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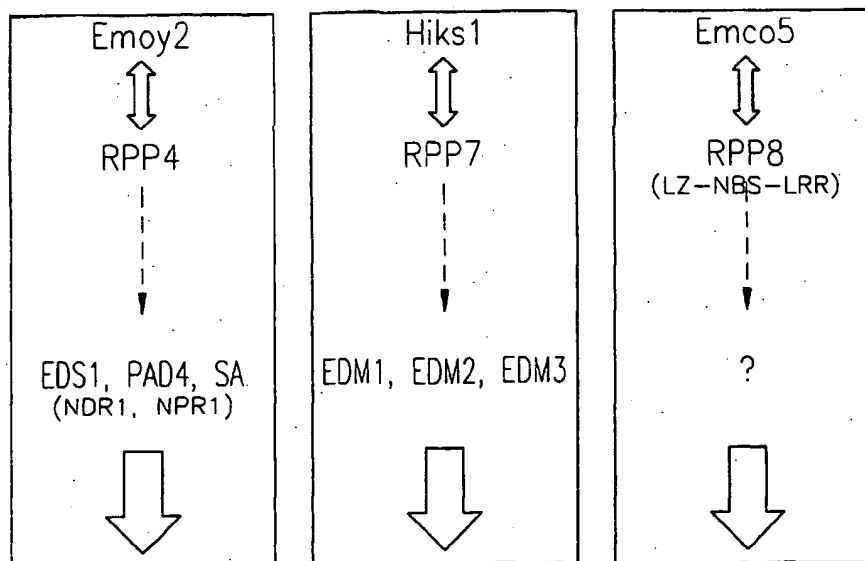
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(54) Title: **PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION**

RPP-DEPENDENT DEFENSE PATHWAYS



R E S I S T A N C E

(57) Abstract: Methods to identify genes, the expression of which is altered in response to pathogen infection, are provided, as well as the genes identified thereby.

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PLANT GENES, THE EXPRESSION OF WHICH ARE ALTERED BY PATHOGEN INFECTION

5

Cross-Reference to Related Applications

This application is a continuation-in-part application of U.S. application Serial No. 60/232,778, filed on September 15, 2000, and of U.S. application Serial No. 60/300,183, filed on June 22, 2001, the disclosures of which are
10 incorporated by reference herein.

Field of the Invention

The present invention generally relates to the field of plant molecular biology, and more specifically to the regulation of gene expression in plants in response to stress, e.g., to pathogen exposure.

15

Background of the Invention

Plants are capable of activating a large array of defense mechanisms in response to pathogen attack. A crucial factor determining the success of these mechanisms is the speed of their activation. Consequently, there is considerable
20 interest in understanding how plants recognize pathogen attack and control expression of defense mechanisms.

Some potential pathogens trigger a very rapid resistance response called gene-for-gene resistance. This occurs when the pathogen carries an avirulence (*avr*) gene that triggers specific recognition by a corresponding host resistance
25 (*R*) gene. *R* gene specificity is generally quite narrow, in most cases only pathogens carrying a particular *avr* gene are recognized. Recognition is thought to be mediated by ligand-receptor binding. *R* genes have been studied extensively in recent years. For a review of *R* genes, see Ellis et al. (1998); Jones et al. (1997); and Ronald (1998).

30 One of the defense mechanisms triggered by gene-for-gene resistance is programmed cell death at the infection site. This is called the hypersensitive response, or HR. Pathogens that induce the HR, or cause cell death by other means, activate a systemic resistance response called systemic acquired resistance (SAR). During SAR, levels of salicylic acid (SA) rise throughout the
35 plant, defense genes such as pathogenesis related (PR) genes are expressed, and the plant becomes more resistant to pathogen attack. SA is a crucial component

of this response. Plants that cannot accumulate SA due to the presence of a transgene that encodes an SA-degrading enzyme (*nahG*), develop a HR in response to challenge by avirulent pathogens, but do not exhibit systemic expression of defense genes and do not develop resistance to subsequent pathogen attack (Ryals et al., 1996). The nature of the systemic signal that triggers SAR is a subject of debate (Shulaev et al., 1995; Vernooji et al., 1994). SA clearly moves from the site of the HR to other parts of the plant, but if this is the signal, it must be effective at extremely low concentration (Willits et al., 1998).

SAR is quite similar to some reactions that occur locally in response to attack by virulent (those that cause disease) or avirulent (those that trigger gene-for-gene resistance) pathogens. In general, activation of defense gene expression occurs more slowly in response to virulent pathogens than in response to avirulent pathogens. Some pathogens trigger expression of defense genes through a different signaling pathway that requires components of the jasmonic acid (JA) and ethylene signaling pathways (Creelman et al., 1997).

One approach to understanding the signal transduction networks that control defense mechanisms is to use genetic methods to identify signaling components and determine their roles within the network. Considerable progress has been made using this approach in *Arabidopsis*-pathogen model systems.

R gene signal transduction

Genes such as *NDRI* and *EDSI*, as well as *DNDI* and the lesion-mimic genes, likely act in signal transduction pathways downstream from *R-avr* recognition. *NDRI* and *EDSI* are required for gene-for-gene mediated resistance to avirulent strains of the bacterial pathogen *Pseudomonas syringae* and the oomycete pathogen *Peronospora parasitica*. Curiously, *ndr1* mutants are susceptible to one set of avirulent pathogens, whereas *eds1* mutants are susceptible to a non-overlapping set (Aarts et al., 1998). The five cloned *R* genes that require *EDSI* all belong to the subset of the nucleotide binding site-leucine rich repeat (NBS-LRR) class of *R* genes that contain sequences similar to the cytoplasmic domains of *Drosophila* Toll and mammalian interleukin 1 transmembrane receptors (TIR-NBS-LRR). The two genes that require *NDRI* belong to the leucine-zipper (LZ-NBS-LRR) subclass of NBS-LRR genes. There is another LZ-NBS-LRR gene, *RPP8*, that does not require *EDSI* or *NDRI*, so

the correlation between *R* gene structure and requirement for *EDS1* or *NDR1* is not perfect. Nevertheless, these results show that *R* genes differ in their requirements for downstream factors and that these differences are correlated with *R* gene structural type.

5 *NDR1* encodes a protein with two predicted transmembrane domains (Century et al. 1997). RPM1, which requires *NDR1* to mediate resistance, is membrane-associated, despite the fact that its primary sequence does not include any likely membrane-integral stretches (Boyes et al., 1998). It is possible that part of the function of *NDR1* is to hold *R* proteins close to the membrane. *EDS1*
10 encodes a protein with blocks of homology to triacyl glycerol lipases (Falk et al., 1999). The significance of this homology is not known, but it is tempting to speculate that *EDS1* is involved in synthesis or degradation of a signal molecule. *EDS1* expression is inducible by SA and pathogen infection, suggesting that *EDS1* may be involved in signal amplification (Falk et al., 1999).

15 It has been extremely difficult to isolate mutations in genes other than the *R* genes that are required for gene-for-gene resistance. A selection procedure was devised (McNellis et al., 1998) on the basis of precisely controlled inducible expression of the *avr* gene *avrRpt2* in plants carrying the corresponding resistance gene *RPS2*. Expression of *avrRpt2* in this background is lethal, as it
20 triggers a systemic HR. It is now possible to select for mutants with subtle defects in gene-for-gene signaling by requiring growth on a concentration of inducer slightly higher than the lethal dose.

Putative plant receptor proteins encoded by *RPP* genes (recognition of *P. parasitica*) mediate specific recognition of *Peronospora* isolates and trigger
25 defense reactions. Recently, McDowell et al. (2000) reported that two members of this class, *RPP7* and *RPP8* (the latter of which encodes a LZ-NBS-LRR type R protein) were not significantly suppressed by mutations in either *EDS1* or *NDR1*, and that *RPP7* resistance was also not compromised by mutations in *EIN2*, *JAR1* or *COI1*, which affect ethylene or jasmonic acid signaling, or in
30 *coil/npr1* or *coil/NahG* backgrounds. The authors suggested that *RPP7* initiates resistance through a novel signaling pathway that is independent of salicylic acid accumulation or jasmonic acid response components.

SA-dependent signaling

SA levels increase locally in response to pathogen attack, and systemically in response to the SAR-inducing signal. SA is necessary and sufficient for activation of *PR* gene expression and enhanced disease resistance.

- 5 Physiological analyses and characterization of certain lesion-mimic mutants strongly suggest that there is a positive autoregulatory loop affecting SA concentrations (Shirasu et al., 1997; Hunt et al., 1997; Weymann et al., 1995). Several mutants with defects in SA signaling have been characterized. These include *npr1*, in which expression of *PR* genes in response to SA is blocked;
- 10 *cpr1*, *cpr5*, and *cpr6*, which constitutively express *PR* genes; the *npr1* suppressor *ssil*; *pad4*, which has a defect in SA accumulation; and *eds5*, which has a defect in *PR1* expression.

- Expression of the defense genes *PR1*, *BG2*, and *PR5* in response to SA treatment requires a gene called *NPR1* or *NIM1*. Mutations in *npr1* abolish
- 15 SAR, and cause enhanced susceptibility to infection by various pathogens (Cao et al., 1994; Delaney et al., 1995; Glazebrook et al., 1996; Shah et al., 1997). *NPR1* appears to be a positive regulator of *PR* gene expression that acts downstream from SA. *NPR1* encodes a novel protein that contains ankyrin repeats (which are often involved in protein-protein interactions (Cao et al.,
- 20 1997; Ryals et al., 1997), and that is localized to the nucleus in the presence of SA (Dong et al., 1998). Consequently, it is unlikely that *NPR1* acts as a transcription factor to directly control *PR* gene expression, but its nuclear localization suggests that it may interact with such transcription factors.

- PAD4* appears to act upstream from SA. In *pad4* plants infected with a
- 25 virulent *P. syringae* strain, SA levels, synthesis of the antimicrobial compound camalexin, and *PR1* expression are all reduced (Zhou et al., 1998). SA is necessary, but not sufficient, for activation of camalexin synthesis (Zhou et al., 1998; Zhao et al., 1996). The camalexin defect in *pad4* plants is reversible by exogenous SA (Zhou et al., 1998). Mutations in *pad4* do not affect SA levels,
- 30 camalexin synthesis, or *PR1* when plants are infected with an avirulent *P. syringae* strain (Zhou et al., 1998). Taken together, these results suggest that *PAD4* is required for signal amplification to activate the SA pathway in response to pathogens that do not elicit a strong defense response (Zhou et al., 1998).

JA-dependent signaling

JA signaling affects diverse processes including fruit ripening, pollen development, root growth, and response to wounding (Creelman et al., 1997). The *jar1* and *coil* mutants fail to respond to JA (Feys et al., 1994; Staswick et al., 1992). *COII* has been cloned, and found to encode protein containing leucine-rich repeats and a degenerate F-box motif (Xie et al., 1998). These features are characteristic of proteins that function in complexes that ubiquitinate protein targeted for degradation.

In the past few years it has become apparent that JA plays an important role in regulation of pathogen defenses. For example, the induction of the defensin gene *PDF1.2* after inoculation of *Arabidopsis* with the avirulent pathogen *Alternaria brassicicola* does not require SA or NPR1, but does require ethylene and JA signaling (Penninck et al., 1996).

SA signaling and JA signaling pathways are interconnected in complicated ways. Studies in other systems have shown that SA signaling and JA signaling are mutually inhibitory (Creelman et al., 1997; Harms et al., 1998). However, synthesis of camalexin in response to *P. syringae* infection is blocked in *nahG* (Zhou et al., 1998; Zhao et al., 1996) and *coil* (Glazebrook, 1999) plants, strongly suggesting that camalexin synthesis requires both SA and JA signaling.

Induced systemic resistance (ISR)

Some rhizosphere-associated bacteria promote disease resistance (van Loon et al., 1998). This phenomenon, called ISR, has been studied using *Pseudomonas fluorescens* strain WCS417r to colonize *Arabidopsis* roots (Pieterse et al., 1996). Colonized plants are more resistant to infection by the fungal pathogen *Fusarium oxysporum* f sp *raphani* and *P. syringae* (Pieterse et al., 1996). ISR occurs in *nahG* plants, indicating that it is not a SA-dependent phenomenon (Pieterse et al., 1996). Rather, ISR appears to be JA- and ethylene-dependent. The observation that ethylene can induce ISR in *jar1* mutants led to the hypothesis that ISR requires a JA signal followed by an ethylene signal (Pieterse et al., 1998). No changes in gene expression associated with ISR have been detected (Pieterse et al., 1998), suggesting that it is different from activation of *PDF1.2* expression by *A. brassicicola*.

Curiously, ISR requires *NPR1* (Pieterse et al., 1996). This was unexpected in light of the fact that *NPR1* was previously known to be involved only in SA-dependent processes and ISR is SA-independent. If the SA-dependent signal is received, *NPR1* mediates a resistance response characterized by *PR1* expression, whereas if the ISR signal is received, *NPR1* mediates a different resistance response. It is difficult to imagine how this could occur, unless *NPR1* is interacting with different 'adapter' molecules to mediate the different signals. The ankyrin repeats found in *NPR1* could function in protein-protein interactions between *NPR1* and adapter proteins. Identification of proteins that interact with *NPR1*, and characterization of plants with loss-of-function mutations affecting those proteins, would be very helpful for understanding how *NPR1* acts in each pathway. It would also be worthwhile to determine if the *ssi1* or *cpr6* mutations suppress the ISR defect of *npr1* mutants.

Relevance to disease resistance

Characterization of the effects of various mutations on resistance to different pathogens has revealed that there is considerable variation in the extent to which pathogens are affected by defense mechanisms. SAR is known to confer resistance to a wide array of pathogens, including bacteria, fungi, oomycetes, and viruses. JA signaling is important for limiting the growth of certain fungal pathogens. In *Arabidopsis*, the SA pathway mutants *npr1* and *pad4* show enhanced susceptibility to *P. syringae* and *P. parasitica* (Cao et al., 1994; Delaney et al., 1995; Shah et al., 1997; Zhou et al., 1998; Glazebrook et al., 1997).

Overexpression of rate-limiting defense response regulators may cause the signaling network to respond faster or more strongly to pathogen attack, thereby improving resistance. For example, overexpression of *NPR1* caused increased resistance to *P. syringae* and *P. parasitica* in a dosage dependent manner (Cao et al., 1998). Moreover, *NPR1*-overexpression had no obvious deleterious effects on plant growth, in contrast to mutations that lead to constitutive overexpression of defense responses, which generally cause dwarfism.

Thus, what is needed is the systematic identification of genes useful to confer resistance to pathogens.

Summary of the Invention

The invention provides an isolated nucleic acid molecule (polynucleotide), e.g., DNA, comprising a plant or fungal nucleotide sequence, the expression of which is altered in response to stress, e.g., pathogen infection.

5 For example, the invention provides a nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising at least a portion of a key effector gene(s) responsible for host resistance to particular pathogens. To provide resistance or tolerance to a pathogen in a plant, this sequence may be overexpressed individually, in the sense or antisense orientation, or in

10 combination with other sequences, to confer improved disease resistance or tolerance to a plant relative to a plant that does not comprise and/or express the sequence. The overexpression may be constitutive, or it may be preferable to express the effector gene(s) from an inducible promoter including a promoter which is responsive to external stimuli, such as chemical application, or to

15 pathogen infection, e.g., so as to avoid possible deleterious effects on plant growth. In one embodiment of the invention, the promoter employed to express the nucleotide sequence of the invention may be one that mediates rapid and transient transcription after pathogen infection. Thus, the invention also provides an isolated nucleic acid molecule comprising a plant nucleotide

20 sequence which alters, e.g., increases or decreases, the transcription of plant genes, e.g., open reading frames, in response to stress, e.g., pathogen infection.

As described herein, *Arabidopsis* plants of differing genotypes were infected with different strains of an oomycete, *P. parasitica*. RNA was isolated from each plant/pathogen pair and employed to prepare probes which were hybridized to a gene

25 chip having nucleic acid sequences (probe sets) corresponding to approximately 8,200 *Arabidopsis* genes. Genes were then identified that were upregulated or downregulated in response to infection, including genes that were dependent on *RPP7* or *RPP8*, which act via unconventional signaling cascades and are not dependent on defense regulators such as EDS1, NDR1, PAD4, NPR1, RAR1, PBS3 or salicylic acid (SA). Among the

30 genes showing strong *Peronospora*-induced expression changes, clusters of genes were identified that were specifically upregulated by *RPP7* or *RPP8*, or both. In particular in one analysis, the expression of 184 genes (SEQ ID NOs:1-211 and 792) related to 217 probe sets was upregulated by either *RPP7* or *RPP8*, or both, while in another analysis the expression of genes related to 194 probe sets (SEQ ID NOs:212-399 and 793) was

upregulated by either *RPP7* or *RPP8*, or both. Further, as described below, promoters of genes that were rapidly and transiently transcribed after *P. parasitica* infection and were *RPP7/8*-dependent were significantly enriched with both novel sequence motifs and potential binding sites of known transcription factors. Specifically, the promoters were significantly enriched with two novel sequence motifs (referred to as "motif 1" and "motif 2"), one of which was similar to binding sites for Myb transcription factors, sequence motifs related to WRKY binding sites, and two other novel sequence motifs ("motif 3" and "motif 4"). Moreover, comparisons between expression signatures of wild type plants as well as the *RPP7* loss of function mutants, and *edm1*, *edm2* and *edm3* mutants, allow for predictions regarding the *RPP7* pathway hierarchy.

In addition, more than 200 genes (SEQ ID NOs:75, 214, 228, 301, 339, 400-684, 792-795) were identified that were specifically controlled by the *RPP4*-dependent pathway, which mediates resistance of the *Arabidopsis* ecotype Col-0 to the *Peronospora* isolate Emoy2. According to their response to SA, an important mediator of local and systemic defense responses, and the protein biosynthesis inhibitor cycloheximide (CHX), these genes were further subcategorized into immediate early and secondary response genes. A set of immediate early SA responsive genes (SEQ ID NOs:150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615, and 526) was found to consist exclusively of regulatory genes. Such genes are likely controlled by transcription factors acting closely downstream of SA. One highly conserved motif in the promoters of these immediate early genes was similar to binding sites of WRKY transcription factors (SEQ ID NOs:757-765). Other conserved promoter motifs appeared to be novel and may facilitate the cloning of their cognate transcription factors. A cluster of SA/CHX super-induced genes was found to show elevated expression ground states in the *npr1* mutant (SEQ ID NOs:214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447 and 551) suggesting an NPR1-dependent de-repression mechanism in the control of some SA responsive immediate early genes.

Thus, the invention provides an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to a pathogen that induces a response mediated by *R* genes, including pathogens such as bacteria, fungi, oomycetes, viruses, nematodes and insects, e.g., aphids (see Hammond-Kosack and Jones (1997), which is specifically incorporated by

reference herein). For example, the plant or fungal nucleotide sequence encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising an open reading frame, the expression of which is altered in response to infection by an oomycete such as *Peronospora*, and is *RPP4*-,
5 *RPP7*-, and/or *RPP8*-dependent. These sequences can be identified by employing an array of nucleic acid samples, e.g., a plurality of oligonucleotides, each plurality corresponding to a different plant gene, on a solid substrate, e.g., a DNA chip, and probes corresponding to nucleic acid from pathogen-infected (e.g., wild-type) plant cells and to nucleic acid from uninfected plant cells or
10 plant cells having a mutation which alters the response to pathogen infection. Thus, genes, the expression of which are altered by pathogen infection, can be systematically identified. Preferably, the nucleotide sequence is from plant DNA, either a dicot or a monocot, which encodes a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading
15 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. More preferably, the nucleotide sequence is from plant DNA that is substantially similar to an *Arabidopsis* nucleic acid segment having any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. The term "substantially similar", when used herein with respect to a polypeptide
20 means a polypeptide corresponding to a reference polypeptide, wherein the polypeptide has substantially the same structure and function as the reference polypeptide, e.g., where only changes in amino acid sequence are those which do not affect the polypeptide function. When used for a polypeptide or an amino acid sequence, the percentage of identity between the substantially similar and
25 the reference polypeptide or amino acid sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, up to at least 99%, where the reference polypeptide is an *Arabidopsis* polypeptide encoded by an open reading
30 frame comprising any one of SEQ ID NOs:1-684 and 792-795, or the complement thereof. However, the percent of identity between the substantially similar and the reference polypeptide may be less than 65% as long as the two polypeptides have the same or similar function, e.g., catalyze the same or similar reaction. Another indication that two polypeptides are substantially similar to

each other is that an agent, e.g., an antibody, which specifically binds to one of the polypeptides, specifically binds to the other.

In its broadest sense, the term "substantially similar", when used herein with respect to a nucleotide sequence, means a nucleotide sequence

5 corresponding to a reference nucleotide sequence, wherein the corresponding sequence is from a gene that encodes a polypeptide having substantially the same structure and function as the polypeptide encoded by a gene comprising the reference nucleotide sequence. The term "substantially similar" is specifically intended to include nucleotide sequences wherein the sequence has been

10 modified to optimize expression in particular cells. The percentage of identity between the substantially similar nucleotide sequence and the reference nucleotide sequence is at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%,

15 96%, 97%, 98%, up to at least 99%, wherein the reference sequence is preferably any one of SEQ ID NOs: 1-684 and 792-795, or the complement thereof. Sequence comparisons may be carried out using a Smith-Waterman sequence alignment algorithm (see e.g., Waterman (1995) or <http://www.uto.usc.edu/software/seqaln/index.html>). The localS program, version 1.16, is

20 preferably used with following parameters: match: 1, mismatch penalty: 0.33, open-gap penalty: 2, extended-gap penalty: 2. Further, a nucleotide sequence that is "substantially similar" to a reference nucleotide sequence hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C,

25 more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC,

30 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 65°C.

Hence, the isolated nucleic acid molecules of the invention also include the orthologs of the *Arabidopsis* sequences disclosed herein, i.e., the corresponding nucleic acid molecules in organisms other than *Arabidopsis*,

including, but not limited to, plants other than *Arabidopsis*, preferably cereal plants, e.g., corn, wheat or rice, as well as rye, turfgrass, sorghum, millet, sugarcane, soybean, barley, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugarbeet, and in fungi. An ortholog is a gene from a different species that
5 encodes a product having the same function as the product encoded by a gene from a reference organism. The encoded ortholog products likely have at least 70% amino acid sequence identity to each other. Hence, the invention includes an isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 70% identity to a polypeptide encoded by one or
10 more of the *Arabidopsis* sequences, although it is also envisioned that orthologous genes to those disclosed herein may encode a polypeptide with less than 70%, e.g., less than 65% amino acid sequence identity, but which polypeptide has the same or similar function. Databases such GenBank or one found at <http://bioserver.myongjiac.kr/rjce.html> (for rice) may be employed to
15 identify sequences related to the *Arabidopsis* sequences, e.g., orthologs in cereal crops such as rice. Alternatively, recombinant DNA techniques such as hybridization or PCR may be employed to identify sequences related to the *Arabidopsis* sequences.

Thus, the invention preferably includes an isolated nucleic acid molecule
20 comprising a plant or fungal nucleotide sequence that encodes a polypeptide that has at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, amino acid sequence identity to an *Arabidopsis* polypeptide encoded by an open reading
25 frame comprising any one of SEQ ID NOs: 1-684 and 792-795, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795. In one embodiment, the isolated nucleic acid molecule is not SEQ ID NOs: 1-684 and
30 792-795. The invention also provides anti-sense nucleic acid molecules corresponding to the open reading frames or genes identified as responsive to pathogen infection. Also provided are expression cassettes, e.g., recombinant vectors, and host cells, comprising the nucleic acid molecule of the invention in either sense or antisense orientation.

Also provided is an isolated nucleic acid molecule comprising a plant or fungal nucleotide sequence comprising a nucleic acid sequence having at least 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and at least 99%, nucleic acid sequence similarity to an *Arabidopsis* open reading frame comprising any one of SEQ ID NOs: 1-684 and 792-795, the complement thereof, or a fragment (portion) thereof which encodes a polypeptide having substantially the same activity as a polypeptide encoded by an open reading frame comprising a corresponding sequence listed in SEQ ID NOs: 1-684 and 792-795.

The nucleic acid molecules of the invention, their encoded polypeptides and compositions thereof, are useful to provide resistance to pathogens and as a diagnostic for the presence or absence of the pathogen by correlating the expression level or pattern of expression of one or more of the nucleic acid molecules of the invention or one or more of the polypeptides encoded thereby. As one embodiment of the invention includes isolated nucleic acid molecules that have increased expression in response to pathogen infection, the invention further provides compositions and methods for enhancing resistance to pathogen infection. The compositions of the invention include plant or fungal nucleotide sequences and the amino acid sequences for the polypeptides or partial-length polypeptides encoded thereby which are useful to provide tolerance or resistance to a plant to a pathogen, preferably by preventing or inhibiting pathogen infection. The resistance or tolerance may be accomplished by decreasing or eliminating expression of a plant gene necessary for pathogen infection and/or replication or by overexpressing a gene product that inhibits pathogen infection and/or replication. Methods of the invention involve stably transforming a plant with one or more of at least a portion of these nucleotide sequences which confer tolerance or resistance operably linked to a promoter capable of driving expression of that nucleotide sequence in a plant cell. By "portion" or "fragment", as it relates to a nucleic acid molecule, sequence or segment of the invention, when it is linked to other sequences for expression, is meant a sequence having at least 80 nucleotides, more preferably at least 150 nucleotides, and still more preferably at least 400 nucleotides. If not employed for expressing, a "portion" or "fragment" means at least 9, preferably 12, more

preferably 15, even more preferably at least 20, consecutive nucleotides, e.g., probes and primers (oligonucleotides), corresponding to the nucleotide sequence of the nucleic acid molecules of the invention. By "resistant" is meant a plant which exhibits substantially no phenotypic changes as a consequence of infection with the pathogen. By "tolerant" is meant a plant which, although it may exhibit some phenotypic changes as a consequence of infection, does not have a substantially decreased reproductive capacity or substantially altered metabolism. Thus, some of the isolated nucleic acid molecules of the invention are useful in a method of combating a pathogen in an agricultural crop. The method comprises introducing to a plant, plant cell, or plant tissue an expression cassette comprising a nucleic acid molecule of the invention so as to yield a transformed differentiated plant, transformed cell or transformed tissue. Transformed cells or tissue can be regenerated to provide a transformed differentiated plant. The transformed differentiated plant preferably expresses the nucleic acid molecule in an amount that confers resistance to the transformed plant to pathogen infection relative to a corresponding nontransformed plant. The present invention also provides a transformed plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields under conditions of pathogen infection and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and probes.

The invention also includes recombinant nucleic acid molecules which have been modified so as to comprise codons other than those present in the unmodified sequence. The recombinant nucleic acid molecules of the invention include those in which the modified codons specify amino acids that are the same as those specified by the codons in the unmodified sequence, as well as those that specify different amino acids, i.e., they encode a variant polypeptide having one or more amino acid substitutions relative to the polypeptide encoded by the unmodified sequence.

The invention further includes a nucleotide sequence which is complementary to one (hereinafter "test" sequence) which hybridizes under stringent conditions with the nucleic acid molecules of the invention as well as RNA which is encoded by the nucleic acid molecule. When the hybridization is performed under stringent conditions, either the test or nucleic acid molecule of invention is preferably supported, e.g., on a membrane or DNA chip. Thus, either a denatured test or nucleic acid molecule of the invention is preferably first bound to a support and hybridization is effected for a specified period of time at a temperature of, e.g., between 55 and 70°C, in double strength citrate buffered saline (SC) containing 0.1% SDS followed by rinsing of the support at the same temperature but with a buffer having a reduced SC concentration. Depending upon the degree of stringency required such reduced concentration buffers are typically single strength SC containing 0.1% SDS, half strength SC containing 0.1% SDS and one-tenth strength SC containing 0.1% SDS.

The present invention also provides a method to identify a gene, the expression of which is altered in response to an external stimulus, e.g., pathogen infection. The method comprises contacting a plurality of samples comprising portions or fragments of isolated nucleic acid molecules with a probe which corresponds to a population of a nucleic acid sequences, the expression of which is altered in response to an external stimulus, so as to form a binary complex. Each sample corresponds to a different gene. Then complex formation is detected or determined. The method may be employed with nucleic acid samples and probes from any organism, e.g., any prokaryotic or eukaryotic organism. Preferably, the nucleic acid sample and probes are from a plant, such as a dicot or monocot. For example, the method comprises contacting a solid substrate comprising a plurality of samples comprising portions or fragments of isolated plant nucleic acid with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from a pathogen infected plant so as to form a complex. Preferred pathogens are those which induce an *R*-gene dependent resistance response. Each individual sample comprises one or more nucleic acid sequences corresponding to a plant gene, e.g., a pool of oligonucleotides corresponding to the same gene or a portion of that gene. The plurality of samples is provided on a DNA chip. A second plurality of samples on a solid substrate, i.e., a DNA chip, each comprising a plurality of samples comprising portions or fragments of

isolated plant nucleic acid is contacted with a probe comprising plant nucleic acid corresponding to at least a portion of RNA from an uninfected or mutant plant or plant cells so as to form a complex. Then complex formation with nucleic acid from infected cells and from uninfected or mutant cells is compared.

5 The invention also provides a method for identifying a plant cell infected with a pathogen, e.g., one that induces a *RPP4*-, *RPP7*- and/or *RPP8*-dependent resistance response. The method comprises contacting nucleic acid obtained from a plant cell suspected of being infected with the pathogen with at least one, preferably at least two, oligonucleotides under conditions effective to amplify at
10 least a portion of a nucleotide sequence in the isolated plant nucleic acid which is substantially similar to at least one of SEQ ID NOs: 1-684 and 792-795, so as to yield an amplified product. Then the presence of the amplified product is detected or determined. The presence of the amplified product, e.g., in an amount that is different than the amount of the corresponding amplified product
15 from an uninfected or mutant plant, corresponding to one or more of SEQ ID NOs: 1-684 and 792-795 or an ortholog thereof, is indicative of pathogen infection.

 The invention provides an additional method for identifying a plant cell infected with a pathogen. The method comprises hybridizing a probe selected
20 from SEQ ID NOs: 1-684 and 792-795 to nucleic acid obtained from a plant cell suspected of being infected with a pathogen. The amount of the probe hybridized to nucleic acid obtained from a cell suspected of being infected with a pathogen is compared to hybridization of the probe to nucleic acid isolated from an uninfected or mutant cell. A change in the amount of the hybridized probe in
25 nucleic acid isolated from a cell suspected of being infected by a pathogen relative to the amount of hybridized probe in nucleic acid isolated from an uninfected or mutant cell is indicative of infection.

 Also provided is an isolated nucleic acid molecule comprising a nucleotide sequence that directs transcription, e.g., a promoter, of a linked
30 nucleic acid segment in a host cell, such as a plant cell, wherein transcription is altered, e.g., increased, in response to a pathogen infection. Preferably, the pathogen is *R*-dependent, and more preferably, one that triggers a response that is dependent on *RPP4*, *RPP7* and/or *RPP8*, such as an oomycete (for example, *Peronospora*). It is preferred that the nucleotide sequence is from plant genomic

DNA which has at least 65%, 66%, 67%, 68%, 69%, 70%, e.g., 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, and even 90% or more, e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, and 99%, nucleotide sequence identity to a sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, e.g., SEQ ID NOs: 774-788, or comprising motifs such as one of SEQ ID NOs: 685-773. Thus, the invention also includes orthologs of *Arabidopsis* promoters. Preferably, the nucleotide sequence includes the promoter region from a gene corresponding to SEQ ID NOs: 1-770 and 792-795, which region preferably includes at least one copy of at least one of the following, e.g., a nucleic acid sequence comprising one of SEQ ID NOs: 685-697 ("motif 1"), SEQ ID NOs: 698-709 ("motif 2"), GGT/CCCA ("motif 3"), GNCCAAA ("motif 4"), or SEQ ID NOs: 710-713, 714-756, or 757-773. The promoter sequence is preferably about 25 to 2000, e.g., 50 to 500 or 100 to 1400, nucleotides in length.

In one embodiment of the invention, the isolated nucleic acid molecule comprises a plant nucleotide sequence which is the promoter region for any one of SEQ ID NOs: 1-684 and 792-795, or is structurally related to the promoter for SEQ ID NOs: 1-684 and 792-795, i.e., is an orthologous promoter, and is linked to a plant structural gene or open reading frame. Hence, the present invention further provides an expression cassette or a recombinant vector containing the nucleic acid molecule, and the vector may be a plasmid. Such cassettes or vectors, when present in a plant, plant cell or plant tissue result in transcription of the linked nucleic acid segment in the plant, plant tissue or plant cell. Transcription of the linked segment is altered in response to pathogen infection, including *Peronospora* infection. For promoters with motif 1, transcription of linked segments may be altered in response to agents or other stimuli that induce Myb-like transcription factors.

Generally, the promoters of the invention may be employed to express a nucleic acid segment that is operably linked to the promoter, for example, an open reading frame or a portion thereof, an anti-sense construct or a transgene. The open reading frame may be obtained from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a

mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a positive selectable marker, a gene affecting plant agronomic characteristics, i.e., yield, standability and the like, or an environment or stress resistance gene, i.e., one or more genes
5 that confer herbicide resistance or tolerance, insect resistance or tolerance, disease resistance or tolerance (viral, bacterial, fungal, oomycete, or nematode), stress tolerance or resistance (as exemplified by resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, salt stress, or oxidative stress), increased yields, food content and makeup, physical appearance, male
10 sterility, drydown, standability, prolificacy, starch properties or quantity, oil quantity and quality, amino acid or protein composition, and the like.

Preferably, the promoters of the invention include a consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743,
15 250 to about 743, 400 to about 743, 600 to about 743, of the promoter sequences from genes comprising any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

In a particular embodiment of the invention said consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40 to about 743, 60 to about 743, 125 to about 743,
20 250 to about 743, 400 to about 743, 600 to about 743, has at least 75%, preferably 80%, more preferably 90% and most preferably 95% sequence identity with a corresponding consecutive stretch of about 25 to 2000, including 50 to 500 or 100 to 250, and up to 1000 or 1500, contiguous nucleotides, e.g., 40
25 to about 743, 60 to about 743, 125 to about 743, 250 to about 743, 400 to about 743, 600 to about 743, of any one of SEQ ID NOs:685-788, 714-756, and 757-773, or the promoter orthologs thereof, which include the minimal promoter region.

The expression cassettes or vectors of the invention may optionally
30 include other regulatory sequences, e.g., transcription terminator sequences, introns and/or enhancers, and may be contained in a host cell. The expression cassette or vector may augment the genome of a transformed plant or may be maintained extrachromosomally. The expression cassette or vector may further have a Ti plasmid and be contained in an *Agrobacterium tumefaciens* cell; it may

be carried on a microparticle, wherein the microparticle is suitable for ballistic transformation of a plant cell; or it may be contained in a plant cell protoplast. Further, the expression cassette can be contained in a plant, plant cell or plant tissue from a dicot or a monocot. In particular, the plant may be a cereal plant.

5 The present invention further provides a method of augmenting a plant genome by contacting plant cells with an expression cassette or vector of the invention, i.e., one having a nucleotide sequence that directs transcription of a linked nucleic acid segment in a plant cell, wherein transcription of the linked segment is altered in response to a pathogen such as an oomycete, e.g.,
10 *Peronospora*, infection, and wherein the nucleic sequence is from plant DNA that has at least 65%, and more preferably at least 70%, identity to the sequence of a promoter from an *Arabidopsis* gene comprising any one of SEQ ID NOs: 1-684 and 792-795, so as to yield transformed plant cells; and regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the
15 differentiated transformed plant expresses the linked fragment in the cells of the plant in response to infection. The present invention also provides a plant prepared by the method, progeny and seed thereof.

A transformed (transgenic) plant of the invention includes plants, the genome of which is augmented by a nucleic acid molecule of the invention, or in
20 which the corresponding gene has been disrupted, e.g., to result in a loss, a decrease or an alteration, in the function of the product encoded by the gene, which plant may also have increased yields and/or produce a better-quality product than the corresponding wild-type plant. The nucleic acid molecules of the invention are thus useful for targeted gene disruption, as well as markers and
25 probes.

The invention also provides a method of plant breeding, e.g., to prepare a crossed fertile transgenic plant. The method comprises crossing a fertile transgenic plant comprising a particular nucleic acid molecule of the invention with itself or with a second plant, e.g., one lacking the particular nucleic acid
30 molecule, to prepare the seed of a crossed fertile transgenic plant comprising the particular nucleic acid molecule. The seed is then planted to obtain a crossed fertile transgenic plant. The plant may be a monocot or a dicot. In a particular embodiment, the plant is a cereal plant.

The crossed fertile transgenic plant may have the particular nucleic acid molecule inherited through a female parent or through a male parent. The second plant may be an inbred plant. The crossed fertile transgenic may be a hybrid. Also included within the present invention are seeds of any of these
5 crossed fertile transgenic plants.

The present invention also provides a method to identify a nucleotide sequence that directs transcription of nucleic acid in the genome of a plant cell in response to pathogen exposure, by contacting a probe comprising plant nucleic acid, e.g., cRNA, isolated from tissues of a plant contacted with the pathogen
10 with a plurality of isolated nucleic acid samples on a plurality of solid substrates, wherein each sample is a plurality of oligonucleotides corresponding to at least a portion of a plant gene, so as to form a complex between at least a portion of the probe and a nucleic acid sample(s) having sequences that are structurally related to the sequences in the probe. Then complex formation is determined or
15 detected to determine which samples represent genes comprising promoters that are responsive to infection with the pathogen. The probe and/or samples may be nucleic acid from a dicot or from a monocot.

A method to shuffle the nucleic acid molecules of the invention is provided. This method involves fragmentation of a (parent) nucleic acid
20 molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-684 and 792-795, the ortholog thereof, or the corresponding gene thereof, followed by religation. This method allows for the production of polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule. Accordingly, the invention provides cells and transgenic plants
25 containing nucleotide sequences produced through shuffling that encode polypeptides having altered activity relative to the polypeptide encoded by the parent nucleic acid molecule.

A computer readable medium containing the nucleic acid sequences of the invention as well as methods of use for the computer readable medium are
30 provided. This medium allows a nucleic acid molecule corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795 to be used as a reference sequence to search against databases. This medium also allows for computer-based manipulation of a nucleic acid sequence

corresponding to a nucleic acid sequence listed in SEQ ID NOs: 1-399, 685-756 and 774-793 or 71, 78, 80, 117, 126, 150, 159, 168, 208, 214, 264-265, 355, 400-657, 659-684, 792-795, and the corresponding gene or polypeptide encoded by the nucleic acid sequence.

5

Brief Description of the Figures

Figure 1 depicts *RPP*-dependent defense pathways.

Figure 2 depicts nucleotide sequences including the promoter region and motifs therein for genes, the expression of which is altered in response to pathogen infection (SEQ ID NOs: 774-788).

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Figure 3 is a schematic of the overlap in genes that are induced early after *P. parasitica* infection and in a *RPP8*-specific manner, genes that are induced late after infection and in a *RPP8*-specific manner, and genes induced early and late after infection in a *RPP7*-specific manner.

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Figure 4 shows a schematic of *RPP4*-pathway, *RPP7*-pathway and *RPP8*-upregulated transcription factor genes.

Detailed Description of the Invention

Definitions

20

The term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form, composed of monomers (nucleotides) containing a sugar, phosphate and a base which is either a purine or pyrimidine. Unless specifically limited, the term encompasses nucleic acids containing known analogs of natural nucleotides which have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences as well as the sequence explicitly indicated.

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Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzner et al., 1991; Ohtsuka et al., 1985; Rossolini et al., 1994). A "nucleic acid fragment" is a fraction of a given nucleic acid molecule. In higher plants, deoxyribonucleic

acid (DNA) is the genetic material while ribonucleic acid (RNA) is involved in the transfer of information contained within DNA into proteins. The term "nucleotide sequence" refers to a polymer of DNA or RNA which can be single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases capable of incorporation into DNA or RNA polymers. The terms "nucleic acid", "nucleic acid molecule", "nucleic acid fragment" or "nucleic acid sequence or segment" may also be used interchangeably with gene, cDNA, DNA and RNA encoded by a gene.

The invention encompasses isolated or substantially purified nucleic acid or protein compositions. In the context of the present invention, an "isolated" or "purified" DNA molecule or an "isolated" or "purified" polypeptide is a DNA molecule or polypeptide that, by the hand of man, exists apart from its native environment and is therefore not a product of nature. An isolated DNA molecule or polypeptide may exist in a purified form or may exist in a non-native environment such as, for example, a transgenic host cell. For example, an "isolated" or "purified" nucleic acid molecule or protein, or biologically active portion thereof, is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In one embodiment, an "isolated" nucleic acid is free of sequences that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences that naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. A protein that is substantially free of cellular material includes preparations of protein or polypeptide having less than about 30%, 20%, 10%, 5%, (by dry weight) of contaminating protein. When the protein of the invention, or biologically active portion thereof, is recombinantly produced, preferably culture medium represents less than about 30%, 20%, 10%, or 5% (by dry weight) of chemical precursors or non-protein-of-interest chemicals. Fragments and variants of the disclosed nucleotide sequences and proteins or partial-length proteins encoded thereby are also encompassed by the present invention. By "fragment" or "portion" is meant a full length or less than

full length of the nucleotide sequence encoding, or the amino acid sequence of, a polypeptide or protein. Alternatively, fragments or portions of a nucleotide sequence that are useful as hybridization probes generally do not encode fragment proteins retaining biological activity. Thus, fragments or portions of a nucleotide sequence may range from at least about 9 nucleotides, about 12 nucleotides, about 20 nucleotides, about 50 nucleotides, about 100 nucleotides or more.

The term "gene" is used broadly to refer to any segment of nucleic acid associated with a biological function. Thus, genes include coding sequences and/or the regulatory sequences required for their expression. For example, gene refers to a nucleic acid fragment that expresses mRNA, functional RNA, or specific protein, including regulatory sequences. Genes also include nonexpressed DNA segments that, for example, form recognition sequences for other proteins. Genes can be obtained from a variety of sources, including cloning from a source of interest or synthesizing from known or predicted sequence information, and may include sequences designed to have desired parameters.

"Naturally occurring" is used to describe an object that can be found in nature as distinct from being artificially produced by man. For example, a protein or nucleotide sequence present in an organism (including a virus), which can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory, is naturally occurring.

A "marker gene" encodes a selectable or screenable trait.

"Selectable marker" is a gene whose expression in a cell gives the cell a selective advantage. The selective advantage possessed by the cells transformed with the selectable marker gene may be due to their ability to grow in the presence of a negative selective agent, such as an antibiotic or a herbicide, compared to the growth of non-transformed cells. The selective advantage possessed by the transformed cells, compared to non-transformed cells, may also be due to their enhanced or novel capacity to utilize an added compound as a nutrient, growth factor or energy source. Selectable marker gene also refers to a gene or a combination of genes whose expression in a cell gives the cell both a negative and/or a positive selective advantage.

The term "chimeric" refers to any gene or DNA that contains 1) DNA

sequences, including regulatory and coding sequences, that are not found together in nature, or 2) sequences encoding parts of proteins not naturally adjoined, or 3) parts of promoters that are not naturally adjoined. Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are
5 derived from different sources, or comprise regulatory sequences and coding sequences derived from the same source, but arranged in a manner different from that found in nature.

A "transgene" refers to a gene that has been introduced into the genome by transformation and is stably maintained. Transgenes may include, for
10 example, DNA that is either heterologous or homologous to the DNA of a particular plant to be transformed. Additionally, transgenes may comprise native genes inserted into a non-native organism, or chimeric genes. The term "endogenous gene" refers to a native gene in its natural location in the genome of an organism. A "foreign" gene refers to a gene not normally found in the host
15 organism but that is introduced by gene transfer.

The terms "protein," "peptide" and "polypeptide" are used interchangeably herein.

By "variants" is intended substantially similar sequences. For nucleotide sequences, variants include those sequences that, because of the degeneracy of
20 the genetic code, encode the identical amino acid sequence of the native protein. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques. Variant nucleotide sequences also include synthetically derived nucleotide sequences, such as those
25 generated, for example, by using site-directed mutagenesis which encode the native protein, as well as those that encode a polypeptide having amino acid substitutions. Generally, nucleotide sequence variants of the invention will have at least 40, 50, 60, to 70%, e.g., preferably 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, to 79%, generally at least 80%, e.g., 81%-84%, at least 85%, e.g.,
30 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, to 98%, sequence identity to the native (endogenous) nucleotide sequence.

"DNA shuffling" is a method to introduce mutations or rearrangements, preferably randomly, in a DNA molecule or to generate exchanges of DNA sequences between two or more DNA molecules, preferably randomly. The

DNA molecule resulting from DNA shuffling is a shuffled DNA molecule that is a non-naturally occurring DNA molecule derived from at least one template DNA molecule. The shuffled DNA preferably encodes a variant polypeptide modified with respect to the polypeptide encoded by the template DNA, and may
5 have an altered biological activity with respect to the polypeptide encoded by the template DNA.

The nucleic acid molecules of the invention can be optimized for enhanced expression in plants of interest. See, for example, EPA035472; WO91/16432; Perlak et al., 1991; and Murray et al., 1989. In this manner, the
10 genes or gene fragments can be synthesized utilizing plant-preferred codons. See, for example, Campbell and Gowri, 1990 for a discussion of host-preferred codon usage. Thus, the nucleotide sequences can be optimized for expression in any plant. It is recognized that all or any part of the gene sequence may be optimized or synthetic. That is, synthetic or partially optimized sequences may
15 also be used. Variant nucleotide sequences and proteins also encompass sequences and protein derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different coding sequences can be manipulated to create a new polypeptide possessing the desired properties. In this manner, libraries of recombinant polynucleotides are
20 generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer, 1994; Stemmer, 1994; Crameri et al., 1997; Moore et al., 1997; Zhang et al., 1997; Crameri et al., 1998; and
25 U.S. Patent Nos. 5,605,793 and 5,837,458.

"Conservatively modified variations" of a particular nucleic acid sequence refers to those nucleic acid sequences that encode identical or essentially identical amino acid sequences, or where the nucleic acid sequence does not encode an amino acid sequence, to essentially identical sequences.
30 Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given polypeptide. For instance the codons CGT, CGC, CGA, CGG, AGA, and AGG all encode the amino acid arginine. Thus, at every position where an arginine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the

encoded protein. Such nucleic acid variations are "silent variations" which are one species of "conservatively modified variations." Every nucleic acid sequence described herein which encodes a polypeptide also describes every possible silent variation, except where otherwise noted. One of skill will
5 recognize that each codon in a nucleic acid (except ATG, which is ordinarily the only codon for methionine) can be modified to yield a functionally identical molecule by standard techniques. Accordingly, each "silent variation" of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

"Recombinant DNA molecule" is a combination of DNA sequences that
10 are joined together using recombinant DNA technology and procedures used to join together DNA sequences as described, for example, in Sambrook et al., Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press (1989).

The terms "heterologous DNA sequence," "exogenous DNA segment" or "heterologous nucleic acid," each refer to a sequence that originates from a
15 source foreign to the particular host cell or, if from the same source, is modified from its original form. Thus, a heterologous gene in a host cell includes a gene that is endogenous to the particular host cell but has been modified through, for example, the use of DNA shuffling. The terms also include non-naturally occurring multiple copies of a naturally occurring DNA sequence. Thus, the
20 terms refer to a DNA segment that is foreign or heterologous to the cell, or homologous to the cell but in a position within the host cell nucleic acid in which the element is not ordinarily found. Exogenous DNA segments are expressed to yield exogenous polypeptides.

A "homologous" DNA sequence is a DNA sequence that is naturally
25 associated with a host cell into which it is introduced.

"Wild-type" refers to the normal gene, or organism found in nature without any known mutation.

"Genome" refers to the complete genetic material of an organism.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or
30 *Agrobacterium* binary vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eukaryotic (e.g. higher plant, mammalian, yeast or fungal cells).

5 "Cloning vectors" typically contain one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of essential biological function of the vector, as well as a marker gene that is suitable for use in the identification and selection of cells transformed with the cloning vector. Marker genes typically
10 include genes that provide tetracycline resistance, hygromycin resistance or ampicillin resistance.

"Expression cassette" as used herein means a DNA sequence capable of directing expression of a particular nucleotide sequence in an appropriate host cell, comprising a promoter operably linked to the nucleotide sequence of
15 interest which is operably linked to termination signals. It also typically comprises sequences required for proper translation of the nucleotide sequence. The coding region usually codes for a protein of interest but may also code for a functional RNA of interest, for example antisense RNA or a nontranslated RNA, in the sense or antisense direction. The expression cassette comprising the
20 nucleotide sequence of interest may be chimeric, meaning that at least one of its components is heterologous with respect to at least one of its other components. The expression cassette may also be one which is naturally occurring but has been obtained in a recombinant form useful for heterologous expression. The expression of the nucleotide sequence in the expression cassette may be under
25 the control of a constitutive promoter or of an inducible promoter which initiates transcription only when the host cell is exposed to some particular external stimulus. In the case of a multicellular organism, the promoter can also be specific to a particular tissue or organ or stage of development.

Such expression cassettes will comprise the transcriptional initiation
30 region of the invention linked to a nucleotide sequence of interest. Such an expression cassette is provided with a plurality of restriction sites for insertion of the gene of interest to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain selectable marker genes.

The transcriptional cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of interest, and a transcriptional and translational termination region functional in plants. The termination region may be native with the transcriptional initiation region, may be native with the DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also, Guerineau et al., 1991; Proudfoot, 1991; Sanfacon et al., 1991; Mogen et al., 1990; Munroe et al., 1990; Ballas et al., 1989; Joshi et al., 1987.

An oligonucleotide corresponding to a nucleic acid molecule of the invention may be about 30 or fewer nucleotides in length (e.g., 9, 12, 15, 18, 20, 21 or 24, or any number between 9 and 30). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16-24 nucleotides in length may be preferred. Those skilled in the art are well versed in the design of primers for use processes such as PCR. If required, probing can be done with entire restriction fragments of the gene disclosed herein which may be 100's or even 1000's of nucleotides in length.

"Coding sequence" refers to a DNA or RNA sequence that codes for a specific amino acid sequence and excludes the non-coding sequences. It may constitute an "uninterrupted coding sequence", i.e., lacking an intron, such as in a cDNA or it may include one or more introns bounded by appropriate splice junctions. An "intron" is a sequence of RNA which is contained in the primary transcript but which is removed through cleavage and re-ligation of the RNA within the cell to create the mature mRNA that can be translated into a protein.

The terms "open reading frame" and "ORF" refer to the amino acid sequence encoded between translation initiation and termination codons of a coding sequence. The terms "initiation codon" and "termination codon" refer to a unit of three adjacent nucleotides ('codon') in a coding sequence that specifies initiation and chain termination, respectively, of protein synthesis (mRNA translation).

A "functional RNA" refers to an antisense RNA, ribozyme, or other RNA that is not translated.

The term "RNA transcript" refers to the product resulting from RNA polymerase catalyzed transcription of a DNA sequence. When the RNA transcript is a perfect complementary copy of the DNA sequence, it is referred to as the primary transcript or it may be a RNA sequence derived from posttranscriptional processing of the primary transcript and is referred to as the mature RNA. "Messenger RNA" (mRNA) refers to the RNA that is without introns and that can be translated into protein by the cell. "cDNA" refers to a single- or a double-stranded DNA that is complementary to and derived from mRNA.

"Regulatory sequences" and "suitable regulatory sequences" each refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences include enhancers, promoters, translation leader sequences, introns, and polyadenylation signal sequences. They include natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. As is noted above, the term "suitable regulatory sequences" is not limited to promoters. However, some suitable regulatory sequences useful in the present invention will include, but are not limited to constitutive plant promoters, plant tissue-specific promoters, plant development specific promoters, inducible plant promoters and viral promoters.

"5' non-coding sequence" refers to a nucleotide sequence located 5' (upstream) to the coding sequence. It is present in the fully processed mRNA upstream of the initiation codon and may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency (Turner et al., 1995).

"3' non-coding sequence" refers to nucleotide sequences located 3' (downstream) to a coding sequence and include polyadenylation signal sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by affecting the addition of polyadenylic acid tracts to the 3' end of the mRNA precursor. The use of different 3' non-coding sequences is exemplified by Ingelbrecht et al., 1989.

The term "translation leader sequence" refers to that DNA sequence portion of a gene between the promoter and coding sequence that is transcribed into RNA and is present in the fully processed mRNA upstream (5') of the translation start codon. The translation leader sequence may affect processing of the primary transcript to mRNA, mRNA stability or translation efficiency.

The term "mature" protein refers to a post-translationally processed polypeptide without its signal peptide. "Precursor" protein refers to the primary product of translation of an mRNA. "Signal peptide" refers to the amino terminal extension of a polypeptide, which is translated in conjunction with the polypeptide forming a precursor peptide and which is required for its entrance into the secretory pathway. The term "signal sequence" refers to a nucleotide sequence that encodes the signal peptide.

The term "intracellular localization sequence" or "signal sequence" refers to a nucleotide sequence that encodes an intracellular targeting signal. An "intracellular targeting signal" is an amino acid sequence that is translated in conjunction with a protein and directs it to a particular sub-cellular compartment. "Endoplasmic reticulum (ER) stop transit signal" refers to a carboxy-terminal extension of a polypeptide, which is translated in conjunction with the polypeptide and causes a protein that enters the secretory pathway to be retained in the ER. "ER stop transit sequence" refers to a nucleotide sequence that encodes the ER targeting signal. Other intracellular targeting sequences encode targeting signals active in seeds and/or leaves and vacuolar targeting signals.

"Promoter" refers to a nucleotide sequence, usually upstream (5') to its coding sequence, which controls the expression of the coding sequence by providing the recognition for RNA polymerase and other factors required for proper transcription. "Promoter" includes a minimal promoter that is a short DNA sequence comprised of a TATA-box and other sequences that serve to specify the site of transcription initiation, to which regulatory elements are added for control of expression. "Promoter" also refers to a nucleotide sequence that includes a minimal promoter plus regulatory elements that is capable of controlling the expression of a coding sequence or functional RNA. This type of promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. Accordingly, an "enhancer" is a DNA sequence which can stimulate promoter activity and may be an innate

element of the promoter or a heterologous element inserted to enhance the level or tissue specificity of a promoter. It is capable of operating in both orientations (normal or flipped), and is capable of functioning even when moved either upstream or downstream from the promoter. Both enhancers and other upstream promoter elements bind sequence-specific DNA-binding proteins that mediate their effects. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even be comprised of synthetic DNA segments. A promoter may also contain DNA sequences that are involved in the binding of protein factors which control the effectiveness of transcription initiation in response to physiological or developmental conditions.

The "initiation site" is the position surrounding the first nucleotide that is part of the transcribed sequence, which is also defined as position +1. With respect to this site all other sequences of the gene and its controlling regions are numbered. Downstream sequences (i.e. further protein encoding sequences in the 3' direction) are denominated positive, while upstream sequences (mostly of the controlling regions in the 5' direction) are denominated negative.

Promoter elements, particularly a TATA element, that are inactive or that have greatly reduced promoter activity in the absence of upstream activation are referred to as "minimal or core promoters." In the presence of a suitable transcription factor, the minimal promoter functions to permit transcription. A "minimal or core promoter" thus consists only of all basal elements needed for transcription initiation, e.g., a TATA box and/or an initiator.

"Constitutive expression" refers to expression using a constitutive or regulated promoter. "Conditional" and "regulated expression" refer to expression controlled by a regulated promoter.

"Constitutive promoter" refers to a promoter that is able to express the gene that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant. Each of the transcription-activating elements do not exhibit an absolute tissue-specificity, but mediate transcriptional activation in most plant parts at a level of $\geq 1\%$ of the level reached in the part of the plant in which transcription is most active.

"Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and

- include both tissue-specific and inducible promoters. It includes natural and synthetic sequences as well as sequences which may be a combination of synthetic and natural sequences. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. New promoters of various types useful in plant cells are constantly being discovered, numerous examples may be found in the compilation by Okamuro et al., 1989. Since in most cases the exact boundaries of regulatory sequences have not been completely defined, DNA fragments of different lengths may have identical promoter activity.
- Typical regulated promoters useful in plants include but are not limited to safener-inducible promoters, promoters derived from the tetracycline-inducible system, promoters derived from salicylate-inducible systems, promoters derived from alcohol-inducible systems, promoters derived from glucocorticoid-inducible system, promoters derived from pathogen-inducible systems, and promoters derived from ecdysome-inducible systems.

"Tissue-specific promoter" refers to regulated promoters that are not expressed in all plant cells but only in one or more cell types in specific organs (such as leaves or seeds), specific tissues (such as embryo or cotyledon), or specific cell types (such as leaf parenchyma or seed storage cells). These also include promoters that are temporally regulated, such as in early or late embryogenesis, during fruit ripening in developing seeds or fruit, in fully differentiated leaf, or at the onset of senescence.

"Inducible promoter" refers to those regulated promoters that can be turned on in one or more cell types by an external stimulus, such as a chemical, light, hormone, stress, or a pathogen.

"Operably-linked" refers to the association of nucleic acid sequences on single nucleic acid fragment so that the function of one is affected by the other. For example, a regulatory DNA sequence is said to be "operably linked to" or "associated with" a DNA sequence that codes for an RNA or a polypeptide if the two sequences are situated such that the regulatory DNA sequence affects expression of the coding DNA sequence (i.e., that the coding sequence or functional RNA is under the transcriptional control of the promoter). Coding sequences can be operably-linked to regulatory sequences in sense or antisense orientation.

"Expression" refers to the transcription and/or translation of an endogenous gene or a transgene in plants. For example, in the case of antisense constructs, expression may refer to the transcription of the antisense DNA only. In addition, expression refers to the transcription and stable accumulation of sense (mRNA) or functional RNA. Expression may also refer to the production of protein.

"Altered levels" refers to the level of expression in transgenic cells or organisms that differs from that of normal or untransformed cells or organisms.

"Overexpression" refers to the level of expression in transgenic cells or organisms that exceeds levels of expression in normal or untransformed cells or organisms.

"Antisense inhibition" refers to the production of antisense RNA transcripts capable of suppressing the expression of protein from an endogenous gene or a transgene.

"Co-suppression" and "transwitch" each refer to the production of sense RNA transcripts capable of suppressing the expression of identical or substantially similar transgene or endogenous genes (U.S. Patent No. 5,231,020).

"Gene silencing" refers to homology-dependent suppression of viral genes, transgenes, or endogenous nuclear genes. Gene silencing may be transcriptional, when the suppression is due to decreased transcription of the affected genes, or post-transcriptional, when the suppression is due to increased turnover (degradation) of RNA species homologous to the affected genes. (English et al., 1996). Gene silencing includes virus-induced gene silencing (Ruiz et al., 1998).

"Silencing suppressor" gene refers to a gene whose expression leads to counteracting gene silencing and enhanced expression of silenced genes. Silencing suppressor genes may be of plant, non-plant, or viral origin. Examples include, but are not limited to HC-Pro, P1-HC-Pro, and 2b proteins. Other examples include one or more genes in TGMV-B genome.

"Transcription stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as polyadenylation signal sequences, capable of terminating transcription. Examples include the 3' non-regulatory regions of genes encoding nopaline synthase and the small subunit of ribulose biphosphate carboxylase.

"Translation stop fragment" refers to nucleotide sequences that contain one or more regulatory signals, such as one or more termination codons in all three frames, capable of terminating translation. Insertion of a translation stop fragment adjacent to or near the initiation codon at the 5' end of the coding sequence will result in no translation or improper translation. Excision of the translation stop fragment by site-specific recombination will leave a site-specific sequence in the coding sequence that does not interfere with proper translation using the initiation codon.

The terms "*cis*-acting sequence" and "*cis*-acting element" refer to DNA or RNA sequences whose functions require them to be on the same molecule. An example of a *cis*-acting sequence on the replicon is the viral replication origin.

The terms "*trans*-acting sequence" and "*trans*-acting element" refer to DNA or RNA sequences whose function does not require them to be on the same molecule.

"Chromosomally-integrated" refers to the integration of a foreign gene or DNA construct into the host DNA by covalent bonds. Where genes are not "chromosomally integrated" they may be "transiently expressed." Transient expression of a gene refers to the expression of a gene that is not integrated into the host chromosome but functions independently, either as part of an autonomously replicating plasmid or expression cassette, for example, or as part of another biological system such as a virus.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" makes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. Preferred, non-limiting examples of such mathematical algorithms are the algorithm of Myers and Miller, 1988; the local homology algorithm of Smith et al., 1981; the homology alignment algorithm of Needleman and Wunsch, 1970; the search-for-similarity-method of Pearson and Lipman, 1988; the algorithm of Karlin and Altschul, 1990, modified as in Karlin and Altschul, 1993.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins et al., 1988; Higgins et al., 1989; Corpet et al., 1988; Huang et al., 1992; and Pearson et al., 1994. The ALIGN program is based on the algorithm of Myers and Miller, *supra*. The BLAST programs of Altschul et al., 1990, are based on the algorithm of Karlin and Altschul *supra*.

Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., 1990). These initial neighborhood word hits act as seeds for initiating searches to find

longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul et al., 1997. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul et al., *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g. BLASTN for nucleotide sequences, BLASTX for proteins) can be used. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, $M=5$, $N=-4$, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989). See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

For purposes of the present invention, comparison of nucleotide sequences for determination of percent sequence identity to the promoter sequences disclosed herein is preferably made using the BlastN program (version 1.4.7 or later) with its default parameters or any equivalent program. By

5 "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by the preferred program.

(c) As used herein, "sequence identity" or "identity" in the context of two

10 nucleic acid or polypeptide sequences makes reference to a specified percentage of residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window, as measured by sequence comparison algorithms or by visual inspection. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions

15 which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g., charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted

20 upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity." Means for making this adjustment are well known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity.

25 Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, e.g., as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

30 (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal

alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

(e)(i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, or 79%, preferably at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, and most preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill in the art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning, and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 70%, more preferably at least 80%, 90%, and most preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions (see below). Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. However, stringent conditions encompass temperatures in the range of about 1°C to about 20°C, depending upon the desired degree of stringency as otherwise qualified herein. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides they encode are substantially identical. This may occur, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is when the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e)(ii) The term "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70%, 71%, 72%, 73%, 74%,

75%, 76%, 77%, 78%, or 79%, preferably 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more preferably at least 90%, 91%, 92%, 93%, or 94%, or even more preferably, 95%, 96%, 97%, 98% or 99%, sequence identity to the reference sequence over a specified comparison window. Preferably, 5 optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, 1970. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by 10 a conservative substitution.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm 15 program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

As noted above, another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under 20 stringent conditions. The phrase "hybridizing specifically to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent conditions when that sequence is present in a complex mixture (e.g., total cellular) DNA or RNA. "Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic 25 acid and embraces minor mismatches that can be accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target nucleic acid sequence.

"Stringent hybridization conditions" and "stringent hybridization wash conditions" in the context of nucleic acid hybridization experiments such as 30 Southern and Northern hybridizations are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize specifically at higher temperatures. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Specificity is typically the function of post-

hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984; $T_m = 81.5^\circ\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m , hybridization, and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with >90% identity are sought, the T_m can be decreased 10°C . Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T , those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T of less than 45°C (aqueous solution) or 32°C (formamide solution), it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993. Generally, highly stringent hybridization and wash conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

An example of highly stringent wash conditions is 0.15 M NaCl at 72°C for about 15 minutes. An example of stringent wash conditions is a 0.2X SSC wash at 65°C for 15 minutes (see, Sambrook, *infra*, for a description of SSC buffer). Often, a high stringency wash is preceded by a low stringency wash to remove background probe signal. An example medium stringency wash for a duplex of, e.g., more than 100 nucleotides, is 1X SSC at 45°C for 15 minutes.

An example low stringency wash for a duplex of, e.g., more than 100 nucleotides, is 4-6X SSC at 40°C for 15 minutes. For short probes (e.g., about 10 to 50 nucleotides), stringent conditions typically involve salt concentrations of less than about 1.5 M, more preferably about 0.01 to 1.0 M, Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is typically at least about 30°C and at least about 60°C for long robes (e.g., >50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. In general, a signal to noise ratio of 2X (or higher) than that observed for an unrelated probe in the particular hybridization assay indicates detection of a specific hybridization. Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the proteins that they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code.

Very stringent conditions are selected to be equal to the T_m for a particular probe. An example of stringent conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or Northern blot is 50% formamide, e.g., hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C.

The following are examples of sets of hybridization/wash conditions that may be used to clone orthologous nucleotide sequences that are substantially identical to reference nucleotide sequences of the present invention: a reference nucleotide sequence preferably hybridizes to the reference nucleotide sequence in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 2X SSC, 0.1% SDS at 50°C, more desirably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 1X SSC, 0.1% SDS at 50°C, more desirably still in 7% sodium dodecyl sulfate (SDS), 0.5

M NaPO₄, 1 mM EDTA at 50°C with washing in 0.5X SSC, 0.1% SDS at 50°C, preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with washing in 0.1X SSC, 0.1% SDS at 50°C, more preferably in 7% sodium dodecyl sulfate (SDS), 0.5 M NaPO₄, 1 mM EDTA at 50°C with
5 washing in 0.1X SSC, 0.1% SDS at 65°C.

By "variant" polypeptide is intended a polypeptide derived from the native protein by deletion (so-called truncation) or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native
10 protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may results form, for example, genetic polymorphism or from human manipulation. Methods for such manipulations are generally known in the art.

Thus, the polypeptides of the invention may be altered in various ways
15 including amino acid substitutions, deletions, truncations, and insertions. Methods for such manipulations are generally known in the art. For example, amino acid sequence variants of the polypeptides can be prepared by mutations in the DNA. Methods for mutagenesis and nucleotide sequence alterations are well known in the art. See, for example, Kunkel, 1985; Kunkel et al., 1987; U.
20 S. Patent No. 4,873,192; Walker and Gaastra, 1983, and the references cited therein. Guidance as to appropriate amino acid substitutions that do not affect biological activity of the protein of interest may be found in the model of Dayhoff et al., 1978, herein incorporated by reference. Conservative substitutions, such as exchanging one amino acid with another having similar
25 properties, are preferred.

Thus, the genes and nucleotide sequences of the invention include both the naturally occurring sequences as well as mutant forms. Likewise, the polypeptides of the invention encompass both naturally occurring proteins as well as variations and modified forms thereof. Such variants will continue to
30 possess the desired activity. The deletions, insertions, and substitutions of the polypeptide sequence encompassed herein are not expected to produce radical changes in the characteristics of the polypeptide. However, when it is difficult to predict the exact effect of the substitution, deletion, or insertion in advance of

doing so, one skilled in the art will appreciate that the effect will be evaluated by routine screening assays.

Individual substitutions deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids (typically less than 5%,
5 more typically less than 1%) in an encoded sequence are "conservatively modified variations," where the alterations result in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. The following five groups each contain amino acids that are conservative
10 substitutions for one another: Aliphatic: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I); Aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); Sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E), Asparagine (N), Glutamine (Q). See also, Creighton, 1984. In addition,
15 individual substitutions, deletions or additions which alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence are also "conservatively modified variations."

"Production tissue" refers to mature, harvestable tissue consisting of non-dividing, terminally-differentiated cells. It excludes young, growing tissue
20 consisting of germline, meristematic, and not-fully-differentiated cells.

"Germline cells" refer to cells that are destined to be gametes and whose genetic material is heritable.

The word "plant" refers to any plant, particularly to seed plant, and "plant cell" is a structural and physiological unit of the plant, which comprises a cell
25 wall but may also refer to a protoplast. The plant cell may be in form of an isolated single cell or a cultured cell, or as a part of higher organized unit such as, for example, a plant tissue, or a plant organ.

"Plant tissue" includes differentiated and undifferentiated tissues or plants, including but not limited to roots, stems, shoots, leaves, pollen, seeds,
30 tumor tissue and various forms of cells and culture such as single cells, protoplast, embryos, and callus tissue. The plant tissue may be in plants or in organ, tissue or cell culture.

The term "altered plant trait" means any phenotypic or genotypic change in a transgenic plant relative to the wild-type or non-transgenic plant host.

The term "transformation" refers to the transfer of a nucleic acid fragment into the genome of a host cell, resulting in genetically stable inheritance. Host cells containing the transformed nucleic acid fragments are referred to as "transgenic" cells, and organisms comprising transgenic cells are referred to as "transgenic organisms". Examples of methods of transformation of plants and plant cells include *Agrobacterium*-mediated transformation (De Blaere et al., 1987) and particle bombardment technology (Klein et al., 1987; U.S. Patent No. 4,945,050). Whole plants may be regenerated from transgenic cells by methods well known to the skilled artisan (see, for example, Fromm et al., 1990).

"Transformed," "transgenic," and "recombinant" refer to a host cell or organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into the genome generally known in the art and are disclosed in Sambrook et al., 1989. See also Innis et al., 1995; and Gelfand, 1995; and Innis and Gelfand, 1999. Known methods of PCR include, but are not limited to, methods using paired primers, nested primers, single specific primers, degenerate primers, gene-specific primers, vector-specific primers, partially mismatched primers, and the like. For example, "transformed," "transformant," and "transgenic" plants or calli have been through the transformation process and contain a foreign gene integrated into their chromosome. The term "untransformed" refers to normal plants that have not been through the transformation process.

A "transgenic plant" is a plant having one or more plant cells that contain an expression vector.

"Transiently transformed" refers to cells in which transgenes and foreign DNA have been introduced (for example, by such methods as *Agrobacterium*-mediated transformation or biolistic bombardment), but not selected for stable maintenance.

"Stably transformed" refers to cells that have been selected and regenerated on a selection media following transformation.

"Transient expression" refers to transgene expression in cells, e.g., after transformation with recombinant virus or by such methods as *Agrobacterium*-mediated transformation, electroporation, or biolistic bombardment, but not selected for its stable maintenance.

"Genetically stable" and "heritable" refer to chromosomally-integrated genetic elements that are stably maintained in the plant and stably inherited by progeny through successive generations.

5 "Primary transformant" and "T0 generation" refer to transgenic plants that are of the same genetic generation as the tissue which was initially transformed (i.e., not having gone through meiosis and fertilization since transformation).

"Secondary transformants" and the "T1, T2, T3, etc. generations" refer to transgenic plants derived from primary transformants through one or more meiotic and fertilization cycles. They may be derived by self-fertilization of
10 primary or secondary transformants or crosses of primary or secondary transformants with other transformed or untransformed plants.

"Significant increase" is an increase that is larger than the margin of error inherent in the measurement technique, preferably an increase by about 2-fold or greater.

15 "Significantly less" means that the decrease is larger than the margin of error inherent in the measurement technique, preferably a decrease by about 2-fold or greater.

I. The Nucleic Acid Molecules of the Invention and Polypeptide Encoded

20 Thereby

This invention relates to isolated plant, e.g., *Arabidopsis* and rice, nucleic acid molecules, sequences and segments (fragments), the expression of which is altered in response to pathogen infection, as well as the endogenous plant promoters for those expressed molecules, sequences or segments. However, the
25 expression of these genes may also be altered in response to non-pathogens, e.g., in response to environmental stimuli. The nucleic acid molecules can be used in pathogen control strategies, e.g., by overexpressing nucleic acid molecules which can confer tolerance to a cell, or by altering the expression of host genes which are required for pathogen infection, e.g., by "knocking out" the expression of at
30 least one genomic copy of the gene. Plants having genetic disruptions in host genes may be less susceptible to infection, e.g., due to a decrease or absence of a host protein needed for infection, or, alternatively, hypersusceptible to infection. Plants that are hypersusceptible to infection may be useful to prepare transgenic

plants as the expression of the gene(s) which was disrupted may be related to gene silencing.

- Preferred sources for the nucleic acid molecules of the invention include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Wolffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wolffella* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).
- Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt, *Biosystematic Investigation on the Family of Duckweeds: The family of*

Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, cauliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens, Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula,

Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia.

- Other vegetable sources (and databases to identify orthologs of the invention) for the nucleic acid sequences of the invention include those are shown in Table 1.

Table 1

FAMILY	LATIN NAME	COMMON NAME	MAP REFERENCES RESOURCES	LINKS
Cucurbitaceae	<i>Cucumis sativus</i>	Cucumber		http://www.cucurbit.org/
	<i>Cucumis melo</i>	Melon		http://genome.cornell.edu/cgc/
	<i>Citrullus lanatus</i>	Watermelon		
	<i>Cucurbita pepo</i>	Squash – summer		
	<i>Cucurbita maxima</i>	Squash - winter		
	<i>Cucurbita moschata</i>	Pumpkin /butternut		
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Solanaceae	<i>Lycopersicon esculentum</i>	Tomato	<ul style="list-style-type: none"> 15x BAC on variety Heinz 1706 order from Clemson Genome center (www.genome.clemson.edu) 11.6x BAC of <i>L. cheesmanii</i> (originates from J. Giovannoni) available from Clemson genome center (www.genome.clemson.edu) EST collection 	genome.cornell.edu/solgenes http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=solgenes http://genome.cornell.edu/tgc/ http://tgrc.ucdavis.edu/

			<p>from TIGR (www.tigr.org/tb/lgi/index.html)</p> <ul style="list-style-type: none"> • EST collection from Clemsom Genome Center (www.genome.clemson.edu) • TAG 99:254-271, 1999 (esculentum x pennelli) • TAG 89:1007-1013, 1994 (peruvianum) • Plant Cell Reports 12:293-297, 1993 (RAPDs) • Genetics 132:1141-1160, 1992 (potato x tomato) • Genetics 120:1095-1105, 1988 (RFLP potato and tomato) • Genetics 115:387-393, 1986 (esculentum x pennelli isozyme and cDNAs) 	
	<i>Capsicum annuum</i>	Pepper		http://neptune.netimages.com/~chile/science.html
	<i>Capsicum frutescens</i>	Chile pepper		
	<i>Solanum melongena</i>	Eggplant		
	(<i>Nicotiana tabacum</i>)	(Tobacco)		
	(<i>Solanum tuberosum</i>)	(Potato)		
	(<i>Petunia x hybrida hort. ex E. Vilm.</i>)	(Petunia)	4x BAC of <i>Petunia hybrida</i> 7984 available from	

			Clemson genome center (www.genome.clemson.edu)	
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Brassicaceae	<i>Brassica oleracea</i> L. var. <i>italica</i>	Broccoli		http://res.agr.ca/ecorc/cwmt/crucifer/traits/index.htm http://geneous.cit.cornell.edu/cabbage/aboutcab.html
	<i>Brassica oleracea</i> L. var. <i>capitata</i>	Cabbage		
	<i>Brassica rapa</i>	Chinese Cabbage		
	<i>Brassica oleracea</i> L. var. <i>botrytis</i>	Cauliflower		
	<i>Raphanus sativus</i> var. <i>niger</i>	Daikon		
	(<i>Brassica napus</i>)	(Oilseed rape)		http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=brassicadb
		Arabidopsis	12x and 6x BACs on Columbia strain available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=agr
Total				http://www.nal.usda.gov/pgdic/Map_proj/
Umbelliferae	<i>Daucus carota</i>	Carrot		
Compositae	<i>Lactuca sativa</i>	Lettuce		
	<i>Helianthus annuus</i>	(Sunflower)		
Total				
Chenopodiaceae	<i>Spinacia oleracea</i>	Spinach		
	(<i>Beta vulgaris</i>)	(Sugar Beet)		
Total				

Leguminosae	<i>Phaseolus vulgaris</i>	Bean	4.3x BAC available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=beangenes
	<i>Pisum sativum</i>	Pea		
	(<i>Glycine max</i>)	(Soybean)	7.5x and 7.9x BACs available from Clemson genome center (www.genome.clemson.edu)	http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase
Total			http://www.nal.usda.gov/pgdic/Map_projects/	
Gramineae	<i>Zea mays</i>	Sweet Corn	Novartis BACs for Mo17 and B73 have been donated to Clemson Genome Center (www.genome.clemson.edu)	
	(<i>Zea mays</i>)	(Field Corn)		http://www.agron.missouri.edu/mnl/
Total			http://www.nal.usda.gov/pgdic/Map_projects/	
Liliaceae	<i>Allium cepa</i>	Onion		
		Leek		
		(Garlic)		
		(Asparagus)		
Total			http://www.nal.usda.gov/pgdic/Map_projects/	

Preferred forage and turf grass nucleic acid sources for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop. Preferably, the nucleic acid sources are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean, barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.), and even more preferably corn and soybean.

According to one embodiment, the present invention is directed to a nucleic acid molecule comprising a nucleotide sequence obtained or obtainable

from any plant gene which encodes a polypeptide having at least 70% amino acid sequence identity to a polypeptide encoded by SEQ ID NOs. 1-684 or 789-795, or a promoter for said gene. Thus, based on the *Arabidopsis* nucleic acid sequences of the present invention, orthologs of those sequences may be

5 identified or isolated from the genome of any desired organism, preferably from another plant, according to well known techniques based on their sequence similarity to the *Arabidopsis* coding sequences, e.g., hybridization, PCR or computer generated sequence comparisons. For example, all or a portion of a particular *Arabidopsis* sequence is used as a probe that selectively hybridizes to

10 other gene sequences present in a population of cloned genomic DNA fragments or cDNA fragments (i.e., genomic or cDNA libraries) from a chosen source organism. Further, suitable genomic and cDNA libraries may be prepared from any cell or tissue of an organism. Such techniques include hybridization screening of plated DNA libraries (either plaques or colonies; see, e.g.,

15 Sambrook et al., 1989) and amplification by PCR using oligonucleotide primers preferably corresponding to sequence domains conserved among related polypeptide or subsequences of the nucleotide sequences provided herein (see, e.g., Innis et al., 1990). These methods are particularly well suited to the isolation of gene sequences from organisms closely related to the organism from

20 which the probe sequence is derived. The application of these methods using the *Arabidopsis* coding sequences as probes is well suited for the isolation of gene sequences from any source organism, preferably other plant species. In a PCR approach, oligonucleotide primers can be designed for use in PCR reactions to amplify corresponding DNA sequences from cDNA or genomic DNA extracted

25 from any plant of interest. Methods for designing PCR primers and PCR cloning are generally known in the art as discussed hereinabove.

In hybridization techniques, all or part of a known nucleotide sequence is used as a probe that selectively hybridizes to other corresponding nucleotide sequences present in a population of cloned genomic DNA fragments or cDNA

30 fragments (i.e., genomic or cDNA libraries) from a chosen organism. The hybridization probes may be genomic DNA fragments, cDNA fragments, RNA fragments, or other oligonucleotides, and may be labeled with a detectable group such as ^{32}P , or any other detectable marker. Thus, for example, probes for hybridization can be made by labeling synthetic oligonucleotides based on the

sequence of the invention. Methods for preparation of probes for hybridization and for construction of cDNA and genomic libraries are generally known in the art and are disclosed in Sambrook et al., 1989. In general, sequences that hybridize to the sequences disclosed herein will have at least 40% to 50%, about 5 60% to 70% and even about 80% 85%, 90%, 95% to 98% or more identity with the disclosed sequences. That is, the sequence similarity of sequences may range, sharing at least about 40% to 50%, about 60% to 70%, and even about 80%, 85%, 90%, 95% to 98% sequence similarity.

The nucleic acid molecules of the invention can also be identified by, for 10 example, a search of known databases for genes encoding polypeptides having a specified amino acid sequence identity. Methods of alignment of sequences for comparison are well known in the art and are described hereinabove.

II. Expression Cassettes of the Invention

15 The present invention also encompasses expression cassettes, preferably in the form of a recombinant vectors comprising the nucleic acid sequences of the invention. In such vectors, the expression cassette comprises regulatory elements for expression of the nucleotide sequences in a host cell capable of expressing the nucleotide sequences. Such regulatory elements usually comprise 20 promoter and termination signals and preferably also comprise elements allowing efficient translation of polypeptides encoded by the nucleic acid sequences of the present invention. For efficient initiation of translation, sequences adjacent to the initiating methionine may require modification. For example, they can be modified by the inclusion of sequences known to be 25 effective in plants. Joshi (1987) has suggested an appropriate consensus for plants and Clontech suggests a further consensus translation initiator (1993/1994 catalog, page 210). These consensus are suitable for use with the nucleotide sequences of this invention. The sequences are incorporated into constructions comprising the nucleotide sequences, up to and including the ATG (whilst 30 leaving the second amino acid unmodified), or alternatively up to and including the GTC subsequent to the ATG (with the possibility of modifying the second amino acid of the transgene).

Vectors comprising the nucleic acid sequences are usually capable of replication in particular host cells, e.g., as extrachromosomal molecules, and are

therefore used to amplify the nucleic acid sequences of this invention in the host cells. In a preferred embodiment, host cells for such vectors are plant cells.

A. Promoters and Enhancers

Expression of the nucleotide sequences in transgenic plants is driven by promoters shown to be functional in plants. The choice of promoter will vary depending on the temporal and spatial requirements for expression, and also depending on the target species. In many cases, expression in multiple tissues is desirable. Although many promoters from dicotyledons have been shown to be operational in monocotyledons and *vice versa*, ideally dicotyledonous promoters are selected for expression in dicotyledons, and monocotyledonous promoters for expression in monocotyledons. However, there is no restriction to the provenance of selected promoters; it is sufficient that they are operational in driving the expression of the nucleotide sequences in the desired cell.

These promoters include, but are not limited to, constitutive, inducible, temporally regulated, developmentally regulated, chemically regulated, stress-responsive, tissue-preferred and tissue-specific promoters. Promoter sequences are known to be strong or weak. A strong promoter provides for a high level of gene expression, whereas a weak promoter provides for a very low level of gene expression. An inducible promoter is a promoter that provides for the turning on and off of gene expression in response to an exogenously added agent, or to an environmental or developmental stimulus. A bacterial promoter such as the P_{tac} promoter can be induced to varying levels of gene expression depending on the level of isothiopyrogalactoside added to the transformed bacterial cells. An isolated promoter sequence that is a strong promoter for heterologous nucleic acid is advantageous because it provides for a sufficient level of gene expression to allow for easy detection and selection of transformed cells and provides for a high level of gene expression when desired.

Preferred promoters that are expressed constitutively include promoters from genes encoding actin or ubiquitin and the CaMV 35S and 19S promoters. The nucleotide sequences of this invention can also be expressed under the regulation of promoters that are chemically regulated. This enables the nucleic acid sequence or encoded polypeptide to be synthesized only when the crop plants are treated with the inducing chemicals. Preferred technology for chemical induction of gene expression is detailed in the published application EP

0 332 104 (to Ciba-Geigy) and U.S. Patent 5,614,395. A preferred promoter for chemical induction is the tobacco PR-1a promoter.

Tissue-specific or tissue-preferential promoters useful in the present invention. Also useful are promoters which confer seed-specific expression, such as those disclosed by Schernthaner et al., 1988; anther (tapetal) specific promoter B6 (Huffman et al.); and pistil-specific promoters such as a modified S13 promoter (Dzelkalns et al., 1993).

Preferred tissue specific expression patterns include green tissue-specific, root-specific, stem-specific, and flower-specific. Promoters suitable for expression in green tissue include many which regulate genes involved in photosynthesis and many of these have been cloned from both monocotyledons and dicotyledons. A preferred promoter is the maize PEPC promoter from the phosphoenol carboxylase gene (Hudspeth & Grula, 1989). A preferred promoter for root-specific expression is that described by de Framond (1991; EP 0 452 269 to Ciba-Geigy). A preferred stem specific promoter is that described in U.S. Patent No. 5,625,136 (to Ciba-Geigy) and which drives expression of the maize *trpA* gene.

Other promoters which direct specific or enhanced expression in certain plant tissues will be known to those of skill in the art in light of the present disclosure. These include, for example, the *rbcS* promoter, specific for green tissue; the *ocs*, *nos*, and *mas* promoters which have higher activity in roots or wounded leaf tissue; a truncated (-90 to +8) 35S promoter which directs enhanced expression in roots, an tubulin gene that directs expression in roots and promoters derived from zein storage protein genes which direct expression in endosperm. It is particularly contemplated that one may advantageously use the 16 bp *ocs* enhancer element from the octopine synthase (*ocs*) gene (Bonchez et al., 1989), especially when present in multiple copies, to achieve enhanced expression in roots.

Preferred plant promoters include, but are not limited to, a promoter such as the CaMV 35S promoter, an enhanced 35S promoter or others such as CaMV 19S, *nos*, *Adh1*, sucrose synthase, α -tubulin, ubiquitin, actin, *cab*, PEPCase or those associated with the R gene complex. Further suitable promoters include the U2 and U5 snRNA promoters from maize, the promoter from alcohol dehydrogenase, the Z4 promoter from a gene encoding the Z4 22 kD zein

protein, the Z10 promoter from a gene encoding a 10 kD zein protein, a Z27 promoter from a gene encoding a 27 kD zein protein, the A20 promoter from the gene encoding a 19 kD -zein protein, inducible promoters, such as the light inducible promoter derived from the pea *rbcS* gene and the actin promoter from rice; seed specific promoters, such as the phaseolin promoter from beans, may also be used. Other promoters useful in the practice of the invention are known to those of skill in the art.

Examples of tissue specific promoters which have been described include the lectin (Vodkin, 1983; Lindstrom et al., 1990,) corn alcohol dehydrogenase 1 (Vogel et al., 1992; Dennis et al., 1984), corn light harvesting complex (Simpson, 1985; Bansal et al., 1992), corn heat shock protein (Odell et al., 1985; Rochester et al., 1986), pea small subunit RuBP carboxylase (Poulsen et al., 1986; Cashmore et al., 1983), Ti plasmid mannopine synthase (Langridge et al., 1989), Ti plasmid nopaline synthase (Langridge et al., 1989), petunia chalcone isomerase (vanTunen et al., 1988), bean glycine rich protein 1 (Keller et al., 1989), truncated CaMV 35s (Odell et al., 1985), potato patatin (Wenzler et al., 1989), root cell (Yamamoto et al., 1990), maize zein (Reina et al., 1990; Kriz et al., 1987; Wandelt et al., 1989; Langridge et al., 1983; Reina et al., 1990), globulin-1 (Belanger et al., 1991), α -tubulin, cab (Sullivan et al., 1989), PEPCase (Hudspeth & Grula, 1989), R gene complex-associated promoters (Chandler et al., 1989), and chalcone synthase promoters (Franken et al., 1991).

Inducible promoters that have been described include the ABA- and turgor-inducible promoters, the promoter of the auxin-binding protein gene (Schwob et al., 1993), the UDP glucose flavonoid glycosyl-transferase gene promoter (Ralston et al., 1988), the MPI proteinase inhibitor promoter (Cordero et al., 1994), and the glyceraldehyde-3-phosphate dehydrogenase gene promoter (Kohler et al., 1995; Quigley et al., 1989; Martinez et al., 1989).

Several tissue-specific regulated genes and/or promoters have been reported in plants. These include genes encoding the seed storage proteins (such as napin, cruciferin, beta-conglycinin, and phaseolin) zein or oil body proteins (such as oleosin), or genes involved in fatty acid biosynthesis (including acyl carrier protein, stearoyl-ACP desaturase, and fatty acid desaturases (*fad 2-1*)), and other genes expressed during embryo development (such as *Bce4*, see, for example, EP 255378 and Kridl et al., 1991). Particularly useful for seed-specific

expression is the pea vicilin promoter (Czako et al., 1992. (See also U.S. Pat. No. 5,625,136, herein incorporated by reference.) Other useful promoters for expression in mature leaves are those that are switched on at the onset of senescence, such as the SAG promoter from Arabidopsis (Gan et al., 1995, 270
5 (5244), 1986-8).

A class of fruit-specific promoters expressed at or during antithesis through fruit development, at least until the beginning of ripening, is discussed in U.S. 4,943,674, the disclosure of which is hereby incorporated by reference. cDNA clones that are preferentially expressed in cotton fiber have been isolated
10 (John et al., 1992). cDNA clones from tomato displaying differential expression during fruit development have been isolated and characterized (Mansson et al., 1985, Slater et al., 1985). The promoter for polygalacturonase gene is active in fruit ripening. The polygalacturonase gene is described in U.S. Patent No. 4,535,060, U.S. Patent No. 4,769,061, U.S. Patent No. 4,801,590, and U.S.
15 Patent No. 5,107,065, which disclosures are incorporated herein by reference.

Other examples of tissue-specific promoters include those that direct expression in leaf cells following damage to the leaf (for example, from chewing insects), in tubers (for example, patatin gene promoter), and in fiber cells (an example of a developmentally-regulated fiber cell protein is E6 (John et al.,
20 1992). The E6 gene is most active in fiber, although low levels of transcripts are found in leaf, ovule and flower.

The tissue-specificity of some "tissue-specific" promoters may not be absolute and may be tested by one skilled in the art using the diphtheria toxin sequence. One can also achieve tissue-specific expression with "leaky"
25 expression by a combination of different tissue-specific promoters (Beals et al., 1997). Other tissue-specific promoters can be isolated by one skilled in the art (see U.S. 5,589,379). Several inducible promoters ("gene switches") have been reported. Many are described in the review by Gatz (1996 and 1997). These include tetracycline repressor system, *Lac* repressor system, copper-inducible
30 systems, salicylate-inducible systems (such as the PR1a system), glucocorticoid- (Aoyama, 1997) and ecdysone-inducible systems. Also included are the benzene sulphonamide- (U.S. Patent No. 5,364,780) and alcohol- (WO 97/06269 and WO 97/06268) inducible systems and glutathione S-transferase promoters. Other studies have focused on genes inducibly regulated in response to

environmental stress or stimuli such as increased salinity, drought, pathogen and wounding. (Graham et al., 1985; Graham et al., 1985, Smith et al., 1986).

Accumulation of metallocarboxypeptidase-inhibitor protein has been reported in leaves of wounded potato plants (Graham et al., 1981). Other plant genes have
5 been reported to be induced methyl jasmonate, elicitors, heat-shock, anaerobic stress, or herbicide safeners.

Frequently it is desirable to have continuous or inducible expression of a DNA sequence throughout the cells of an organism in a tissue-independent manner. For example, increased resistance of a plant to infection by soil- and air
10 borne pathogens might be accomplished by genetic manipulation of the plant's genome to comprise a continuous promoter operably linked to a heterologous or homologous pathogen-resistance gene such that pathogen-resistance proteins are continuously expressed throughout the plant's tissues.

Alternatively, it might be desirable to inhibit expression of a native DNA
15 sequence within a plant's tissues to achieve a desired phenotype. In this case, such inhibition might be accomplished with transformation of the plant to comprise a constitutive, tissue-independent promoter operably linked to an antisense nucleotide sequence, such that constitutive expression of the antisense sequence produces an RNA transcript that interferes with translation of the
20 mRNA of the native DNA sequence.

Other elements include those that can be regulated by endogenous or exogenous agents, e.g., by DNA binding proteins such as zinc finger proteins, including naturally occurring zinc finger proteins or chimeric zinc finger proteins (see, e.g., U.S. Patent No. 5,789,538, WO 99/48909; WO 99/45132; WO
25 98/53060; WO 98/53057; WO 98/53058; WO 00/23464; WO 95/19431; and WO 98/54311) or myb-like transcription factors. For example, a chimeric zinc finger protein may include amino acid sequences which bind to a specific DNA sequence (the zinc finger) and amino acid sequences that activate (e.g., GAL 4 sequences) or repress the transcription of the sequences linked to the specific
30 DNA sequence.

B. 5' and 3' Sequences

In addition to promoters, a variety of 3' transcriptional terminators are also available for use in the present invention. Transcriptional terminators are responsible for the termination of transcription and correct mRNA

polyadenylation. The 3' nontranslated regulatory DNA sequence preferably includes from about 50 to about 1,000, more preferably about 100 to about 1,000, nucleotide base pairs and contains plant transcriptional and translational termination sequences. Appropriate transcriptional terminators and those which are known to function in plants include the CaMV 35S terminator, the trnI terminator, the nopaline synthase terminator, the pea rbcS E9* terminator, the terminator for the T7 transcript from the octopine synthase gene of *Agrobacterium tumefaciens*, and the 3' end of the protease inhibitor I or II genes from potato or tomato, although other 3' elements known to those of skill in the art can also be employed.

The 5' regulatory region of the expression cassette may also include other enhancing sequences. Numerous sequences have been found to enhance gene expression in transgenic plants. These include sequences which have been shown to enhance expression such as intron sequences (e.g., from *Adhl*, *bronzel* or the sucrose synthase intron) and viral leader sequences (e.g., from TMV, MCMV and AMV). For example, a number of non-translated leader sequences derived from viruses are known to enhance expression. Specifically, leader sequences from Tobacco Mosaic Virus (TMV), Maize Chlorotic Mottle Virus (MCMV), and Alfalfa Mosaic Virus (AMV) have been shown to be effective in enhancing expression (e.g., Gallie et al., 1987; Skuzeski et al., 1990). Other leaders known in the art include but are not limited to: Picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5 noncoding region) (Elroy-Stein et al., 1989); Potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison et al., 1986); MDMV leader (Maize Dwarf Mosaic Virus); Human immunoglobulin heavy-chain binding protein (BiP) leader, (Macejak et al., 1991); Untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), (Jobling et al., 1987; Tobacco mosaic virus leader (TMV), (Gallie et al., 1989; and Maize Chlorotic Mottle Virus leader (MCMV) (Lommel et al., 1991. See also, Della-Cioppa et al., 1987.

C. Targeting Sequences

It may be preferable to target expression of the nucleotide sequences of the present invention to different cellular localizations in the plant. In some cases, localization in the cytosol may be desirable, whereas in other cases, localization in some subcellular organelle, e.g., the nucleus, may be preferred. Subcellular

localization of transgene encoded enzymes is undertaken using techniques well known in the art. Typically, the DNA encoding the target peptide from a known organelle-targeted gene product is manipulated and fused upstream of the nucleotide sequence. Many such target sequences are known for the chloroplast and their functioning in heterologous constructions has been shown. The expression of the nucleotide sequences of the present invention is also targeted to the endoplasmic reticulum or to the vacuoles of the host cells. Techniques to achieve this are well-known in the art.

D. Marker Genes

In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the preselected nucleic acid sequence or segment. "Marker genes" are genes that impart a distinct phenotype to cells expressing the marker gene and thus allow such transformed cells to be distinguished from cells that do not have the marker. Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can 'select' for by chemical means, i.e., through the use of a selective agent (e.g., a herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing, i.e., by 'screening' (e.g., the R-locus trait). Of course, many examples of suitable marker genes are known to the art and can be employed in the practice of the invention.

Included within the terms selectable or screenable marker genes are also genes which encode a "secretable marker" whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected by their catalytic activity. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA; small active enzymes detectable in extracellular solution (e.g., α -amylase, β -lactamase, phosphinothricin acetyltransferase); and proteins that are inserted or trapped in the cell wall (e.g., proteins that include a leader sequence such as that found in the expression unit of extensin or tobacco PR-S).

With regard to selectable secretable markers, the use of a gene that encodes a polypeptide that becomes sequestered in the cell wall, and which polypeptide

includes a unique epitope is considered to be particularly advantageous. Such a secreted antigen marker would ideally employ an epitope sequence that would provide low background in plant tissue, a promoter-leader sequence that would impart efficient expression and targeting across the plasma membrane, and
5 would produce protein that is bound in the cell wall and yet accessible to antibodies. A normally secreted wall protein modified to include a unique epitope would satisfy all such requirements.

Elements of the present disclosure are exemplified in detail through the use of particular marker genes. However in light of this disclosure, numerous other
10 possible selectable and/or screenable marker genes will be apparent to those of skill in the art in addition to the one set forth herein below. Therefore, it will be understood that the following discussion is exemplary rather than exhaustive. In light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the present invention renders possible the
15 introduction of any gene, including marker genes, into a recipient cell to generate a transformed plant cell, e.g., a monocot cell.

Possible selectable markers for use in connection with the present invention include, but are not limited to, a *neo* gene, which codes for kanamycin resistance and can be selected for using kanamycin, G418, a gene encoding
20 resistance to bleomycin, and the like; a *bar* gene which codes for bialaphos resistance; a gene which encodes an altered EPSP synthase protein thus conferring glyphosate resistance; a nitrilase gene such as *bxn* from *Klebsiella ozaenae* which confers resistance to bromoxynil; a mutant acetolactate synthase gene (ALS) which confers resistance to imidazolinone, sulfonyleurea or other
25 ALS-inhibiting chemicals (European Patent Application 154,204, 1985); a methotrexate-resistant DHFR gene; a dalapon dehalogenase gene that confers resistance to the herbicide dalapon; or a mutated anthranilate synthase gene that confers resistance to 5-methyl tryptophan. Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a
30 suitable chloroplast transit peptide, CTP (European Patent Application 0 218 571, 1987).

An illustrative embodiment of a selectable marker gene capable of being used in systems to select transformants is the genes that encode the enzyme phosphinothricin acetyltransferase, such as the *bar* gene from *Streptomyces*

hygroscopicus or the *pat* gene from *Streptomyces viridochromogenes* (U.S. Patent No. 5,550,318). The enzyme phosphinothricin acetyltransferase (PAT) inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, causing rapid accumulation of ammonia and cell death. The success in using this selective system in conjunction with monocots was particularly surprising because of the major difficulties which have been reported in transformation of cereals.

Screenable markers that may be employed include, but are not limited to, a β -glucuronidase or *uidA* gene (GUS) which encodes an enzyme for which various chromogenic substrates are known; an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues; a β -lactamase gene, which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a *xyIE* gene which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene; a tyrosinase gene which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to form the easily detectable compound melanin; a β -galactosidase gene, which encodes an enzyme for which there are chromogenic substrates; a luciferase (*lux*) gene, which allows for bioluminescence detection; or an aequorin gene, which may be employed in calcium-sensitive bioluminescence detection, or a green fluorescent protein.

Genes from the maize R gene complex are contemplated to be particularly useful as screenable markers. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. Maize strains can have one, or as many as four, R alleles which combine to regulate pigmentation in a developmental and tissue specific manner. A gene from the R gene complex was applied to maize transformation, because the expression of this gene in transformed cells does not harm the cells. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line carries dominant alleles for genes encoding the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2), but carries a recessive allele at the R locus, transformation of any cell from that line with R will result in red pigment formation. Exemplary lines include Wisconsin 22

which contains the rg-Stadler allele and TR112, a K55 derivative which is r-g, b, Pl. Alternatively any genotype of maize can be utilized if the C1 and R alleles are introduced together.

A further screenable marker contemplated for use in the present invention is firefly luciferase, encoded by the *lux* gene. The presence of the *lux* gene in transformed cells may be detected using, for example, X-ray film, scintillation counting, fluorescent spectrophotometry, low-light video cameras, photon counting cameras or multiwell luminometry. It is also envisioned that this system may be developed for populational screening for bioluminescence, such as on tissue culture plates, or even for whole plant screening.

E. Other Sequences

A vector of the invention can also further comprise plasmid DNA. Plasmid vectors include additional DNA sequences that provide for easy selection, amplification, and transformation of the expression cassette in prokaryotic and eukaryotic cells, e.g., pUC-derived vectors such as pUC8, pUC9, pUC18, pUC19, pUC23, pUC119, and pUC120, pSK-derived vectors, pGEM-derived vectors, pSP-derived vectors, or pBS-derived vectors. The additional DNA sequences include origins of replication to provide for autonomous replication of the vector, additional selectable marker genes, preferably encoding antibiotic or herbicide resistance, unique multiple cloning sites providing for multiple sites to insert DNA sequences or genes encoded in the expression cassette, and sequences that enhance transformation of prokaryotic and eukaryotic cells.

Another vector that is useful for expression in both plant and prokaryotic cells is the binary Ti plasmid (as disclosed in Schilperoort et al., U.S. Patent No. 4,940,838) as exemplified by vector pGA582. This binary Ti plasmid vector has been previously characterized by An, cited *supra*. This binary Ti vector can be replicated in prokaryotic bacteria such as *E. coli* and *Agrobacterium*. The *Agrobacterium* plasmid vectors can be used to transfer the expression cassette to dicot plant cells, and under certain conditions to monocot cells, such as rice cells. The binary Ti vectors preferably include the nopaline T DNA right and left borders to provide for efficient plant cell transformation, a selectable marker gene, unique multiple cloning sites in the T border regions, the *colE1* replication of origin and a wide host range replicon. The binary Ti vectors carrying an

expression cassette of the invention can be used to transform both prokaryotic and eukaryotic cells, but is preferably used to transform dicot plant cells.

Virtually any DNA may be used for delivery to recipient cells to ultimately produce fertile transgenic plants in accordance with the present invention. For example, DNA segments in the form of vectors and plasmids, or linear DNA fragments, in some instance containing only the DNA element to be expressed in the plant, and the like, may be employed.

Vectors, plasmids, cosmids, YACs (yeast artificial chromosomes) and DNA segments for use in transforming such cells will, of course, generally comprise the cDNA, gene or genes which one desires to introduce into the cells. These DNA constructs can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired. The DNA segment or gene chosen for cellular introduction will often encode a protein which will be expressed in the resultant recombinant cells, such as will result in a screenable or selectable trait and/or which will impart an improved phenotype to the regenerated plant. However, this may not always be the case, and the present invention also encompasses transgenic plants incorporating non-expressed transgenes.

20 III. Transformation

The expression cassettes of the present invention can be introduced into a host cell, e.g., a plant cell, in a number of art-recognized ways. Those skilled in the art will appreciate that the choice of method might depend on the type of cell, e.g., monocotyledonous or dicotyledonous, targeted for transformation. Vectors which may be used to transform plant tissue with the expression cassettes of the present invention include both *Agrobacterium* vectors and ballistic vectors, as well as vectors suitable for DNA-mediated transformation, e.g., direct uptake or via electroporation. However, cells other than plant cells may be transformed with the expression cassettes of the invention.

Suitable methods of transforming plant cells include, but are not limited to, microinjection (Crossway et al., 1986), direct DNA transfer to plant cells by PEG precipitation; liposomes; electroporation (Riggs et al., 1986, *Agrobacterium*-mediated transformation (Hinchey et al., 1988), direct gene transfer (Paszkowski et al., 1984), and ballistic particle acceleration using

devices available from Agracetus, Inc., Madison, Wis. and BioRad, Hercules, Calif. (see, for example, Sanford et al., U.S. Pat. No. 4,945,050; and McCabe et al., 1988). Also see, Weissinger et al., 1988; Sanford et al., 1987 (onion); Christou et al., 1988 (soybean); McCabe et al., 1988 (soybean); Datta et al., 1990 (rice); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Klein et al., 1988 (maize); Fromm et al., 1990 (maize); and Gordon-Kamm et al., 1990 (maize); Svab et al., 1990 (tobacco chloroplast); Koziel et al., 1993 (maize); Shimamoto et al., 1989 (rice); Christou et al., 1991 (rice); European Patent Application EP 0 332 581 (orchardgrass and other Pooideae); Vasil et al., 1993 (wheat); Weeks et al., 1993 (wheat).

In one embodiment, a nucleotide sequence of the present invention is directly transformed into the plastid genome. Plastid transformation technology is extensively described in U.S. Patent Nos. 5,451,513, 5,545,817, and 5,545,818, in PCT application no. WO 95/16783, and in McBride et al., 1994.

The basic technique for chloroplast transformation involves introducing regions of cloned plastid DNA flanking a selectable marker together with the gene of interest into a suitable target tissue, e.g., using biolistics or protoplast transformation (e.g., calcium chloride or PEG mediated transformation). The 1 to 1.5 kb flanking regions, termed targeting sequences, facilitate orthologous recombination with the plastid genome and thus allow the replacement or modification of specific regions of the plastome. Initially, point mutations in the chloroplast 16S rRNA and rps12 genes conferring resistance to spectinomycin and/or streptomycin are utilized as selectable markers for transformation (Svab et al., 1990; Staub et al., 1992). This resulted in stable homoplasmic transformants at a frequency of approximately one per 100 bombardments of target leaves. The presence of cloning sites between these markers allowed creation of a plastid targeting vector for introduction of foreign genes (Staub et al., 1993). Substantial increases in transformation frequency are obtained by replacement of the recessive rRNA or r-protein antibiotic resistance genes with a dominant selectable marker, the bacterial *aadA* gene encoding the spectinomycin-detoxifying enzyme aminoglycoside-3'-adenyltransferase (Svab et al., 1993). Other selectable markers useful for plastid transformation are known in the art and encompassed within the scope of the invention. Typically, approximately 15-20 cell division cycles following transformation are required to reach a

homoplastidic state. Plastid expression, in which genes are inserted by orthologous recombination into all of the several thousand copies of the circular plastid genome present in each plant cell, takes advantage of the enormous copy number advantage over nuclear-expressed genes to permit expression levels that can readily exceed 10% of the total soluble plant protein. In a preferred embodiment, a nucleotide sequence of the present invention is inserted into a plastid targeting vector and transformed into the plastid genome of a desired plant host. Plants homoplastic for plastid genomes containing a nucleotide sequence of the present invention are obtained, and are preferentially capable of high expression of the nucleotide sequence.

Agrobacterium tumefaciens cells containing a vector comprising an expression cassette of the present invention, wherein the vector comprises a Ti plasmid, are useful in methods of making transformed plants. Plant cells are infected with an *Agrobacterium tumefaciens* as described above to produce a transformed plant cell, and then a plant is regenerated from the transformed plant cell. Numerous *Agrobacterium* vector systems useful in carrying out the present invention are known. For example, U.S. Pat. No. 4,459,355 discloses a method for transforming susceptible plants, including dicots, with an *Agrobacterium* strain containing the Ti plasmid. The transformation of woody plants with an *Agrobacterium* vector is disclosed in U.S. Patent No. 4,795,855. Further, U.S. Patent No. 4,940,838 to Schilperoort et al. discloses a binary *Agrobacterium* vector (i.e., one in which the *Agrobacterium* contains one plasmid having the vir region of a Ti plasmid but no T region, and a second plasmid having a T region but no vir region) useful in carrying out the present invention.

It is particularly preferred to use the binary type vectors of Ti and Ri plasmids of *Agrobacterium* spp. Ti-derived vectors transform a wide variety of higher plants, including monocotyledonous and dicotyledonous plants, such as soybean, cotton, rape, tobacco, and rice (Pacciotti et al., 1985; Byrne et al., 1987; Sukhapinda et al., 1987; Lorz et al., 1985; Potrykus, 1985; Park et al., 1985; Hiei et al., 1994). The use of T-DNA to transform plant cells has received extensive study and is amply described (EP 120516; Hoekema, 1985; Knauf, et al., 1983; and An. et al., 1985). For introduction into plants, the nucleotide sequences of the invention can be inserted into binary vectors as described in the examples.

Transformation of plants can be undertaken with a single DNA molecule or multiple DNA molecules (i.e., co-transformation), and both these techniques are suitable for use with the expression cassettes of the present invention.

Numerous transformation vectors are available for plant transformation, and the
 5 expression cassettes of this invention can be used in conjunction with any such vectors. The selection of vector will depend upon the preferred transformation technique and the target species for transformation.

Preferred plant cells for transformation include, but are not limited to, cells from plant such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B.*
 10 *juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus*
 15 *tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa
 20 (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.),
 25 oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L. miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L.*
 30 *valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofieldia* (*Wl. caudata*, *Wl. denticulata*, *Wl. gladiata*, *Wl. hyalina*, *Wl. lingulata*, *Wl. repunda*, *Wl. rotunda*, and *Wl. neotropica*).

Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,

5 Biosystematic Investigation on the Family of Duckweeds: The family of *Lemnaceae* - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis*

10 such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and

15 chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*);

20 redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils,

25 chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g., trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula,

30 blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry, apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry,

nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,

5 Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia. Other vegetables are in Table 1.

10 Preferred forage and turf grass for use in the methods of the invention include alfalfa, orchard grass, tall fescue, perennial ryegrass, creeping bent grass, and redtop.

Preferably, plants of the present invention are crop plants and in particular cereals (for example, corn, alfalfa, sunflower, rice, *Brassica*, canola, soybean,

15 barley, soybean, sugarbeet, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, and the like), and even more preferably rice, corn and soybean.

In a preferred embodiment, the host cells are monocot or dicot cells, including, but are not limited to, wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince,

20 cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage, brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry,

25 chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut, nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g.,

30 lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia,

Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. More preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be
5 regenerated into a transgenic plant.

Any plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a vector of the present invention. The term "organogenesis," as used herein, means a process by which shoots and roots are developed sequentially from meristematic centers; the
10 term "embryogenesis," as used herein, means a process by which shoots and roots develop together in a concerted fashion (not sequentially), whether from somatic cells or gametes. The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen,
15 embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristems, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem).

The choice of plant tissue source for transformation will depend on the nature of the host plant and the transformation protocol. Useful tissue sources
20 include callus, suspension culture cells, protoplasts, leaf segments, stem segments, tassels, pollen, embryos, hypocotyls, tuber segments, meristematic regions, and the like. The tissue source is selected and transformed so that it retains the ability to regenerate whole, fertile plants following transformation, i.e., contains totipotent cells. Type I or Type II embryonic maize callus and
25 immature embryos are preferred *Zea mays* tissue sources. Selection of tissue sources for transformation of monocots is described in detail in U.S. Application Serial No. 08/112,245 and PCT publication WO 95/06128 (incorporated herein by reference).

For certain plant species, different antibiotic or herbicide selection markers
30 may be preferred. Selection markers used routinely in transformation include the nptII gene which confers resistance to kanamycin and related antibiotics (Messing & Vierra, 1982); Bevan et al., 1983), the *bar* gene which confers resistance to the herbicide phosphinothricin (White et al., 1990, Spencer et al., 1990), the *hph* gene which confers resistance to the antibiotic hygromycin

(Blochinger & Diggelmann), and the *dhfr* gene, which confers resistance to methotrexate (Bourouis et al., 1983).

Thus, the present invention also provides a transformed (transgenic) plant cell, *in planta* or *ex planta*, including, but not limited to, a transformed plant cell

5 from plants such as corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet

10 (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Cofea* spp.), coconut (*Cocos*

15 *nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond

20 (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers; duckweed (*Lemna*, see WO 00/07210, which includes members of the family *Lemnaceae*. There are known four genera and 34 species of duckweed as follows: genus *Lemna* (*L. aequinoctialis*, *L. disperma*, *L. ecuadoriensis*, *L. gibba*, *L. japonica*, *L. minor*, *L.*

25 *miniscula*, *L. obscura*, *L. perpusilla*, *L. tenera*, *L. trisulca*, *L. turionifera*, *L. valdiviana*); genus *Spirodela* (*S. intermedia*, *S. polyrrhiza*, *S. punctata*); genus *Woffia* (*Wa. angusta*, *Wa. arrhiza*, *Wa. australina*, *Wa. borealis*, *Wa. brasiliensis*, *Wa. columbiana*, *Wa. elongata*, *Wa. globosa*, *Wa. microscopica*, *Wa. neglecta*) and genus *Wofieldia* (*W1. caudata*, *W1. denticulata*, *W1. gladiata*,

30 *W1. hyalina*, *W1. lingulata*, *W1. repunda*, *W1. rotunda*, and *W1. neotropica*). Any other genera or species of *Lemnaceae*, if they exist, are also aspects of the present invention. *Lemna gibba*, *Lemna minor*, and *Lemna miniscula* are preferred, with *Lemna minor* and *Lemna miniscula* being most preferred. *Lemna* species can be classified using the taxonomic scheme described by Landolt,

Biosystematic Investigation on the Family of Duckweeds: The family of Lemnaceae - A Monograph Study. Geobotanischen Institut ETH, Stiftung Rubel, Zurich (1986)); vegetables including tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans
 5 (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*),
 10 carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum. Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*), Douglas-fir (*Pseudotsuga
 15 menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek,
 20 soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, etc. Legumes include, but are not limited to, *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, *Lotus*, e.g.,
 25 trefoil, lens, e.g., lentil, and false indigo, *Acacia*, aneth, artichoke, arugula, blackberry, canola, cilantro, clementines, escarole, eucalyptus, fennel, grapefruit, honey dew, jicama, kiwifruit, lemon, lime, mushroom, nut, okra, orange, parsley, persimmon, plantain, pomegranate, poplar, radiata pine, radicchio, Southern pine, sweetgum, tangerine, triticale, vine, yams, apple, pear, quince, cherry,
 30 apricot, melon, hemp, buckwheat, grape, raspberry, chenopodium, blueberry, nectarine, peach, plum, strawberry, watermelon, eggplant, pepper, caluliflower, Brassica, e.g., broccoli, cabbage, brussels sprouts, onion, carrot, leek, beet, broad bean, celery, radish, pumpkin, endive, gourd, garlic, snapbean, spinach, squash, turnip, asparagus, and zucchini and ornamental plants include impatiens,

Begonia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Agertum, Amaranthus, Antihirrhinum, Aquilegia, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura, Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossos, and Zinnia, as well
 5 as from vegetables including those described in Table 1.

In a preferred embodiment, the transformed cells, include, but are not limited to, transformed wheat, corn (maize), rice, oat, barley, millet, rye, rape and alfalfa, as well as asparagus, tomato, egg plant, apple, pear, quince, cherry, apricot, pepper, melon, lettuce, cauliflower, *Brassica*, e.g., broccoli, cabbage,
 10 brussels sprout, sugar beet, sugar cane, sweetcorn, onion, carrot, leek, cucumber, tobacco, aubergine, beet, broad bean, carrot, celery, chicory, cotton, radish, pumpkin, hemp, buckwheat, orchardgrass, creeping bent top, redtop, ryegrass, tobacco, turfgrass, tall fescue, cow pea, endive, gourd, grape, raspberry, chenopodium, blueberry, pineapple, avocado, mango, banana, groundnut,
 15 nectarine, papaya, garlic, pea, peach, peanut, pepper, pineapple, plum, potato, safflower, snap bean, spinach, squashes, strawberry, sunflower, sorghum, sweet potato, turnip, watermelon, legumes such as *Arachis*, e.g., peanuts, *Vicia*, e.g., crown vetch, hairy vetch, adzuki bean, mung bean, and chickpea, *Lupinus*, e.g., lupine, trifolium, *Phaseolus*, e.g., common bean and lima bean, *Pisum*, e.g., field
 20 bean, *Melilotus*, e.g., clover, *Medicago*, e.g., alfalfa, Lotus, e.g., trefoil, lens, e.g., lentil, and false indigo, and the like; and ornamental crops including Impatiens, Begonia, Petunia, Pelargonium, Viola, Cyclamen, Verbena, Vinca, Tagetes, Primula, Saint Paulia, Ageratum, Amaranthus, Anthirrhinum, Aquilegia, Chrysanthemum, Cineraria, Clover, Cosmo, Cowpea, Dahlia, Datura,
 25 Delphinium, Gerbera, Gladiolus, Gloxinia, Hippeastrum, Mesembryanthemum, Salpiglossis, Zinnia, and the like. Preferably, the host cells are monocot cells such as maize, rice, wheat, barley, oats, and sorghum, which can be regenerated into a transgenic plant.

30 IV. Identification of Transgenic Plants

To confirm the presence of the preselected nucleic acid segment(s) or "transgene(s)" in the regenerating plants, a variety of assays may be performed. Such assays include, for example, "molecular biological" assays well known to those of skill in the art, such as Southern and Northern blotting, *in situ*

hybridization and nucleic acid-based amplification methods such as PCR or RT-PCR; "biochemical" assays, such as detecting the presence of a protein product, e.g., by immunological means (ELISAs and Western blots) or by enzymatic function; plant part assays, such as leaf or root assays; and also, by analyzing the
5 phenotype of the whole regenerated plant, e.g., for disease or pest resistance.

DNA may be isolated from cell lines or any plant parts to determine the presence of the preselected nucleic acid segment through the use of techniques well known to those skilled in the art. Note that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

10 The presence of nucleic acid elements introduced through the methods of this invention may be determined by polymerase chain reaction (PCR). Using this technique discreet fragments of nucleic acid are amplified and detected by gel electrophoresis. This type of analysis permits one to determine whether a preselected nucleic acid segment is present in a stable transformant, but does not
15 prove integration of the introduced preselected nucleic acid segment into the host cell genome. In addition, it is not possible using PCR techniques to determine whether transformants have exogenous genes introduced into different sites in the genome, i.e., whether transformants are of independent origin. It is contemplated that using PCR techniques it would be possible to clone fragments
20 of the host genomic DNA adjacent to an introduced preselected DNA segment.

Positive proof of DNA integration into the host genome and the independent identities of transformants may be determined using the technique of Southern hybridization. Using this technique specific DNA sequences that were introduced into the host genome and flanking host DNA sequences can be
25 identified. Hence the Southern hybridization pattern of a given transformant serves as an identifying characteristic of that transformant. In addition it is possible through Southern hybridization to demonstrate the presence of introduced preselected DNA segments in high molecular weight DNA, i.e., confirm that the introduced preselected DNA segment has been integrated into
30 the host cell genome. The technique of Southern hybridization provides information that is obtained using PCR, e.g., the presence of a preselected DNA segment, but also demonstrates integration into the genome and characterizes each individual transformant.

It is contemplated that using the techniques of dot or slot blot hybridization which are modifications of Southern hybridization techniques one could obtain the same information that is derived from PCR, e.g., the presence of a preselected DNA segment.

5 Both PCR and Southern hybridization techniques can be used to demonstrate transmission of a preselected DNA segment to progeny. In most instances the characteristic Southern hybridization pattern for a given transformant will segregate in progeny as one or more Mendelian genes (Spencer et al., 1992); Laursen et al., 1994) indicating stable inheritance of the gene. The
10 nonchimeric nature of the callus and the parental transformants (R_0) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus, R_0 plants and R_1 progeny that segregated for the transformed gene.

Whereas DNA analysis techniques may be conducted using DNA isolated
15 from any part of a plant, RNA may only be expressed in particular cells or tissue types and hence it will be necessary to prepare RNA for analysis from these tissues. PCR techniques may also be used for detection and quantitation of RNA produced from introduced preselected DNA segments. In this application of PCR it is first necessary to reverse transcribe RNA into DNA, using enzymes
20 such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique will demonstrate the presence of an RNA species and give information
25 about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and will only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the preselected
30 DNA segment in question, they do not provide information as to whether the preselected DNA segment is being expressed. Expression may be evaluated by specifically identifying the protein products of the introduced preselected DNA segments or evaluating the phenotypic changes brought about by their expression.

Assays for the production and identification of specific proteins may make use of physical-chemical, structural, functional, or other properties of the proteins. Unique physical-chemical or structural properties allow the proteins to be separated and identified by electrophoretic procedures, such as native or
5 denaturing gel electrophoresis or isoelectric focussing, or by chromatographic techniques such as ion exchange or gel exclusion chromatography. The unique structures of individual proteins offer opportunities for use of specific antibodies to detect their presence in formats such as an ELISA assay. Combinations of approaches may be employed with even greater specificity such as Western
10 blotting in which antibodies are used to locate individual gene products that have been separated by electrophoretic techniques. Additional techniques may be employed to absolutely confirm the identity of the product of interest such as evaluation by amino acid sequencing following purification. Although these are among the most commonly employed, other procedures may be additionally
15 used.

Assay procedures may also be used to identify the expression of proteins by their functionality, especially the ability of enzymes to catalyze specific chemical reactions involving specific substrates and products. These reactions may be followed by providing and quantifying the loss of substrates or the
20 generation of products of the reactions by physical or chemical procedures. Examples are as varied as the enzyme to be analyzed.

Very frequently the expression of a gene product is determined by evaluating the phenotypic results of its expression. These assays also may take many forms including but not limited to analyzing changes in the chemical
25 composition, morphology, or physiological properties of the plant. Morphological changes may include greater stature or thicker stalks. Most often changes in response of plants or plant parts to imposed treatments are evaluated under carefully controlled conditions termed bioassays.

30 V. Utility

Once an expression cassette of the invention has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. Particularly preferred plants of the invention

include the agronomically important crops listed above. The genetic properties engineered into the transgenic seeds and plants described above are passed on by sexual reproduction and can thus be maintained and propagated in progeny plants. The present invention also relates to a transgenic plant cell, tissue, organ, seed or plant part obtained from the transgenic plant. Also included within the invention are transgenic descendants of the plant as well as transgenic plant cells, tissues, organs, seeds and plant parts obtained from the descendants.

Preferably, the expression cassette in the transgenic plant is sexually transmitted. In one preferred embodiment, the coding sequence is sexually transmitted through a complete normal sexual cycle of the R0 plant to the R1 generation. Additionally preferred, the expression cassette is expressed in the cells, tissues, seeds or plant of a transgenic plant in an amount that is different than the amount in the cells, tissues, seeds or plant of a plant which only differs in that the expression cassette is absent.

The transgenic plants produced herein are thus expected to be useful for a variety of commercial and research purposes. Transgenic plants can be created for use in traditional agriculture to possess traits beneficial to the grower (e.g., agronomic traits such as resistance to water deficit, pest resistance, herbicide resistance or increased yield), beneficial to the consumer of the grain harvested from the plant (e.g., improved nutritive content in human food or animal feed), or beneficial to the food processor (e.g., improved processing traits). In such uses, the plants are generally grown for the use of their grain in human or animal foods. However, other parts of the plants, including stalks, husks, vegetative parts, and the like, may also have utility, including use as part of animal silage or for ornamental purposes. Often, chemical constituents (e.g., oils or starches) of maize and other crops are extracted for foods or industrial use and transgenic plants may be created which have enhanced or modified levels of such components.

Transgenic plants may also find use in the commercial manufacture of proteins or other molecules, where the molecule of interest is extracted or purified from plant parts, seeds, and the like. Cells or tissue from the plants may also be cultured, grown *in vitro*, or fermented to manufacture such molecules.

The transgenic plants may also be used in commercial breeding programs, or may be crossed or bred to plants of related crop species. Improvements

encoded by the expression cassette may be transferred, e.g., from maize cells to cells of other species, e.g., by protoplast fusion.

The transgenic plants may have many uses in research or breeding, including creation of new mutant plants through insertional mutagenesis, in order to identify beneficial mutants that might later be created by traditional mutation and selection. An example would be the introduction of a recombinant DNA sequence encoding a transposable element that may be used for generating genetic variation. The methods of the invention may also be used to create plants having unique "signature sequences" or other marker sequences which can be used to identify proprietary lines or varieties.

Thus, the transgenic plants and seeds according to the invention can be used in plant breeding which aims at the development of plants with improved properties conferred by the expression cassette, such as tolerance of viruses or other pests, or other stresses. The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate descendant plants. Depending on the desired properties different breeding measures are taken. The relevant techniques are well known in the art and include but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also include the sterilization of plants to yield male or female sterile plants by mechanical, chemical or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both parental lines. Thus, the transgenic seeds and plants according to the invention can be used for the breeding of improved plant lines which for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance can be obtained which, due to their optimized genetic "equipment", yield harvested product of better quality than products which were not able to tolerate comparable adverse developmental conditions.

VI. A Computer Readable Medium

The invention also provides a computer readable medium having stored thereon a data structure containing nucleic acid sequences having at least 70% sequence identity to a nucleic acid sequence selected from those listed in SEQ ID Nos: 1-795 as well as complementary, ortholog, and variant sequences thereof. Storage and use of nucleic acid sequences on a computer readable medium is well known in the art. (See for example U.S. Patent Nos. 6,023,659; 5,867,402; 5,795,716) Examples of such medium include, but are not limited to, magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory. Accordingly, the nucleic acid sequences contained on the computer readable medium may be compared through use of a module that receives the sequence information and compares it to other sequence information. Examples of other sequences to which the nucleic acid sequences of the invention may be compared include those maintained by the National Center for Biotechnology Information (NCBI)(<http://www.ncbi.nlm.nih.gov/>) and the Swiss Protein Data Bank. A computer is an example of such a module that can read and compare nucleic acid sequence information. Accordingly, the invention also provides the method of comparing a nucleic acid sequence of the invention to another sequence. For example, a sequence of the invention may be submitted to the NCBI for a Blast search as described herein where the sequence is compared to sequence information contained within the NCBI database and a comparison is returned. The invention also provides nucleic acid sequence information in a computer readable medium that allows the encoded polypeptide to be optimized for a desired property. Examples of such properties include, but are not limited to, increased or decreased: thermal stability, chemical stability, hydrophylicity, hydrophobicity, and the like. Methods for the use of computers to model polypeptides and polynucleotides having altered activities are well known in the art and have been reviewed. (Lesyng et al., 1993; Surles et al., 1994; Koehl et al., 1996; Rossi et al., 2001).

The invention will be further described by the following examples which is not intended to limit the scope of the invention.

Example 1GeneChip Standard ProtocolQuantitation of total RNA

Total RNA from plant tissue is extracted and quantified.

- 5 1. Quantify total RNA using GeneQuant

1 OD₂₆₀=40 mg RNA/ml; A260/A280=1.9 to about 2.1

2. Run gel to check the integrity and purity of the extracted RNA

Synthesis of double-stranded cDNA

- 10 Gibco/BRL SuperScript Choice System for cDNA Synthesis (Cat#1B090-019)

was employed to prepare cDNAs. T7-(dT)₂₄ oligonucleotides were prepared

and purified by HPLC. (5'-

- 15 GGCCAGTGAATTGTAATACGACTCACTATAGGGAGGCGG-(dT)₂₄-3'(SEQ ID NO:800).

Step 1. Primer hybridization:

Incubate at 70°C for 10 minutes

Quick spin and put on ice briefly

- 20 Step 2. Temperature adjustment:

I Incubate at 42°C for 2 minutes

Step 3. First strand synthesis:

DEPC-water- 1 µl

RNA (10 µg final)-10 µl

- 25 T7=(dT)₂₄ Primer (100 pmol final)-1 µl pmol

5X 1st strand cDNA buffer-4 µl

0.1M DTT (10 mM final)- 2 µl

10 mM dNTP mix (500 µM final)-1 µl

Superscript II RT 200 U/µl- 1 µl

- 30 Total of 20 µl

Mix well

Incubate at 42°C for 1 hour

Step 4. Second strand synthesis:

Place reactions on ice, quick spin

- DEPC-water- 91 μ l
 5X 2nd strand cDNA buffer- 30 μ l
 mM dNTP mix (250 mM final) - 3 μ l
E. coli DNA ligase (10 U/ μ l)-1 μ l
 5 *E. coli* DNA polymerase 1-10 U/ μ l- 4 μ l
 RnaseH 2U/ μ l -1 μ l
 T4 DNA polymerase 5 U/ μ l-2 μ l
 0.5 M EDTA (0.5 M final)--10 μ l
 Total 162 μ l
 10 Mix/spin down/incubate 16°C for 2 hours

Step 5. Completing the reaction:

Incubate at 16°C for 5 minutes

Purification of double stranded cDNA

- 15 1. Centrifuge PLG (Phase Lock Gel, Eppendorf 5 Prime, Inc., PI-188233)
 at 14,000X, transfer 162 μ l of cDNA to PLG
 2. Add 162 μ l of Phenol:Chloroform:Isoamyl alcohol (pH 8.0), centrifuge
 2 minutes
 3. Transfer the supernatant to a fresh 1.5 ml tube, add
 20 Glycogen (5 mg/ml) 2
 0.5 M NH₄OAC (0.75xVol) 120
 ETOH (2.5xVol, -20 °C) 400
 4. Mix well and centrifuge at 14,000X for 20 minutes
 5. Remove supernatant, add 0.5 ml 80% EtOH (-20°C)
 25 6. Centrifuge for 5 minutes, air dry or by speed vac for 5-10 minutes
 7. Add 44 μ l DEPC H₂O

Analyze of quantity and size distribution of cDNA

Run a gel using 1 μ l of the double-stranded synthesis product

30 Synthesis of biotinylated cRNA

(use Enzo BioArray High Yield RNA Transcript Labeling Kit Cat#900182)

- Purified cDNA 22 μ l
 10X Hy buffer 4 μ l
 10X biotin ribonucleotides 4 μ l

10X DTT	4 μ l
10X Rnase inhibitor mix	4 μ l
<u>20X T7 RNA polymerase</u>	<u>2 μl</u>
Total	40 μ l

- 5 Centrifuge 5 seconds, and incubate for 4 hours at 37°C
Gently mix every 30-45 minutes

Purification and quantification of cRNA

(use Qiagen Rneasy Mini kit Cat# 74103)

- 10 Determine concentration and dilute to 1 μ g/ μ l concentration

Fragmentation of cRNA

cRNA (1 μ g/ μ l)	15 μ l
5X Fragmentation Buffer*	6 μ l
15 DEPC H ₂ O	<u>9 μl</u>
	30 μ l

*5x Fragmentation Buffer

1M Tris (pH8.1)	4.0 ml
20 MgOAc	0.64 g
KOAc	0.98 g
DEPC H ₂ O	
Total	20 ml
Filter Sterilize	

25

Array wash and staining

Stringent Wash Buffer**

Non-Stringent Wash Buffer***

SAPE Stain****

- 30 Antibody Stain*****

Wash on fluidics station using the appropriate antibody amplification protocol

**Stringent Buffer: 12X MES 83.3 ml, 5 M NaCl 5.2 ml, 10% Tween 1.0 ml, H₂O 910 ml,

Filter Sterilize

***Non-Stringent Buffer: 20X SSPE 300 ml, 10% Tween 1.0 ml, H₂O 698 ml,
Filter Sterilize, Antifoam 1.0.

****SAPE stain: 2X Stain Buffer 600 µl, BSA 48 µl, SAPE 12µl, H₂O 540 µl.

5 *****Antibody Stain: 2X Stain Buffer 300 µl, H₂O 266.4 µl, BSA 24 ul, Goat
IgG 6 µl, Biotinylated Ab 3.6 µl

Example 2Identification of *Arabidopsis* Genes Induced by *Peronospora* Infection

10

To define the transcriptional profile for *Peronospora*-induced and/or *RPP7*- and *RPP8*- dependent genes, four *Arabidopsis* lines were infected with one of two different *P. parasitica* isolates (see Table 2). One *Arabidopsis* line was Col-0::*RPP8* which carries the cloned *RPP8* genomic clone (*RPP8* mediates resistance of the ecotype La-er against Emco5; McDowell et al. 1998) and is
15 Emco5 resistant. Wild-type Col-0 plants are Emco5 susceptible. *RPP7* mediates resistance of *Arabidopsis* against the *Peronospora* isolate Hiks1, and occurs naturally in Col-0. Another *Arabidopsis* line had a loss of function *rpp7* mutant allele (Col-0 (*rpp7*)) (McDowell et al., 2000). Finally, three mutants in the
20 signaling pathway for *RPP7*, i.e., they lack a *RPP7*-mediated response, were identified, i.e., *edm1*, *edm2* and *edm3*, and a line with one of the mutant alleles, i.e., *edm1*, was used.

RNA samples were collected from two week old seedlings at three time points, 0, 12 and 24 hours post infection with 100,000 spores/ml. Twelve hours
25 post-inoculation was determined to be an appropriate time point for analysis of both incompatible interactions, based on trypan blue staining of HR sites and *PR-1* and *sen1* induction. Forty-eight hours post-inoculation was determined to be a time point where both compatible interactions exhibit dense hyphal growth and both *PR-1* and *sen1* expression. Three independent sets of RNA were
30 pooled.

Table 2

<u>Plant</u>	<u><i>Peronospora</i> isolate</u>	<u>Time of RNA collection</u>
Col-0 (<i>RPP7</i> , <i>incomp.</i>)	Hiks1	0, 12, 48 hours
35 Col-0 (<i>rpp7</i> , <i>comp.</i>)	Hiks1	0, 12, 48 hours

Col-0 (<i>edm1, comp.</i>)	Hiks1	0, 12, 48 hours
Col-0 (<i>tgRPP8, incomp.</i>)	Emco5	0, 12, 48 hours
Col-0 (<i>rpp8, comp.</i>)	Emco5	0, 12, 48 hours

5 RNAs were labeled as described in Example 1 and hybridized to an Affymetrix Gene Chip having sequences corresponding to about 8,200 *Arabidopsis* genes. The data collected from these chips was employed to determine:

- 1) the difference, if any, between *RPP7* and *RPP8* triggered signaling (and how these profiles compare to other profiles, for example, to the profiles of *RPM1* and *RPS2*);
- 2) which portion of the transcriptional response is *R* dependent;
- 3) which genes are either commonly or uniquely induced during two different compatible interactions;
- 4) which genes are specifically activated during the incompatible interactions (gleaned by comparison with isogenic compatible controls) and, hence, may be important for the plant's defense against *Peronospora*;
- 5) which genes whose expression is a prerequisite for induced defense reactions against *Peronospora*; and
- 6) which genes are specifically repressed during the incompatible interactions, which may be required for successful Oomycete infections.

Results

Genes Expressed Early and Transiently After Infection

The normalized "average difference" (AD) from the chip experiments were processed as follows. All values together with the respective gene identifiers were loaded in EXCEL. Genes having, for a given treatment, AD values of 25 or less were considered as being not expressed. To reduce spurious background fluctuation, this cut off level was elevated to 75 for most of the analyses and normalized all AD values of 75 or less. For all five infection time courses, the AD values were divided by the corresponding 0 hour time point AD value. To visualize differences in gene expression ground states between the four experimental *Arabidopsis* lines, the following ratios were calculated for the 0 hour AD values: Col-0 (from Emco5 series)/Col-0-*RPP8* and *rpp7*/Col-0 (from Hiks1 series) and *edm1*/Col-0 (from Hiks1 series). These ratios indicate whether

a given gene is up- or down-regulated by the *RPP7* or *RPP8* pathway, respectively. The resulting set of 18 expression ratio series was then loaded into CLUSTER (Eisen et al., 1998). The AD values were log transformed (base 2) and filtered to include only genes in the final data set that showed at least a 3-
 5 fold expression change (which equals a 1.6-fold change of the log transformed values). These criteria were fulfilled by 464 genes that define the final data set. With this data set Average linkage clustering was performed (uncentered correlation). The resulting clustergram was displayed using TREEVIEW (Eisen et al., 1998). A second clustergram was generated in the same way applying a cut
 10 off value of 50 on the normalized AD values. This clustergram includes 619 genes (probe sets).

Based on these clustergrams, gene clusters showing distinct expression behaviors were defined. Cluster cR7/R8 (see Table 3) contained genes that are early and transiently upregulated early and transiently after *P. parasitica*
 15 infection of *Arabidopsis* in an *RPP7/8* dependent manner. Upregulation by the *RPP8* pathway was generally stronger. Strong induced expression of cR7/R8 genes was detectable 12 hours after Emco5 infection in Col-0(*tgRPP8*) plants (incompatible interaction), whereas no elevated expression can be observed 48 hours post infection in the same plants (as compared to untreated control plants).
 20 Only weakly elevated or no elevated expression was detected at all tested time points in Col-0 plants (compatible interaction). After Hiks1 infection, elevated expression of these genes was only observed in Col-0 plants (incompatible interaction) after 12 hours. At no other time point following Hiks1 infection was substantially elevated expression of these genes observed. The expression ground
 25 state of these genes is similar in all four *Arabidopsis* lines.

Table 3

20245 s at	cut off = 75
18716 At	
18022 at	
14609 at	
17014 s at	
17051 s at	
19640 at	
14248 at	
13176 _at	

15978 at cut off +50
 17014 s at
 14609 at
 13764 at
 16649 s at Subcluster A
 13215 s at
 17653 at
 17008 at
 15042 at
 12778_r_at

14614 at
 17051 s at
 14248 at Subcluster B
 20245 s at
 19640 at
 18716 at
 18022_at

17500 s at
 13217 s at
 18928 at

The cR7/R8 cluster was originally defined using the clustergram based on a cut off value of 75 and comprised only 9 genes. Applying a cut off value of 50, the cluster became larger, comprising 21 genes, which could be divided into two subclusters (Table 4). Subcluster cR7/R8 A includes genes strongly and transiently upregulated by the *RPP8* pathway, but either not, or only faintly, upregulated by the *RPP7* pathway. Members of subcluster B showed pronounced upregulation by both *RPP* pathways after 12 hours and also elevated expression during compatible Emco5 infections in Col-0.

10

Table 4

<u>Subcluster A</u>	
<u>Gene-identifier (probe set)</u>	<u>Related to</u>
15978_at	X68592.6_at
17014_s_at*	atu05206_s_at
14609_at	AC002340.147_at
16649_s_at+	athorf_s_at
	CafferoylCoAmethyltrans_s_a
13215_s_at ⁺	t
17653_at	AL035679.144_at
17008_at	AC006585.212_at

15042_at	AL021961.3_at
12778_r_at	AC006577.16_r_at

Subcluster B

<u>Gene-identifier (probe set)</u>	<u>Related to</u>
14614_at	AC004165.66_at
17051_s_at	af098947_s_at
14248_at	PAD3_at
20245_s_at	AC005309.97_s_at
19640_at	AC004561.78_at
18716_at	X91916_at
18022_at	AJ010971_at
17500_s_at [†]	athcallga_s_at
13217_s_at [†]	calmodulinlike_s_at
18928_at	AC002333.181_at

*Genes printed in **bold** were identified using a cut off value of 75; all others were identified using a cut off value of 50.

[†]The probe sets 16649 and 13215 as well as 17500 and 13217 correspond to the same genes.

Thus, the predominant feature of genes of the cR7/R8 cluster is more pronounced expression along with *RPP7* and *RPP8* mediated *Peronospora* resistance in comparison to the corresponding compatible interactions. Expression of these genes peaks in around 12 hours post infection and returns to ground state by 48 hours post infection. Hence, increased transcript levels of these genes coincide with the time window of decision between disease or resistance. Within 48 hours after infection with each tested *Peronospora* isolate, the plant either responds with HR and hinders development of oomycete hyphae or allows successful infection.

Identification of Conserved Sequence Motifs Within cR7/R8 Upstream Regions

To identify potential *cis*-elements involved in the specific regulation of cR7/R8 genes, stretches comprising 1.1 to 1.2 kb localized directly upstream of the translation start sites of coding regions from this cluster were collected from genomic *Arabidopsis* sequences (see Figure 2). Two motif search algorithms were used to recognize conserved motifs: AlignAce (Roth et al., 1998) and MEME (Bailey and Elkan, 1994). A search with AlignAce (default settings) revealed two conserved motifs within a set of 8 promoters comprising 7 from the originally defined cR7R8 using a cut off value of 75 and the promoter of a gene encoding a putative Myb-like transcription factor (Martin & Paz-Ares, 1997)

(probe set 13176, SEQ ID NO:36), which shows a similar expression behavior as cR7/R8. The AlignAce output is shown below in Table 5:

Table 5

Motif 1	MAP Score:	SEQ ID NO.	Corresponding Probe Set
*****	6.87857		
CAACAATTAT	0 36 1	685	17014
CAACTATGTC	0 981 1	686	17014
CAACAATGAC	1 934 0	687	20245
CAACAATGAC	2 271 1	688	14609
AAACAATGAT	2 1184 1	689	14609
CAACATTGAC	3 163 0	690	17051
CAACATTGTT	3 298 0	691	17051
CAACAATGTT	4 613 1	692	19640
CAACTATGAT	4 791 0	693	19640
CAACAATGAT	4 1064 0	694	19640
CAAAAATGAT	7 397 0	695	17008
CAACATTGAT	7 415 1	696	17008
CATATCA/TA/TTGAC (Consensus)		697	N.A.

5

Motif 2	MAP Score:	SEQ ID NO.	Corresponding Probe Set
***** **	2.22382		
TTTGGGCAAAA	1 368 0	698	20245
GTTGGGTCAAA	1 739 0	699	20245
GATGGGCACAA	2 691 0	700	14609
GATGGGCCAAA	3 700 0	701	17051
GATGGGTATAA	4 344 0	702	19640
GATGGGACTAA	5 98 1	703	14248
TTTGGGCCTAA	5 971 1	704	14248
TATGGGCCCAA	5 1012 0	705	14248
CTTGGGACAAA	7 579 1	706	17008
GATGGGTCAAC	7 1009 0	707	17008
CATGGGAATAA	7 1072 1	708	17008
NATTGGGNC/ANAA (Consensus)		709	N.A.

For each motif, examples from cR7/R8 promoters are listed. Nucleotides evaluated by AlignAce as being conserved are indicated by a "*" above the examples. Besides motifs 1 and 2, a variety of additional ones were found by AlignAce, which, however, consisted almost exclusively of Ts and As. These motifs probably do not constitute functional *cis*-elements. Promoter sequences

10

are generally enriched in As or Ts (A/T content in cR7/R8 promoters is 70%) and regulatory *cis*-elements usually contain also Cs or Gs.

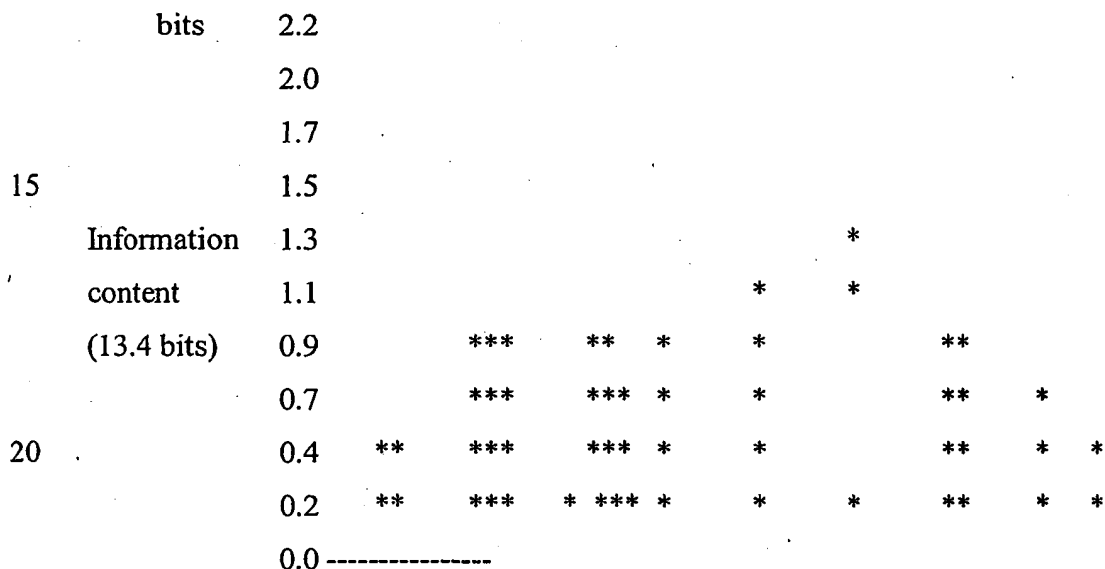
Motif 1 (CAACA/TA/TTGA/TC/T, SEQ ID NO:710) resembles the type I Myb binding site consensus (MBS;T/CAACT/GG), which is bound by animal
 5 and some plant Myb transcription factors (Yang & Klessig, 1996). The 3' portion of the motif 1 consensus allows overlap with binding sites of WRKY (TTTGACC/T; Eulgem et al., 2000) or TGA-bZIP transcription factors (TGACG; Schindler et al. 1992). Interestingly, a gene encoding a putative Myb-like transcription factor (gene identification number 13176) is upregulated along
 10 with cR7/R8 genes in an *RPP7/RPP8*-dependent, early and transient manner. The factor encoded by this gene may be a regulator of cR7/R8 genes. Motif 1 is particularly enriched in promoters of the originally defined cR7/R8 cluster (cut off = 75). This motif, which consists of six strictly defined positions and four positions allowing two base pairs each, should occur by random roughly once per
 15 20,000 bp in each of both possible orientations (assuming a T/A content of 70% and a G/C content of 30%. In the 8,441 bp of cR7/R8 promoter sequences, the motif occurs 9 times (roughly 20 times the statistically expected frequency). Consistent with the statistical expectation, motif 1 occurs only two times within
 15,873 bp from a set of control promoters of genes showing no defense related
 20 expression (data not shown).

In the extended set of cR7/R8 genes (cut off = 50), the enrichment of motif 1 is less striking. It occurs only 9 times within 16,519 bp in total and, more importantly, none of the promoters added to the set by lowering the cut off value contains this motif. Thus, if motif 1 is involved in the specific regulation
 25 of cR7/R8 genes it cannot alone be responsible for the particular expression features of these genes, and may rather be responsible for the more pronounced R7/R8-triggered expression of members of the originally defined cluster (cut off = 75).

Motif 2 (A/TTGGGNC/ANAA; SEQ ID NO:711) does not resemble any
 30 other known plant *cis*-element. The consensus sequence consists of six strictly defined positions, two positions with two alternatives and two positions with four alternatives; and, hence, should occur by random once per 10,000 bp. Motif 2 can be found 10 times within 8,441 bp of the promoters from the originally defined cR7/R8 (cut off = 75) and 14 times within 16,519 bp of the extended

cR7/R8 promoter set. Thus, its occurrence in cR7/R8 promoters is roughly 10 times the statistical expectation. Motif 2 is absent in the 15,873 bp of promoters of genes showing no defense related expression (data not shown). It is, however, also enriched in the promoters of previously defined clusters of defense related genes, such as the PR1 regulon (SAR genes) and SOMc3 (genes up regulated in Ws-0 after infection with avirulent Noco2; data not shown). The latter two clusters may also include genes sharing expression features with cR7/R8 genes. In addition to AlignAce, a motif 2-like sequence was also recognized by MEME. Within the extended set of cR7/R8 promoters, MEME found the following

10 sequence stretch to be conserved:



Multilevel Consensus sequence T/C TTT G/C A/T/G C/T

25 CCAAG/A/CAA/GAC/A (SEQ ID NO:712)

The reverse complement of this consensus sequence is (positions with three alternatives were given as "N") given below with motif 2 for comparison:

30 MEME motif: G/T T C/T T N T T G G G N G/C A A A A/C (SEQ ID NO:713)

Motif 2: T G G G N A N/C A A (SEQ ID NO:714)

MEME was run using the default settings of “advanced MEME” choosing the options “one motif per sequence”, “narrow motifs” and “additional strand: reverse complement”.

To confirm these results, Northern blots using probes of representatives of each cluster are performed. In addition, T-DNA lines are screened for knock out in Myb-like gene (AL031394.56_at) and selected members of cR7/R8, such as RNS1 (atu05206_s_at) or the gene encoding a calmodulin-like protein (identification number 13217_s_at). Also, yeast one hybrid screens are performed to clone transcription factors binding to motifs 1 and 2, or other identified motifs. Transgenic *Arabidopsis* plants carrying fusions of GUS with a representative promoter from cR7/R8 can be used to further evaluate the functional significance of motifs 1 and 2, and to perform a genetic screening for mutants impaired in regulation of cR7/R8 genes.

15 Genes Induced by *Peronospora* Infection in a Manner that Requires RPP7 or RPP8

The data sets described above were employed to identify genes that were induced by *Peronospora* infection and were RPP7/8-dependent. All expression values less than 5 were set to 5. Using ratios calculated in Excel, and database sorting using Access, a subset of genes was identified whose expression depends on RPP7 or RPP8 using the following criteria:

Col Hiks1 12 hour/Col untreated > 2.5 AND Col Hiks1 12 hour > 30
AND Col Hiks1 12 hour/Col rpp7 Hiks1 12 hour > 2
OR
25 Col Hiks1 48 hour/Col untreated > 2.5 AND Col Hiks1 48 hour > 30
AND Col Hiks1 48 hour/Col rpp7 Hiks1 48 hour > 2
OR
Col RPP8 Emco5 12 hour/Col RPP8 no treatment > 2.5 AND Col RPP8
Emco5 12 hour > 30 AND Col RPP8 Emco5 12 hour/Col (rpp8) Emco5
30 12 hour > 2
OR
Col RPP8 Emco5 48 hour/Col RPP8 no treatment AND Col RPP8
Emco5 48 hour > 30 AND Col RPP8 Emco5 48 hour/Col (rpp8) Emco5
48 hour > 2

This yielded 217 probe sets ("RPP7 or 8") which correspond to sequences, the expression of which were increased by at least 2.5 fold and were *RPP7*- or *RPP8*-dependent (Table 6).

5

Table 6

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
12630_at (AF024504.13_AT)	gb AAFI8681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]

12777_i_at (AC006577.16_I_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12779_f_at (AC006577.16_F_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
12989_s_at (AC004077.149_S_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]

13154_s_at (AC002333.210_S_AT)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13697_at (NI16_AT)	No hits found.

13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14096_at (AC002291.12_AT)	No hits found. emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14110_i_at (AL035528.279_I_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	
14141_at (NOVARTIS31_AT)	No hits found less than or equal to 1e-15. dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14145_at (NOVARTIS35_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
14146_at (NOVARTIS36_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	
14201_at (NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15. emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
14223_at (NOVARTIS9_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
14232_at (NOVARTIS95_AT)	

14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from <i>Arabidopsis thaliana</i> and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [<i>Arabidopsis thaliana</i>]
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [<i>Arabidopsis thaliana</i>]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [<i>Arabidopsis</i>
14256_f_at (PAL1-INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [<i>Arabidopsis thaliana</i>]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [<i>Arabidopsis thaliana</i>]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [<i>Arabidopsis</i> <i>thaliana</i>]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [<i>Arabidopsis thaliana</i>]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [<i>Arabidopsis thaliana</i>]
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [<i>Arabidopsis thaliana</i>]
14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [<i>Arabidopsis thaliana</i>]
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [<i>Arabidopsis thaliana</i>]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [<i>Arabidopsis thaliana</i>]
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [<i>Arabidopsis</i> <i>thaliana</i>]
14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [<i>Arabidopsis thaliana</i>]
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [<i>Arabidopsis thaliana</i>]
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [<i>Arabidopsis thaliana</i> <i>thaliana</i>]
14682_i_at (WT1012A_RC_I_AT)	No hits found.
14691_at (WT1096_AT)	No hits found.

14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15.
14763_at (X86958.1_AT)	emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAD28243.1 (AF121356_1) (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]

15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16150_s_at (ATHPEAR_S_AT)	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
16357_at (AF149413.38_AT)	gb AAD40144.1 AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucine rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16365_at (AC003974.136_AT)	gb AAC04495.1 (AC003974) putative disease resistance protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
16817_s_at (AL096882.91_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]
17068_s_at (ATHRLPKA_S_AT)	gb AAA32857.1 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17413_s_at (AJ006961.4_S_AT)	emb CAA67551.1 (X99097) peroxidase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]

17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
17499_s_at (AF107726_S_AT)	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
17500_s_at (ATHCALLGA_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17775_at (AC004392.2_AT)	gb AAC28500.1 (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	emb CAB52675.1 (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAB87112.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

18590_at (AJ222713.4_AT)	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana] gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	gb AAC33239.1 (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
18969_g_at (AF163823.4_G_AT)	emb CAB41722.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
19158_at (X95738.2_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	

19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20232_s_at (AL022347.12_S_AT)	emb CAA18460.1 (AL022347) protein kinase-like protein [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate

	synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1 (AC005896) putative C2H2- type zinc finger protein [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]

The functions of RPP7 and RPP8 are independent of *PAD4*, *NDR1*, *NahG*, *COI1*, and *EDS1*. Consequently, it is unlikely that genes whose expression is reduced in *pad4* or *NahG* backgrounds are important for RPP7- or RPP8- mediated resistance. Although data from *Peronospora* infection of *pad4* or *nahG* plants was not available, data from *Pseudomonas syringae* (ES4326) infection of *pad4* and *NahG* plants was available and employed to determine which genes depended on *PAD4* or were interfered with by *NahG*. Resistance to *P. syringae* mediated by *RPS2* requires *NDR1* function. Genes whose expression requires *RPS2* are less likely to be important for RPP7 or RPP8 mediated resistance than genes whose expression is independent of *RPS2*. Gene expression data was available for wild-type plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, and *rps2* mutant plants infected with *Pseudomonas syringae* pv. tomato DC3000 *avrRpt2*, 6 hours after infection.

EDM1 is required for resistance mediated by RPP7. Thus, genes whose expression requires *EDM1* are likely to be important for RPP7-mediated resistance. Gene expression data was available for an *edm1* mutant (see above).

The data from the 7 additional data sets (Col Psm ES4326 30 hour; Col Mock 30 hour; Col *NahG* Psm ES4226 30 hour; Col *pad4* Psm ES4326 30 hour; Col water control; Col DC3000 *avrRpt2* and *rps2* DC3000 *avrPrt2* was added to the 217 probe sets in "RPP7 or 8". The following sets were identified:

edm1:

Col edm1 Hiks1 12 hour/Col Hiks1 12 hour < 0.5 OR Col edm1 Hiks1
48 hour/Col Hiks1 48 hour < 0.5.

rps2:

- 5 Col DC3000 *avrRpt2* 6 hour/Col water control > 2 AND *rps2* DC3000
avrRpt2 6 hour/Col DC3000 *avrRpt2* 6 hour < 0.5.

pad4 or NahG:

- 10 Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col pad4 Psm
ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

OR

Col Psm ES4326 30 hour/Col Mock 30 hour > 2 AND Col NahG Psm
ES4326 30 hour/Col Psm ES4326 30 hour < 0.5.

- 15 There are 8 possible combinations of these three sets. Access was used to divide
the 217 probe sets into 8 sets, numbered 2-9 (considering the whole set of 217
probe sets as set 1) as shown in Tables 7 and 8:

Table 7

20	<u>Set</u>	<u>Content</u>	<u>Number of probe</u>
		<u>sets</u>	
	2	RPP7 or 8 not edm1 not rps2 not pad4 or NahG	62 probe sets
	3	edm1 not rps2 not pad4 or NahG	50 probe sets
	4	rps2 not edm1 not pad4 or NahG	14 probe sets
25	5	pad4 or NahG not edm1 not rps2	21 probe sets
	6	edm1 and rps2 not pad4 or NahG	23 probe sets
	7	edm1 and pad4 or NahG not rps2	25 probe sets
	8	rps2 and pad4 or NahG not edm1	8 probe sets
	9	edm1 and rps2 and pad4 or NahG	<u>14 probe sets</u>
30	Total		217 probe sets

Table 8

2 RPP7 or 8 not edm1 not rps2
not pad4 or NahG

ProbeSet	Description
12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
12777_i_at (AC006577.16_I_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSDL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12779_f_at (AC006577.16_F_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSDL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana]
13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
13696_at (NI115_AT)	No hits found less than or equal to 1e-15.
13880_s_at (AL049480.183_S_AT)	emb CAB39611.1 (AL049480) possible apospory-associated like protein [Arabidopsis thaliana]
13966_at (AL022023.172_AT)	emb CAA17775.1 (AL022023) putative protein [Arabidopsis thaliana]
14111_s_at (AL035528.279_S_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]

14145_at (NOVARTIS35_AT)	dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
14256_f_at (PAL1-INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
15042_at (AL021961.3_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
15523_s_at (AL078637.213_S_AT)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
16083_s_at (AF153283_S_AT)	gb AAD34615.1 AF153283_1 (AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]
16257_at (AC004138.105_AT)	gb AAC32915.1 (AC004138) putative nucleoside triphosphatase [Arabidopsis thaliana]
16298_at (AL021890.71_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
16299_at (AL024486.185_AT)	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
16522_at (X77500.2_AT)	emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]
16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
17051_s_at (AF098947_S_AT)	gb AAD09952.1 (AF098947) CTF2B [Arabidopsis thaliana]

17083_s_at (ATU18770_S_AT)	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
17464_at (AC000132.72_AT)	gb AAB60752.1 (AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475, gb ATTS4362 come from this gene. [Arabidopsis thaliana]
17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
18216_at (X95573.2_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18217_g_at (X95573.2_G_AT)	gb AAF24959.1 AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
18591_at (X74756.2_AT)	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]
18625_at (AC005278.22_AT)	gb AAC72125.1 (AC005278) ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene. [Arabidopsis thaliana]
18844_at (AC005315.131_AT)	gb AAC33239.1 (AC005315) putative ligand- gated ion channel protein [Arabidopsis thaliana]
18908_i_at (AF055848.2_I_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
18920_at (AC002338.11_AT)	gb AAC16927.1 (AC002338) putative laccase [Arabidopsis thaliana]
18983_s_at (AL049730.104_S_AT)	emb CAB41722.1 (AL049730) pEARLI 1- like protein [Arabidopsis thaliana]
19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

19982_at (AC002986.28_AT)	gb AAC17040.1 (AC002986) Similarity to A. thaliana gene product F21M12.20, gb AC000132. EST gb Z25651 comes from this gene. [Arabidopsis thaliana]
20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
20620_g_at (AC005896.161_G_AT)	gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]

Duplicates

12777 and 12779 (lipase)
 12889 and 20291 (ASA1)
 12908 and 16536 (ERF5)
 17464 and 19982 (RLK5)
 18216 and 18217 (T22C5.18)
 18908 and 18909 (subtilisin-like protease)
 20238 and 20239 (beta-fructofuranosidase)

3 edm1 without rps2 without pad4orNahG

ProbeSet	Description
12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]

	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
12500_s_at (AF081067.3_S_AT)	[Arabidopsis thaliana]
	gb AAC14413.1 (AF049236) unknown
12521_at (AF049236.28_AT)	[Arabidopsis thaliana]
	emb CAA57944.1 (X82624) SRG2At
12574_at (X82624.2_AT)	[Arabidopsis thaliana]
	gb AAD25772.1 AC006577_8 (AC006577)
	Belongs to the PF00657
	Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene. [Arabidopsis thaliana]
12778_r_at (AC006577.16_R_AT)	
	gb AAC63850.1 (U73786) ACC synthase
12891_at (ATACS6_AT)	[Arabidopsis thaliana]
	gb AAC63850.1 (U73786) ACC synthase
12892_g_at (ATACS6_G_AT)	[Arabidopsis thaliana]
	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2
12905_s_at (ATERF2_S_AT)	[Arabidopsis thaliana]
	gb AAC13947.1 (AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]
12916_s_at (ATHCOR1_S_AT)	
13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
13198_i_at (ATTS0190_I_AT)	
	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
13435_at (AF003102.3_AT)	
	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
13631_at (AC002387.185_AT)	
14096_at (AC002291.12_AT)	No hits found.
	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
14223_at (NOVARTIS9_AT)	
	gb AAF16756.1 AC010155_9 (AC010155)
14232_at (NOVARTIS95_AT)	F3M18.20 [Arabidopsis thaliana]
14254_s_at (PAL1-MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
14614_at (AC004165.66_AT)	
14691_at (WT1096_AT)	No hits found.
	gb AAA32835.1 (M96073)
	phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14838_s_at (M96073.6_S_AT)	
	gb AAB53975.1 (U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
15161_s_at (ATU90522_S_AT)	

15532_r_at (AL078637.191_R_AT)	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana] dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
15629_s_at (AB003280_S_AT)	gb AAB80922.1 (AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]
15665_s_at (AF022658_S_AT)	emb CAB45796.1 (AL080252) putative protein [Arabidopsis thaliana]
16232_s_at (AL080252.77_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
16609_s_at (AB008104_S_AT)	emb CAB51412.1 (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
16817_s_at (AL096882.91_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
16981_s_at (U35829.2_S_AT)	gb AAD23027.1 AC006585_22 (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
17008_at (AC006585.212_AT)	gb AAC48925.1 (U05206) ribonuclease [Arabidopsis thaliana]
17014_s_at (ATU05206_S_AT)	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
17500_s_at (ATHCALLGA_S_AT)	dbj BAA28538.1 (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
17522_s_at (D78606_S_AT)	emb CAB38823.1 (AL035679) putative protein [Arabidopsis thaliana]
17653_at (AL035679.144_AT)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
17744_s_at (AC004684.168_S_AT)	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
17843_s_at (AC002391.150_S_AT)	emb CAB52675.1 (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
18022_at (AJ010971_AT)	gb AAB87112.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
18551_at (AC002391.163_AT)	gb AAF26754.1 AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
18716_at (X91916_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
18946_at (Y11788.1_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
19171_at (AC002335.160_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
19177_at (X99923.1_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
19182_at (AL031804.245_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
19284_at (AC003028.196_AT)	

19672_at (AC005687.19_AT) gb|AAC36019.1| (AC005687) RAP2.6
[Arabidopsis thaliana]
19762_at (AL035527.204_AT) emb|CAB36812.1| (AL035527) peptide
transporter-like protein [Arabidopsis thaliana]
19892_at (AC005770.30_AT) gb|AAC79626.1| (AC005770) putative
protease inhibitor [Arabidopsis thaliana]
20232_s_at emb|CAA18460.1| (AL022347) protein
(AL022347.12_S_AT) kinase-like protein [Arabidopsis thaliana]
20429_s_at (Z97336.167_S_AT) emb|CAB10219.1| (Z97336) hypothetical
protein [Arabidopsis thaliana]
emb|CAA63012.1| (X91919) LEA76
homologue type1 [Arabidopsis thaliana]
Arabidopsis thaliana. ESTs gb|N97082,
gb|Z27056 and gb|Z29902 come from this
gene.
20641_at (X91919.1_AT)

Duplicates

12905 and 16609 (ERF2)

13188 and 16981 (thioredoxin h)

12891 and 12892 (ACC
synthase)

14838 (phosphoribosyl
anthranilate transferase) has a
duplicate in set 2 (14620).
Counted in set 2

14254 (PAL1) has a duplicate in
set 2 (14256) Counted in set 2.

12778 (lipase) has duplicates in
set 2 (12777 and 12779) Counted
in set 2.

4 rps2 without edm1 without pad4orNahG

ProbeSet

12278_at (AJ011674.2_AT)

Description

emb|CAA09731.1| (AJ011674) receptor-like
protein kinase, RLK3 [Arabidopsis thaliana]
emb|CAA18468.1| (AL022347)

serine/threonine kinase-like protein

12360_at (AL022347.131_AT)

[Arabidopsis thaliana]

13154_s_at

gb|AAB64047.1| (AC002333) putative

(AC002333.210_S_AT)

endochitinase [Arabidopsis thaliana]

gb|AAC31756.1| (U68017) heat shock

13273_s_at (HSF4_S_AT)

transcription factor 4 [Arabidopsis thaliana]

gb|AAD25552.1|AC005850_9 (AC005850)

Highly Similar to Mlo proteins [Arabidopsis

13685_s_at (MLOLIKE2_S_AT) thaliana]

14141_at (NOVARTIS31_AT) No hits found less than or equal to 1e-15.

15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
16053_i_at (Y14251.4_I_AT)	emb CAA74639.1 (Y14251) glutathione S-transferase [Arabidopsis thaliana]
16995_at (AC002391.188_AT)	gb AAB87114.1 (AC002391) unknown protein [Arabidopsis thaliana]
18054_at (AJ238846_AT)	emb CAB54517.1 (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
18224_s_at (AL021890.57_S_AT)	emb CAA17150.1 (AL021890) putative protein [Arabidopsis thaliana]
19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
20223_at (AL022347.145_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
20365_s_at (AC005850.19_S_AT)	gb AAD25552.1 AC005850_9 (AC005850). Highly Similar to Mlo proteins [Arabidopsis thaliana]

Duplicates

12360 and 20223 (serine threonine kinase)
13685 and 20365 (similar to Mlo)

5 pad4orNahG without rps2 without edm1

ProbeSet	Description
12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
13751_at (NOVARTIS127_AT)	gb AAF16751.1 AC010155_4 (AC010155) F3M18.8 [Arabidopsis thaliana]
13764_at (NOVARTIS22_AT)	gb AAD39641.1 AC007591_6 (AC007591) F9L1.6 [Arabidopsis thaliana]

14146_at (NOVARTIS36_AT)	gb AAD25550.1 AC005850_7 (AC005850) Hypothetical protein [Arabidopsis thaliana]
15778_at (X98676.2_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15779_g_at (X98676.2_G_AT)	emb CAA67234.1 (X98676) zinc finger protein [Arabidopsis thaliana]
15859_at (AC006587.164_AT)	gb AAD21491.1 (AC006587) unknown protein [Arabidopsis thaliana]
16360_at (AL031187.126_AT)	emb CAA20203.1 (AL031187) receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]
16578_s_at (ATHRPRP1B_S_AT)	emb CAB68132.1 (AL137080) beta-1, 3- glucanase 2 (BG2) [Arabidopsis thaliana]
16914_s_at (AL049500.57_S_AT)	emb CAB39936.1 (AL049500) osmotin precursor [Arabidopsis thaliana]
17097_s_at (ATU66345_S_AT)	gb AAC49697.1 (U66345) calreticulin [Arabidopsis thaliana]
17278_at (AC000107.5_AT)	gb AAD36959.1 AC000107_5 (AC000107) F17F8.5 [Arabidopsis thaliana]
17485_s_at (Z97340.345_S_AT)	emb CAB10405.1 (Z97340) beta-1, 3- glucanase class I precursor [Arabidopsis thaliana]
19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]

Duplicates:

15778 and 15779 (zinc finger
protein)

**6 edm1 and rps2 without
pad4orNahG**

ProbeSet

12630_at (AF024504.13_AT)
13100_at (AC003680.50_AT)
13115_at (AC000375.44_AT)
13187_i_at
(ATTHIRED4_I_AT)
13189_s_at
(ATTHIRED4_S_AT)

Description

gb|AAF18681.1|AF024504_11 (AF024504)
unknown protein [Arabidopsis thaliana]
gb|AAC06158.1| (AC003680) putative
cytochrome P450 [Arabidopsis thaliana]
gb|AAB60774.1| (AC000375) ESTs
gb|U75592,gb|T13956,gb|T43869 come from
from this gene. [Arabidopsis thaliana]
gb|AAC49356.1| (U35829) thioredoxin h
[Arabidopsis thaliana]
gb|AAC49356.1| (U35829) thioredoxin h
[Arabidopsis thaliana]

13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
13217_s_at (CALMODULINLIKE_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
14083_at (AC005662.56_AT)	gb AAC78535.1 (AC005662) putative embryo-abundant protein [Arabidopsis thaliana]
14116_at (AF077407.30_AT)	gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
14682_i_at (WT1012A_RC_I_AT)	No hits found.
15641_s_at (AF117063_S_AT)	gb AAD10829.1 (AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]
15978_at (X68592.6_AT)	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
16061_s_at (AB004796_S_AT)	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana]
16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
17511_s_at (AF067605_S_AT)	gb AAB71482.1 (AC002294) similar to S- linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
17899_at (Z97339.197_AT)	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]
18012_s_at (AJ002295_S_AT)	emb CAB59428.1 (AJ002295) inositol-1,4,5- trisphosphate 5-Phosphatase [Arabidopsis thaliana]

19640_at (AC004561.78_AT) gb|AAC95192.1| (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Duplicates

13187 and 13189 (thioredoxin h)
There are two duplicates of this in set 3 (13188 and 16981) Count it in set 3.

13215 and 16649 (putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase)
13285 and 16091 (heat shock protein 83)
13217 (calmodulin-like) has a duplicate in set 3 (17500). Count in set 3

16105 (hsf4) has a duplicate in set 4 (13273) Count in set 4

7 pad4orNahG and edm1 without rps2

ProbeSet	Description
14110_i_at (AL035528.279_I_AT)	emb CAB36854.1 (AL035528) putative disease resistance protein [Arabidopsis thaliana]
14148_at (NOVARTIS38_AT)	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
14709_at (WT788_AT)	No hits found less than or equal to 1e-15.
14882_at (AL022605.63_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
15616_s_at (ATHPRO25A_S_AT)	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]

15846_at (AC006067.63_AT) gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]
 15847_g_at (AC006067.63_G_AT) gb|AAD15461.1| (AC006067) unknown protein [Arabidopsis thaliana]
 15970_s_at (X71794.2_S_AT) emb|CAA50677.1| (X71794) peroxidase [Arabidopsis thaliana]
 16150_s_at (ATHPEAR_S_AT) emb|CAB41718.1| (AL049730) pEARLI 1 [Arabidopsis thaliana]
 16357_at (AF149413.38_AT) gb|AAD40144.1|AF149413_25 (AF149413) contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]
 16365_at (AC003974.136_AT) gb|AAC04495.1| (AC003974) putative disease resistance protein [Arabidopsis thaliana]
 17068_s_at (ATHRLPKA_S_AT) gb|AAA32857.1| (M84658) receptor-like protein kinase [Arabidopsis thaliana]
 17413_s_at (AJ006961.4_S_AT) emb|CAA67551.1| (X99097) peroxidase [Arabidopsis thaliana]
 17499_s_at (AF107726_S_AT) gb|AAD19610.1| (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
 17775_at (AC004392.2_AT) gb|AAC28500.1| (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb|AF020814 from Pisum sativum. [Arabidopsis thaliana]
 18590_at (AJ222713.4_AT) emb|CAA10955.1| (AJ222713) unnamed protein product [Arabidopsis thaliana]
 18968_at (AF163823.4_AT) gb|AAD45127.1|AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
 18969_g_at (AF163823.4_G_AT) gb|AAD45127.1|AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
 20287_at (Y14590.5_AT) emb|CAA74930.1| (Y14590) class IV chitinase [Arabidopsis thaliana]
 20288_g_at (Y14590.5_G_AT) emb|CAA74930.1| (Y14590) class IV chitinase [Arabidopsis thaliana]

Duplicates

14249 and 14250 (PAD4)

14704 and 15846 and 15847
(unknown protein)

18968 and 18969
(endoxyloglucan transferase)

20287 and 20288 (class IV chitinase)
 14110 (putative disease-resistance gene) is an incomplete probe set with very low signal. It has a duplicate (14111) in set 2. Count in set 2.
 14672 (trp synthase alpha) has a duplicate in set 2 (17487) Counted in set 2.

8 rps2 and pad4orNahG without edm1

ProbeSet	Description
13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
13818_s_at (AC006218.175_S_AT)	gb AAD15433.1 (AC006218) putative aspartate aminotransferase [Arabidopsis thaliana]
14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis-related PR-1-like protein [Arabidopsis thaliana]
17930_s_at (AJ006960.4_S_AT)	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]

Duplicates:

14635 and 17128 (PR-1)

9 edm1 and rps2 and pad4orNahG

ProbeSet	Description
12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]

12989_s_at (AC004077.149_S_AT) 13697_at (NI16_AT)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana] No hits found.
14201_at (NOVARTIS73_AT) 14202_at (NOVARTIS73_RC_AT)	No hits found less than or equal to 1e-15. No hits found less than or equal to 1e-15.
14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana] emb CAA50677.1 (X71794) peroxidase
14638_s_at (PRXCB_S_AT)	[Arabidopsis thaliana] emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
14763_at (X86958.1_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
15116_f_at (AF121356_F_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
17544_s_at (ATU40856_S_AT)	gb AAB64049.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
17840_s_at (AC002333.223_S_AT)	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
18567_at (AC004411.25_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
20269_at (AC002387.237_AT)	

Duplicates

12879 and 17544 (AIG1)

14201 and 14202 (Novartis 73)

14638 (peroxidase) has a
duplicate in set 7 (15970).
Counted in set 7.

The first set (set 2 above) do not require *EDM1* and are not affected by *rps2*, *pad4* or *NahG*. These genes are less likely to be important for resistance mediated by *RPP7* and *RPP8* than the genes in the second set (set 3 above). The

5 genes in the second set require *EDM1* but are not affected by *rps2*, *pad4* or *NahG*. These genes are more likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the third set (set 4 above) are affected by *rps2*, do not require *EDM1*, and are not affected by *pad4* or *NahG*. The genes in the

10 fourth (set 5 above), seventh (set 8 above) and eight (set 9 above) sets include genes that are affected by *pad4* or *NahG*, and so are less likely to be important for resistance mediated by *RPP7* and *RPP8*. The genes in the sixth set (set 7 above) require *RPP7* or *RPP8* for increased expression after infection by

Peronospora and are affected by *rps2*. These genes are also less likely to be important for resistance mediated by *RPP7* and *RPP8*.

Duplicates were identified by sorting "RPP7 or 8" by description, which put duplicated genes adjacent to one another. Most duplicates were in the same set, but there were nine cases of duplicates that had one probe set in one set, and another in another set. Examination of the data revealed that in these cases, the expression values were close to the cut-offs used to define the various sets. If one copy met the criteria, e.g., for *rps2*-dependent, but the other copy did not, the gene was classified as not *rps2*-dependent. Duplicates are noted. One hundred eighty four unique genes remained (SEQ ID NOs:1-211 and 792, Table 9 and Table 10).

Table 9

SEQ ID NO	ProbeSet	Description
1	12007_at (Z99708.249_AT)	emb CAB16829.1 (Z99708) putative protein [Arabidopsis thaliana]
2	12091_at (AC004450.116_AT)	gb AAC64313.1 (AC004450) unknown protein [Arabidopsis thaliana]
3	12115_at (AL033545.26_AT)	emb CAA22152.1 (AL033545) extensin-like protein [Arabidopsis thaliana]
4	12240_at (AL078579.130_AT)	emb CAB43974.1 (AL078579) putative protein [Arabidopsis thaliana]
5	12278_at (AJ011674.2_AT)	emb CAA09731.1 (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis thaliana]
6	12307_at (AC002392.162_AT)	gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis thaliana]
7	12332_s_at (AB023448.2_S_AT)	dbj BAA82810.1 (AB023448) basic endochitinase [Arabidopsis thaliana]
8	12341_s_at (AL021637.176_S_AT)	emb CAA16619.1 (AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
9	12349_s_at (X84728.6_S_AT)	gb AAA17993.1 (M91192) phenylalanine ammonia-lyase [Trifolium subterraneum]
10	12360_at (AL022347.131_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
11	20223_at (AL022347.145_AT)	emb CAA18468.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]

	12500_s_at (AF081067.3_S_AT)	gb AAC32192.1 (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
12	12521_at (AF049236.28_AT)	gb AAC14413.1 (AF049236) unknown [Arabidopsis thaliana]
13	12538_at (AF033205.2_AT)	gb AAC02973.1 (AF033205) putative pectin methylesterase [Arabidopsis thaliana]
14	12556_at (AL079344.155_AT)	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
15	12574_at (X82624.2_AT)	emb CAA57944.1 (X82624) SRG2At [Arabidopsis thaliana]
16	12630_at (AF024504.13_AT)	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
17	12642_at (AC006920.138_AT)	gb AAD22285.1 AC006920_9 (AC006920) unknown protein [Arabidopsis thaliana]
18		gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene.
19	12777_i_at (AC006577.16_I_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene.
20	12778_r_at (AC006577.16_R_AT)	gb AAD25772.1 AC006577_8 (AC006577) Belongs to the PF 00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb T44453, gb T04815, gb T45993, gb R30138, gb AI099570 and gb T22281 come from this gene.
21	12779_f_at (AC006577.16_F_AT)	[Arabidopsis thaliana]
22	12879_s_at (AIG1_S_AT)	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
23	17744_s_at (AC004684.168_S_A T)	gb AAC23646.1 (AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
24	12889_s_at (ASA1_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]
25	20291_s_at (M92353.4_S_AT)	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]

26	12891_at (ATACS6_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
27	12892_g_at (ATACS6_G_AT)	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
28	12905_s_at (ATERF2_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
29	16609_s_at (AB008104_S_AT)	dbj BAA32419.1 (AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]
30	12908_s_at (ATERF5_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
31	16536_s_at (AB008107_S_AT)	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]
32	12916_s_at (ATHCOR1_S_AT)	gb AAC13947.1 (AF021244) coronatine- induced protein 1 [Arabidopsis thaliana]
33	12933_r_at (ATPR1TAN_R_AT)	emb CAA65420.1 (X96600) pathogenesis- related protein 1 [Arabidopsis thaliana]
34	12989_s_at (AC004077.149_S_A T)	gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
35	13067_s_at (AC003114.16_S_AT)	gb AAC24083.1 (AC003114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana]
36	13100_at (AC003680.50_AT)	gb AAC06158.1 (AC003680) putative cytochrome P450 [Arabidopsis thaliana]
37	13115_at (AC000375.44_AT)	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]
38	13154_s_at (AC002333.210_S_A T)	gb AAB64047.1 (AC002333) putative endochitinase [Arabidopsis thaliana]
39	13176_at (AL031394.56_AT)	emb CAA20567.1 (AL031394) putative protein [Arabidopsis thaliana]
40	13187_i_at (ATTHIRED4_I_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
41	13188_r_at (ATTHIRED4_R_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
42	13189_s_at (ATTHIRED4_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
43	16981_s_at (U35829.2_S_AT)	gb AAC49356.1 (U35829) thioredoxin h [Arabidopsis thaliana]
44	13198_i_at (ATTS0190_I_AT)	emb CAA16892.1 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

45	13215_s_at (CAFFEROYLCOAMETHYLTRANS_S_AT) T)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
46	16649_s_at (ATHORF_S_AT)	gb AAF16576.1 AC012563_29 (AC012563) putative S-adenosyl-L-methionine:trans- caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]
47	13217_s_at (CALMODULINLIK E_S_AT)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
48	17500_s_at (ATHCALLGA_S_A T)	emb CAB42906.1 (AL049862) calmodulin- like protein [Arabidopsis thaliana]
49	13273_s_at (HSF4_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
50	16105_s_at (ATU68017_S_AT)	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
51	13277_i_at (HSP176A_I_AT)	emb CAA74399.1 (Y14070) Heat Shock Protein 17.6A [Arabidopsis thaliana]
52	13285_s_at (HSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
53	16091_s_at (ATHHSP83_S_AT)	gb AAA32822.1 (M62984) heat shock protein 83 [Arabidopsis thaliana]
54	13381_at (AC006580.8_AT)	gb AAD22369.1 AC006580_1 (AC006580) NAM (no apical meristem)-like protein [Arabidopsis thaliana]
	13435_at (AF003102.3_AT)	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
55	13588_at (AL021961.24_AT)	emb CAA17552.1 (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]
56	13627_at (AL035394.196_AT)	emb CAA23036.1 (AL035394) putative Na ⁺ /H ⁺ -exchanging protein [Arabidopsis thaliana]
57	13631_at (AC002387.185_AT)	gb AAB82634.1 (AC002387) putative transketolase precursor [Arabidopsis thaliana]
58	13659_at (AL022347.46_AT)	emb CAA18462.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
59	13685_s_at (MLOLIKE2_S_AT)	gb AAD25552.1 AC005850_9 (AC005850) Highly Similar to Mlo proteins [Arabidopsis thaliana]

		gb AAD25552.1 AC005850_9 (AC005850)
	20365_s_at	Highly Similar to Mlo proteins [Arabidopsis
60	(AC005850.19_S_AT)	thaliana]
61	13696_at (NI15_AT)	No hits found less than or equal to 1e-15.
no cds	13697_at (NI16_AT)	No hits found.
	13751_at	gb AAF16751.1 AC010155_4 (AC010155)
62	(NOVARTIS127_AT)	F3M18.8 [Arabidopsis thaliana]
	13764_at	gb AAD39641.1 AC007591_6 (AC007591)
63	(NOVARTIS22_AT)	F9L1.6 [Arabidopsis thaliana]
	13818_s_at	gb AAD15433.1 (AC006218) putative
	(AC006218.175_S_A	aspartate aminotransferase [Arabidopsis
64	T)	thaliana]
	13880_s_at	emb CAB39611.1 (AL049480) possible
	(AL049480.183_S_A	apospory-associated like protein
65	T)	[Arabidopsis thaliana]
	13966_at	emb CAA17775.1 (AL022023) putative
66	(AL022023.172_AT)	protein [Arabidopsis thaliana]
		gb AAC78535.1 (AC005662) putative
	14083_at	embryo-abundant protein [Arabidopsis
67	(AC005662.56_AT)	thaliana]
	14096_at	
68	(AC002291.12_AT)	No hits found.
	14110_i_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_I_AT	disease resistance protein [Arabidopsis
69)	thaliana]
	14111_s_at	emb CAB36854.1 (AL035528) putative
	(AL035528.279_S_A	disease resistance protein [Arabidopsis
70	T)	thaliana]
		gb AAC26243.1 (AF077407) contains
		similarity to sugar transporters (Pfam:
	14116_at	sugar_tr.hmm, score: 395.39) [Arabidopsis
71	(AF077407.30_AT)	thaliana]
	14141_at	
72	(NOVARTIS31_AT)	No hits found less than or equal to 1e-15.
		dbj BAA22813.1 (D26015) CND41,
	14145_at	chloroplast nucleoid DNA binding protein
73	(NOVARTIS35_AT)	[Nicotiana tabacum]
	14146_at	gb AAD25550.1 AC005850_7 (AC005850)
74	(NOVARTIS36_AT)	Hypothetical protein [Arabidopsis thaliana]
	14148_at	gb AAF34713.1 AF224762_1 (AF224762)
75	(NOVARTIS38_AT)	SigA binding protein [Arabidopsis thaliana]
	14201_at	
76	(NOVARTIS73_AT)	No hits found less than or equal to 1e-15.
	14202_at	
	(NOVARTIS73_RC_	
77	AT)	No hits found less than or equal to 1e-15.
	14223_at	emb CAA19683.1 (AL024486) putative
78	(NOVARTIS9_AT)	protein [Arabidopsis thaliana]

79	14232_at (NOVARTIS95_AT)	gb AAF16756.1 AC010155_9 (AC010155) F3M18.20 [Arabidopsis thaliana]
80	14248_at (PAD3_AT)	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
81	14249_i_at (PAD4_I_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
82	14250_r_at (PAD4_R_AT)	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
83	14254_s_at (PAL1- MRNA_S_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
84	14256_f_at (PAL1- INTRON_F_AT)	gb AAD18156.2 (AC006260) phenylalanine ammonia lyase (PAL1) [Arabidopsis thaliana]
85	14278_at (AL022373.295_AT)	emb CAA18503.1 (AL022373) hypothetical protein [Arabidopsis thaliana]
86	14320_at (AC005956.54_AT)	gb AAD23719.1 AC005956_8 (AC005956) putative RING zinc finger protein [Arabidopsis thaliana]
87	14381_at (AC002521.68_AT)	gb AAC05341.1 (AC002521) unknown protein [Arabidopsis thaliana]
88	14443_at (AC000348.23_AT)	gb AAB61498.1 (AC000348) T7N9.22 [Arabidopsis thaliana]
89	14609_at (AC002340.147_AT)	gb AAC02748.1 (AC002340) putative cytochrome P450 [Arabidopsis thaliana]
90	14614_at (AC004165.66_AT)	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
91	14620_s_at (PAT1_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
92	14838_s_at (M96073.6_S_AT)	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
93	14621_at (PDF1.2_AT)	gb AAC31244.1 (AC004747) putative antifungal protein [Arabidopsis thaliana]
94	14635_s_at (PR.1_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
95	17128_s_at (ATHRPRP1A_S_AT)	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
96	14638_s_at (PRXCB_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]

97	15970_s_at (X71794.2_S_AT)	emb CAA50677.1 (X71794) peroxidase [Arabidopsis thaliana]
98	14672_s_at (TSA1_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
99	17487_s_at (U18993.2_S_AT)	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
100	14673_s_at (TSB2_S_AT)	gb AAA32879.1 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
101	14682_i_at (WT1012A_RC_I_AT)	No hits found.
102	14691_at (WT1096_AT)	No hits found.
103	14704_s_at (WT768_RC_S_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
104	15846_at (AC006067.63_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
105	15847_g_at (AC006067.63_G_AT)	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
106	14709_at (WT788_AT)	No hits found less than or equal to 1e-15. emb CAA60521.1 (X86958) protein kinase catalytic domain (fragment) [Arabidopsis thaliana]
107	14763_at (X86958.1_AT)	emb CAA18753.1 (AL022605) putative protein [Arabidopsis thaliana]
108	14882_at (AL022605.63_AT)	emb CAA17549.1 (AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]
109	15042_at (AL021961.3_AT)	
110	15116_f_at (AF121356_F_AT)	gb AAD28243.1 AF121356_1 (AF121356) peroxiredoxin TPx2 [Arabidopsis thaliana]
111	15161_s_at (ATU90522_S_AT)	gb AAB53975.1 (U90522) lysine- ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]
112	15366_at (U93215.38_AT)	gb AAB63077.1 (U93215) unknown protein [Arabidopsis thaliana]
113	15415_at (AF000657.28_AT)	gb AAB72169.1 (AF000657) hypothetical protein [Arabidopsis thaliana]
114	15431_at (AL030978.64_AT)	emb CAA19722.1 (AL030978) putative protein [Arabidopsis thaliana]
115	15523_s_at (AL078637.213_S_A T)	emb CAB45071.1 (AL078637) putative protein [Arabidopsis thaliana]
116	15532_r_at (AL078637.191 R A	emb CAB45069.1 (AL078637) putative protein [Arabidopsis thaliana]

T)

- 15616_s_at
(ATHPRO25A_S_AT) emb|CAA08794.1| (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
117) dbj|BAA24440.1| (AB010407)
- 15629_s_at
(AB003280_S_AT) phosphoglycerate dehydrogenase
118 [Arabidopsis thaliana]
gb|AAD10829.1| (AF117063) putative
- 15641_s_at
(AF117063_S_AT) inositol polyphosphate 5-phosphatase At5P2
119 [Arabidopsis thaliana]
gb|AAB80922.1| (AF022658) putative c2h2
- 15665_s_at
(AF022658_S_AT) zinc finger transcription factor [Arabidopsis
120; 682 thaliana]
- 15778_at
(X98676.2_AT) emb|CAA67234.1| (X98676) zinc finger
121 protein [Arabidopsis thaliana]
- 15779_g_at
(X98676.2_G_AT) emb|CAA67234.1| (X98676) zinc finger
122 protein [Arabidopsis thaliana]
- 15859_at
(AC006587.164_AT) gb|AAD15461.1| (AC006067) unknown
123 protein [Arabidopsis thaliana]
- 15978_at
(X68592.6_AT) gb|AAD15461.1| (AC006067) unknown
124 protein [Arabidopsis thaliana]
- 16053_i_at
(Y14251.4_I_AT) emb|CAA74639.1| (Y14251) glutathione S-
125 transferase [Arabidopsis thaliana]
- 16061_s_at
(AB004796_S_AT) gb|AAB97145.1| (AF000977) MEK1
126 [Arabidopsis thaliana] thaliana
gb|AAD34615.1|AF153283_1 (AF153283)
- 16083_s_at
(AF153283_S_AT) putative progesterone-binding protein
127 homolog [Arabidopsis thaliana]
- 16150_s_at
(ATHPEAR_S_AT) emb|CAB41718.1| (AL049730) pEARLI 1
128 [Arabidopsis thaliana]
- 16232_s_at
(AL080252.77_S_AT) emb|CAB45796.1| (AL080252) putative
129 protein [Arabidopsis thaliana]
gb|AAC32915.1| (AC004138) putative
- 16257_at
(AC004138.105_AT) nucleoside triphosphatase [Arabidopsis
130 thaliana]
- 16298_at
(AL021890.71_AT) emb|CAA17152.1| (AL021890) putative
131 protein [Arabidopsis thaliana]
- 16299_at
(AL024486.185_AT) emb|CAA19705.1| (AL024486) putative
132 protein [Arabidopsis thaliana]
- gb|AAD40144.1|AF149413_25 (AF149413)
contains similarity to protein kinase domains
(Pfam F00069, Score=162.6, E=6.8e-45,
N=1) and leucine rich repeats (Pfam
PF00560, Score=210.7, E=2.2e-59, N=10)
- 16357_at
(AF149413.38_AT) [Arabidopsis thaliana]
emb|CAA20203.1| (AL031187) receptor-like
- 16360_at
(AL031187.126_AT) serine/threonine protein kinase ARK3
134 [Arabidopsis thaliana]

- 135 16365_at (AC003974.136_AT) gb|AAC04495.1| (AC003974) putative disease resistance protein [Arabidopsis thaliana]
- 136 16578_s_at (ATHRPRP1B_S_AT) emb|CAB68132.1| (AL137080) beta-1, 3-glucanase 2 (BG2) [Arabidopsis thaliana]
- 137 16817_s_at (AL096882.91_S_AT) emb|CAB51412.1| (AL096882) ACC synthase (AtACS-6) [Arabidopsis thaliana]
- 138 16914_s_at (AL049500.57_S_AT) emb|CAB39936.1| (AL049500) osmotin precursor [Arabidopsis thaliana]
- 139 16995_at (AC002391.188_AT) gb|AAB87114.1| (AC002391) unknown protein [Arabidopsis thaliana]
- 140 17008_at (AC006585.212_AT) gb|AAD23027.1| (AC006585_22) (AC006585) putative tyrosine aminotransferase [Arabidopsis thaliana]
- 141 17014_s_at (ATU05206_S_AT) gb|AAC48925.1| (U05206) ribonuclease [Arabidopsis thaliana]
- 142 17051_s_at (AF098947_S_AT) gb|AAD09952.1| (AF098947) CTF2B [Arabidopsis thaliana]
- 143 17068_s_at (ATHRLPKA_S_AT) gb|AAA32857.1| (M84658) receptor-like protein kinase [Arabidopsis thaliana]
- 144 17083_s_at (ATU18770_S_AT) gb|AAD25838.1| (AC006951_17) (AC006951) putative indole-3-glycerol phosphate synthase [Arabidopsis thaliana]
- 145 17097_s_at (ATU66345_S_AT) gb|AAC49697.1| (U66345) calreticulin [Arabidopsis thaliana]
- 146 17278_at (AC000107.5_AT) gb|AAD36959.1| (AC000107_5) (AC000107) F17F8.5 [Arabidopsis thaliana]
- 147 17413_s_at (AJ006961.4_S_AT) emb|CAA67551.1| (X99097) peroxidase [Arabidopsis thaliana]
- 148 17464_at (AC000132.72_AT) gb|AAB60752.1| (AC000132) Similar to A. thaliana receptor-like protein kinase (gb|RLK5_ARATH). ESTs gb|ATTS0475, gb|ATTS4362 come from this gene. [Arabidopsis thaliana]
- 149 17485_s_at (Z97340.345_S_AT) emb|CAB10405.1| (Z97340) beta-1, 3-glucanase class I precursor [Arabidopsis thaliana]
- 150 17499_s_at (AF107726_S_AT) gb|AAD19610.1| (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
- 151 17511_s_at (AF067605_S_AT) gb|AAB71482.1| (AC002294) similar to S-linalool synthase gp|U58314|1491939 [Arabidopsis thaliana]
- 152 17522_s_at (D78606_S_AT) dbj|BAA28538.1| (D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]
- 153 17544_s_at (ATU40856_S_AT) gb|AAC49282.1| (U40856) AIG1 [Arabidopsis thaliana]

- 154 17653_at (AL035679.144_AT) emb|CAB38823.1| (AL035679) putative protein [Arabidopsis thaliana]
gb|AAC28500.1| (AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb|AF020814 from Pisum sativum. [Arabidopsis thaliana]
- 155 17775_at (AC004392.2_AT)
- 156 17840_s_at (AC002333.223_S_A T) gb|AAB64049.1| (AC002333) putative endochitinase [Arabidopsis thaliana]
- 157 17843_s_at (AC002391.150_S_A T) gb|AAB87109.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
- 158 17899_at (Z97339.197_AT) emb|CAB10339.1| (Z97339) hypothetical protein [Arabidopsis thaliana]
- 159 17930_s_at (AJ006960.4_S_AT) emb|CAA07352.1| (AJ006960) peroxidase [Arabidopsis thaliana]
- 160 18012_s_at (AJ002295_S_AT) emb|CAB59428.1| (AJ002295) inositol-1,4,5-trisphosphate 5-Phosphatase [Arabidopsis thaliana]
- 161 18022_at (AJ010971_AT) emb|CAB52675.1| (AJ010971) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
- 162 18054_at (AJ238846_AT) emb|CAB54517.1| (AJ238846) SGP1 monomeric G-protein [Arabidopsis thaliana]
- 163 18216_at (X95573.2_AT) gb|AAF24959.1|AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 164 18217_g_at (X95573.2_G_AT) gb|AAF24959.1|AC012375_22 (AC012375) T22C5.18 [Arabidopsis thaliana]
- 165 18551_at (AC002391.163_AT) gb|AAB87112.1| (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
gb|AAC34217.1| (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
- 166 18567_at (AC004411.25_AT)
- 167 18590_at (AJ222713.4_AT) emb|CAA10955.1| (AJ222713) unnamed protein product [Arabidopsis thaliana]
- 168; 665 18591_at (X74756.2_AT) emb|CAA52772.1| (X74756) ATAF2 [Arabidopsis thaliana]
gb|AAC72125.1| (AC005278) ESTs
gb|H36966, gb|R65511, gb|T42324 and gb|T20569 come from this gene.
- 169 18625_at (AC005278.22_AT) [Arabidopsis thaliana]
- 170 18716_at (X91916_AT) gb|AAF26754.1|AC007396_3 (AC007396) T4O12.6 [Arabidopsis thaliana]
gb|AAC33239.1| (AC005315) putative ligand-gated ion channel protein [Arabidopsis thaliana]
- 171 18844_at (AC005315.131_AT)
- 172 18908_i_at (AF055848.2_I_AT) gb|AAC62611.1| (AF055848) subtilisin-like protease [Arabidopsis thaliana]

173	18909_s_at (AF055848.2_S_AT)	gb AAC62611.1 (AF055848) subtilisin-like protease [Arabidopsis thaliana]
174	18946_at (Y11788.1_AT)	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
175	18968_at (AF163823.4_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
176	18969_g_at (AF163823.4_G_AT)	gb AAD45127.1 AF163823_1 (AF163823) endoxyloglucan transferase [Arabidopsis thaliana]
177	18983_s_at (AL049730.104_S_AT)	emb CAB41722.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
178	19158_at (X95738.2_AT)	emb CAA65053.1 (X95738) proline transporter 2 [Arabidopsis thaliana]
179	19171_at (AC002335.160_AT)	gb AAB64325.1 (AC002335) putative trypsin inhibitor [Arabidopsis thaliana]
180	19177_at (X99923.1_AT)	emb CAA68191.1 (X99923) male sterility 2-like protein [Arabidopsis thaliana]
181	19182_at (AL031804.245_AT)	emb CAA21214.1 (AL031804) putative protein [Arabidopsis thaliana]
182	19229_at (AC003027.39_AT)	gb AAD10694.1 (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
183	19247_at (AF071527.44_AT)	gb AAD11587.1 AAD11587 (AF071527) hypothetical protein [Arabidopsis thaliana]
184	19284_at (AC003028.196_AT)	gb AAC27173.1 (AC003028) putative anthocyanidin synthase [Arabidopsis thaliana]
185	19415_at (AL080253.32_AT)	emb CAB45805.1 (AL080253) putative protein [Arabidopsis thaliana]
186	19594_i_at (X98321.2_I_AT)	emb CAA66965.1 (X98321) peroxidase [Arabidopsis thaliana]
187	19640_at (AC004561.78_AT)	gb AAC95192.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
188	19664_at (AL050351.172_AT)	emb CAB43638.1 (AL050351) NAD(P)H oxidoreductase, isoflavone reductase-like protein [Arabidopsis thaliana]
189	19672_at (AC005687.19_AT)	gb AAC36019.1 (AC005687) RAP2.6 [Arabidopsis thaliana]
190	19762_at (AL035527.204_AT)	emb CAB36812.1 (AL035527) peptide transporter-like protein [Arabidopsis thaliana]
191	19892_at (AC005770.30_AT)	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
192	19894_at (AJ001809.1_AT)	emb CAA05025.1 (AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

193	19914_at (AC005727.175_AT)	gb AAC79593.1 (AC005727) unknown protein [Arabidopsis thaliana]
194	19951_at (AC005395.47_AT)	gb AAC42241.1 (AC005395) unknown protein [Arabidopsis thaliana]
195	19991_at (AC007017.124_AT)	gb AAD21459.1 (AC007017) similar to harpin-induced protein hin1 from tobacco [Arabidopsis thaliana]
196	20189_at (AC005489.2_AT)	gb AAD32864.1 AC005489_2 (AC005489) F14N23.2 [Arabidopsis thaliana]
197	20232_s_at (AL022347.12_S_AT)	emb CAA18469.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
198	20238_at (X74514.2_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
199	20239_g_at (X74514.2_G_AT)	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
200	20245_s_at (AC005309.97_S_AT)	emb CAA05625.1 (AJ002584) AtMRP4 [Arabidopsis thaliana] thaliana]
201	20246_s_at (AF084037.3_S_AT)	gb AAC95354.1 (AF084037) receptor-like protein kinase [Arabidopsis thaliana]
202	20269_at (AC002387.237_AT)	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
203	20287_at (Y14590.5_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
204	20288_g_at (Y14590.5_G_AT)	emb CAA74930.1 (Y14590) class IV chitinase [Arabidopsis thaliana]
205	20331_at (AC007168.86_AT)	gb AAD23617.1 AC007168_8 (AC007168) putative aspartate aminotransferase [Arabidopsis thaliana]
206	20368_at (AC005314.38_AT)	gb AAC36163.1 (AC005314) putative serpin [Arabidopsis thaliana]
207	20420_at (AL024486.131_AT)	emb CAA19698.1 (AL024486) putative chitinase [Arabidopsis thaliana]
208	20429_s_at (Z97336.167_S_AT)	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
209	20620_g_at (AC005896.161_G_A T)	gb AAC98070.1 (AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
210	20625_at (AL049658.102_AT)	emb CAB41131.1 (AL049658) hypothetical protein [Arabidopsis thaliana]
211	20641_at (X91919.1_AT)	emb CAA63012.1 (X91919) LEA76 homologue type1 [Arabidopsis thaliana]
789	18224_s_at (AL021890.57_S_AT)	Arabidopsis thaliana. ESTs gb N97082, gb Z27056 and gb Z29902 come from this gene.
790	16522_at (X77500.2_AT)	emb CAA17152.1 (AL021890) putative protein [Arabidopsis thaliana]
		emb CAA54631.1 (X77500) amino acid transporter [Arabidopsis thaliana]

		gb AAC17040.1 (AC002986) Similarity to
		A. thaliana gene product F21M12.20,
		gb AC000132. EST gb Z25651 comes from
791	19982_at (AC002986.28_AT)	this gene. [Arabidopsis thaliana]
	18920_at	gb AAC16927.1 (AC002338) putative
367	(AC002338.11_AT)	laccase [Arabidopsis thaliana]
212	12324_i_at	AC007212
793	12345_at	L36246
213	12500_s_at	AF081067
214; 662	12505_s_at	AC005309
215	12608_i_at	S70188
216	12642_at	AC006920
217	12746_i_at	AL096882
218	12748_f_at	AL096882
219	12761_s_at	AC006577
220	12773_at	AC005727
221	12778_r_at	AC006577
222	12798_at	AC003028
223	12802_at	AL022373
	12842_s_at	No hits found less than or equal to 1e-15
224	12843_s_at	AC007195
	12845_s_at	AJ004810
225	12879_s_at	U40856
226	12891_at	U73786
227	12892_g_at	U73786
228; 658	12904_s_at	AB008103
229	12905_s_at	AB008104
230	12908_s_at	AB008107
231	12909_s_at	Z97343
232	12911_s_at	X84229
233	12916_s_at	AF021244
234	13138_at	AL096882
235	13177_at	AL049640
236	13178_at	U93215
237	13187_i_at	U35829
238	13189_s_at	U35829
239	13198_i_at	AL021749
240	13212_s_at	AL137080
241	13217_s_at	AL049862
242	13258_s_at	AC005309
243	13273_s_at	U68017
244	13284_s_at	AJ002551
245	13604_at	AC000104
246	13615_at	AC002332
247	13617_at	AC006592
248	13718_at	Z72152
249	13771_at	AC006593
250	13785_at	AC007087
251	14052_at	AC004122

252	14096_at	AC002291
253	14097_at	AC005309
254	14116_at	AF077407
255	14141_at	AC011437
256; 683	14148_at	AF224762
257	14196_at	AC012563
258	14201_at	AL163972
259	14219_at	AC068667
260	14223_at	AL024486
261	14248_at	AC007357
262	14250_r_at	AL050300
263	14595_at	AL022580
264	14608_at	AC007357
265	14614_at	AC004165
266	14621_at	AC004747
267	14627_i_at	X76609
268	14628_r_at	X76609
269	14635_s_at	AC005398
270	14636_s_at	AC013258
271	14643_s_at	AC006836
272	14672_s_at	U18993
273	14675_s_at	D85191
274	14691_at	AP002046
275	14704_s_at	AC006067
276	14706_r_at	AL137189
277	14709_at	AP002046
278	14711_s_at	AF085279
279	14731_s_at	AF014960
280	14784_at	AC005310
281	14951_at	AL049481
282	15057_at	AL035440
283	15085_s_at	AL031018
284	15105_s_at	Z14987
285	15116_f_at	AF121356
286	15125_f_at	D85190
287	15141_s_at	D85191
288	15145_s_at	D64155
289	15154_s_at	AL096860
290	15161_s_at	U90522
291	15178_s_at	U43489
292	15216_s_at	U75198
293	15431_at	AL030978
294	15496_at	AC006282
295	15523_s_at	AL078637
296	15593_s_at	U54561
297	15611_s_at	L22567
298	15616_s_at	AJ009696
299	15622_s_at	U43945

300	15629_s_at	AB010407
301	15665_s_at	AF022658
302	15680_s_at	D42061
303	15846_at	AC006067
304	15847_g_at	AC006067
305	15866_s_at	AC005770
306	15950_at	AC006429
307	15954_at	U72155
308	15978_at	X68592
309	16038_s_at	L04173
310	16063_s_at	AB008103
311	16105_s_at	U68017
312	16150_s_at	AL049730
313	16153_s_at	AC013258
314	16393_s_at	AC006436
315	16412_s_at	AL022603
316	16442_s_at	AJ002551
317	16504_s_at	Z97335
318	16510_at	AL034567
319	16536_s_at	AB008107
320	16539_s_at	Z97343
321	16569_s_at	L23968
322	16578_s_at	AL137080
323	16609_s_at	AB008104
324	16620_s_at	AF051338
325	16637_s_at	Z97336
326	16817_s_at	AL096882
327	16864_i_at	AL133248
328	16951_i_at	AC005662
329	16952_s_at	AC005662
330	16981_s_at	U35829
331	17014_s_at	U05206
332	17033_s_at	U83179
333	17054_s_at	AF134128
334	17073_s_at	AC006836
335	17119_s_at	AF132212
336	17123_s_at	AF106087
337	17128_s_at	AC005398
338	17187_at	AF128396
339; 669	17303_s_at	AC005499
340; 663	17379_at	AC018721
341	17386_at	AC006264
342	17413_s_at	X99097
343	17499_s_at	AF107726
344	17500_s_at	AL049862
345	17544_s_at	U40856
346	17567_at	AL162751
347	17886_at	AC004484

348	17899_at	Z97339
349	17917_s_at	AC004261
350	17961_at	AC007323
351	17963_at	AL049730
352	18003_at	AF188334
	18064_r_at	No hits found
	18069_at	No hits found
	18070_r_at	No hits found
353	18216_at	AC012375
354	18217_g_at	AC012375
355	18235_at	AC000348
356	18252_at	AL096882
357	18255_at	AC005770
358	18272_at	AF002109
359	18533_at	AL021684
360	18556_at	AC006264
361	18590_at	AJ222713
362	18591_at	X74756
363	18607_s_at	U78721
364	18635_at	AC004005
365	18716_at	AC007396
366	18876_at	AF002109
367	18920_at	AC002338
368	18928_at	AC002338
369	19034_at	AL021768
370	19171_at	AC002335
371	19178_at	AB035137
372	19182_at	AL031804
373	19251_at	AL035538
374	19640_at	AC004561
375	19977_at	AL049659
376	20017_at	AC004521
377	20034_i_at	A71607
378	20201_at	AL078470
379	20227_s_at	AB027252
380	20269_at	AC002387
381	20297_at	AC007153
382	20314_s_at	AL096882
383	20335_s_at	Y14208
384	20429_s_at	Z97336
385	20585_s_at	AC005309
386	20641_at	X91919
387	12333_at	AJ286345
388	14028_at	
389	14295_s_at	Z54356
390	14965_at	AC002329
391	15969_s_a	AJ133036
392	15982_s_a	X98190

393	16461_I_at	AC004683
394	16462_s_a	AC004683
395	16514_at	AL035538
396	17549_s_a	L37126
397	18706_s_a	X75782
398	19594_i_at	X98321
399	20555_s_a	AL080318
400	16212_at	gb AAD17366.1 (AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana]
794	14985_s_at	gb AAC32233.2 (AC005168) unknown protein [Arabidopsis thaliana]
401	16411_s_at	emb CAB71046.1 (AL137898) shaggy-like kinase beta [Arabidopsis thaliana]
402	15920_i_at	gb AAD39561.1 AC007067_1 (AC007067) T10024.1 [Arabidopsis thaliana]
403	16299_at	emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana]
404	18445_at	gb AAC98458.1 (AC005851) putative glucosyltransferase [Arabidopsis thaliana]
405	19215_at	gb AAC23400.1 (AC004005) putative methyl chloride transferase [Arabidopsis thaliana]
406	16439_at	emb CAA50905.1 (X72022) ORF1 [Arabidopsis thaliana]
407	16047_at	gb AAD20710.1 (AC006300) unknown protein [Arabidopsis thaliana]
408	18003_at	gb AAF01328.1 AF188334_1 (AF188334) Toll/interleukin-1 receptor-like protein [Arabidopsis thaliana]
409	20429_s_at	emb CAB10219.1 (Z97336) hypothetical protei [Arabidopsis thaliana]
410	17917_s_at	gb AAD12002.1 (AC004261) calcium binding protein (CaBP-22) [Arabidopsis thaliana]
411	17963_at	emb CAB41717.1 (AL049730) pEARLI 1-like protein [Arabidopsis thaliana]
412	16150_s_at	emb CAB41718.1 (AL049730) pEARLI 1 [Arabidopsis thaliana]
413	20239_g_at	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
414	20238_at	emb CAA52619.1 (X74514) beta-fructofuranosidase [Arabidopsis thaliana]
415	15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
416	18591_at	emb CAA52772.1 (X74756) ATAF2 [Arabidopsis thaliana]

		gb AAC26243.1 (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]
417	14116_at	
		gb AAC72120.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb 84105 and gb A1100071 come from this gene. [Arabidopsis thaliana]
418	12759_at	gb AAC18809.1 (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
419	19060_at	
420	12998_at	emb CAB41863.1 (AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]
421	13172_s_at	gb AAD30608.1 AC007369_18 (AC007369) Sugar transporter [Arabidopsis thaliana]
422	14709_at	No hits found less than or equal to 1e-15.
423	15931_at	gb AAD41420.1 AC007727_9 (AC007727) F8K7.9 [Arabidopsis thaliana]
424	20369_s_at	emb CAB41109.1 (AL049656) ammonium transport protein (AMT1) [Arabidopsis thaliana]
425	14201_at	No hits found less than or equal to 1e-15.
426	14691_at	No hits found.
75	14148_at	gb AAF34713.1 AF224762_1 (AF224762) SigA binding protein [Arabidopsis thaliana]
426	16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2 [Arabidopsis thaliana]
427	13625_s_at	emb CAB42924.1 (AL049862) putative disease resistance protein [Arabidopsis thaliana]
428	13702_s_at	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
429	17886_at	gb AAC14530.1 (AC004484) unknown protein [Arabidopsis thaliana]
430	12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
431	12353_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase [Arabidopsis thaliana]
432	17899_at	emb CAB10339.1 (Z97339) hypothetical protein [Arabidopsis thaliana]

		emb CAB43665.1 (AL050352) Ca ²⁺ -transporting ATPase-like protein [Arabidopsis thaliana]
433	18894_at	
		gb AAB64024.1 (AC002333) putative glucosyltransferase [Arabidopsis thaliana]
434	14978_at	emb CAA19683.1 (AL024486) putative protein [Arabidopsis thaliana]
435	14223_at	gb AAC05342.1 (AC002521) putative protein kinase [Arabidopsis thaliana]
436	16109_s_at	gb AAD28055.1 AC007166_3 (AC007166) putative protein kinase [Arabidopsis thaliana]
437	18820_at	gb AAC72865.1 (AF104919) similar to class I chitinases (Pfam: PF00182, E=1.2e-142, N=1) [Arabidopsis thaliana]
438	20345_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein [Arabidopsis thaliana]
439	14170_at	gb AAD38519.1 AF138281_1 (AF138281) phospholipase D-gamma-2 [Arabidopsis thaliana]
440	15143_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel [Arabidopsis thaliana]
441	17499_s_at	emb CAB37511.1 (AL035540) Phospholipase like protein [Arabidopsis thaliana]
442	20590_at	
		gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase family. ESTs gb T45045 and gb AA394473 come from this gene. [Arabidopsis thaliana]
443	14608_at	emb CAA18465.1 (AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]
444	13550_at	emb CAA71371.1 (Y10342) putative amidase [Arabidopsis thaliana]
445	13355_at	gb AAC78521.1 (AC005312) putative glutathione S-transferase [Arabidopsis thaliana]
446	13564_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]
447	19845_g_at	gb AAC32912.1 (AC004138) putative glutathione S-transferase [Arabidopsis thaliana]
448	12764_f_at	gb AAB16855.1 (U71122) pyruvate decarboxylase [Arabidopsis thaliana]
449	17922_at	

		emb CAA66863.1 (X98190) peroxidase
450	15982_s_at	ATP2a [Arabidopsis thaliana]
		gb AAD39285.1 AC007576_8 (AC007576)
451	12227_at	Unknown protein [Arabidopsis thaliana]
		emb CAB45975.1 (AL080318) copper amine
		oxidase like protein (fragment2)
452	20555_s_at	[Arabidopsis thaliana]
		emb CAB37510.1 (AL035540)
		monooxygenase 2 (MO2) [Arabidopsis
453	19844_at	thaliana]
		gb AAC31242.1 (AC004747) unknown
454	13985_s_at	protein [Arabidopsis thaliana]
		gb AAD41421.1 AC007727_10 (AC007727)
		ESTs gb N96028, gb F14286, gb T20680,
		gb F14443, gb AA657300 and gb N65244
455	13548_at	come from this gene. [Arabidopsis thaliana]
		gb AAA32775.1 (L22567) cor78
456	15611_s_at	[Arabidopsis thaliana]
		gb AAD25759.1 AC007060_17 (AC007060)
		Strong similarity to F19I3.2 gi 3033375
		putative berberine bridge enzyme from
		Arabidopsis thaliana BAC gb AC004238.
457	19840_s_at	EST gb R90518 comes from this gene.
		emb CAA67340.1 (X98808) peroxidase
458	15985_at	ATP3a [Arabidopsis thaliana]
		gb AAD32844.1 AC007658_3 (AC007658)
459	14584_at	unknown protein [Arabidopsis thaliana]
		gb AAD36948.1 AF069441_8 (AF069441)
460	15422_at	hypothetical protein [Arabidopsis thaliana]
		gb AAB61076.1 (AF007271)
		A_TM021B04.14 gene product [Arabidopsis
461	20150_at	thaliana]
		gb AAC33239.1 (AC005315) putative
		ligand-gated ion channel protein
462	18844_at	[Arabidopsis thaliana]
		emb CAA20203.1 (AL031187) receptor-like
		serine/threonine protein kinase ARK3
463	16360_at	[Arabidopsis thaliana]
		gb AAB87113.1 (AC002391) putative
464	20292_at	protein kinase [Arabidopsis thaliana]
		gb AAC18798.1 (AC003671) F17O7.4
465	14554_at	[Arabidopsis thaliana]
		gb AAC19273.1 (AF069298) similar to
		several small proteins (~100 aa) that are
		induced by heat, auxin, ethylene and
		wounding such as Phaseolus aureus indole-3-
		acetic acid induced protein ARG
466	18604_at	(SW:32292) [Arabidopsis thaliana]

467	16061_s_at	gb AAB97145.1 (AF000977) MEK1 [Arabidopsis thaliana] thaliana] dbj BAA22813.1 (D26015) CND41, chloroplast nucleoid DNA binding protein
468	14145_at	[Nicotiana tabacum] dbj BAA04870.1 (D21843) MAP kinase
469	16144_s_at	[Arabidopsis thaliana] gb AAC49697.1 (U66345) calreticulin
470	17097_s_at	[Arabidopsis thaliana] gb AAB71447.1 (AC000098) Similar to Arabidopsis Fe(II) transport protein
471	19718_at	(gb U27590). [Arabidopsis thaliana] gb AAC25507.1 (AC003979) T22J18.6
472	14298_g_at	[Arabidopsis thaliana] gb AAD12037.1 (AC002392) putative receptor-like protein kinase [Arabidopsis
473	12307_at	thaliana] emb CAA18460.1 (AL022347) protein
474	20232_s_at	kinase-like protein [Arabidopsis thaliana] gb AAF19738.1 AC012463_12 (AC012463) T2E6.14 [Arabidopsis thaliana]
475	19322_at	gb AAF07386.1 AC010675_9 (AC010675) putative peptide transporter [Arabidopsis
476	14224_at	thaliana] gb AAD39269.1 AC007203_1 (AC007203) Putative UDP-glucose:sterol
477	14270_at	glucosyltransferase [Arabidopsis thaliana] emb CAB39671.1 (AL049483) putative
478	15479_at	protein [Arabidopsis thaliana] gb AAD41981.1 AC006438_13 (AC006438) unknown protein [Arabidopsis thaliana]
479	14090_i_at	gb AAB05099.1 (U39944) BELL1 [Arabidopsis thaliana]
480	16162_s_at	gb AAB70415.1 (AC000106) Similar to Beta integral membrane protein (gb U43629).
481	20149_at	[Arabidopsis thaliana] gb AAD15574.1 (AC006340) unknown
482	12765_at	protein [Arabidopsis thaliana] gb AAC63643.1 (AC005309) putative
214	12505_s_at	CONSTANS-like B-box zinc finger protein [Arabidopsis thaliana] gb AAC79588.1 (AC005727) putative RING
483	13140_at	zinc finger ankyrin protein [Arabidopsis thaliana] gb AAC72124.1 (AC005278) ESTs
484	15022_at	gb H37641 and gb AA651422 come from this gene. [Arabidopsis thaliana]

485	16306_at	emb CAB41935.1 (AL049751) putative protein [Arabidopsis thaliana] gb AAC26246.1 (AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
486	18611_at	emb CAB43428.1 (AL050300) putative protein [Arabidopsis thaliana]
487	20199_at	emb CAA18626.1 (AL022580) putative protein [Arabidopsis thaliana]
488	14595_at	gb AAD31337.1 AC007354_10 (AC007354) Strong similarity to gb Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF 01326 Pyruvate phosphate dikinase, PEP/pyruvate binding domain. EST gb N96757 comes from this gene.
489	12532_at	[Arabidopsis thaliana]
490	19977_at	emb CAB41162.1 (AL049659) putative protein [Arabidopsis thaliana] gb AAC79594.1 (AC005727) putative membrane channel protein [Arabidopsis thaliana]
491	12773_at	gb AAD32870.1 AC005489_8 (AC005489) F14N23.8 [Arabidopsis thaliana]
492	19632_at	emb CAA16957.1 (AL021811) putative protein [Arabidopsis thaliana]
493	19359_s_at	emb CAA78712.1 (Z14988) glycine rich protein [Arabidopsis thaliana]
494	14716_f_at	gb AAC19269.1 (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
495	13648_at	gb AAD41977.1 AC006438_9 (AC006438) unknown protein [Arabidopsis thaliana]
496	12768_at	gb AAC69134.1 (U78721) putative auxin-regulated protein [Arabidopsis thaliana]
497	16422_at	gb AAC26203.1 (AF053747) dormancy-associated protein [Arabidopsis thaliana]
498	15131_s_at	emb CAB38829.1 (AL035679) drought-inducible cysteine proteinase RD19A precursor
499	14659_s_at	emb CAB38829.1 (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
500	14658_s_at	emb CAB36513.1 (AL035440) putative protein [Arabidopsis thaliana]
501	15057_at	emb CAB56039.1 (AJ133786) gigantea protein [Arabidopsis thaliana]
502	17581_g_at	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
503	18567_at	

504	17047_s_at	gb AAC68674.1 (AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]
505	15105_s_at	emb CAA78711.1 (Z14987) glycine rich protein [Arabidopsis thaliana]
506	14196_at	gb AAF16557.1 AC012563_10 (AC012563) unknown protein [Arabidopsis thaliana]
507	17599_s_at	gb AAD50976.1 AF170494_1 (AF170494) ionotropic glutamate receptor ortholog GLR6 [Arabidopsis thaliana]
508	18556_at	gb AAD29803.1 AC006264_11 (AC006264) cyclophilin (CYP2) [Arabidopsis thaliana]
509	16486_at	gb AAB04606.1 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana]
510	18272_at	gb AAB95293.1 (AF002109) unknown protein [Arabidopsis thaliana]
795	12219_at	gb AAD31373.1 AC006053_15 (AC006053) unknown protein [Arabidopsis thaliana]
511	20446_s_at	gb AAC80600.1 (AC005106) T25N20.21 [Arabidopsis thaliana]
512	12561_at	emb CAA16701.1 (AL021687) putative protein [Arabidopsis thaliana]
513	12060_at	gb AAD46000.1 AC005916_12 (AC005916) Contains similarity to gb AF113001 silencing mediator of retinoic acid and thyroid hormone receptor alpha and gb AF109179 cyclin T1 from Mus musculus. ESTs gb N95317, gb Z29139 and gb Z30853 come from this gene. [Arabidopsis thaliana]
514	18235_at	gb AAB61480.1 (AC000348) T7N9.4 [Arabidopsis thaliana]
515	14021_r_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana]
516	14020_i_at	emb CAA04134.1 (AJ000497) Starch branching enzyme II [Arabidopsis thaliana]
517	16011_s_at	emb CAA44630.1 (X62818) Metallothionein-like protein [Arabidopsis thaliana]
518	17033_s_at	gb AAD09232.1 (U83179) unknown [Arabidopsis thaliana]
519	16050_at	gb AAD24630.1 AC006919_10 (AC006919) putative fructose bisphosphate aldolase [Arabidopsis thaliana]

520	19692_at	gb AAC14039.1 (AC003981) F22O13.13 [Arabidopsis thaliana]
521	19181_s_at	gb AAC39464.1 (AF053065) late embryogenesis abundant protein homolog [Arabidopsis thaliana]
792	13435_at	gb AAC49775.1 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
522	17128_s_at	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
523	14635_s_at	gb AAC69381.1 (AC005398) pathogenesis- related PR-1-like protein [Arabidopsis thaliana]
524	15846_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
525	15847_g_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
526	14704_s_at	gb AAD15461.1 (AC006067) unknown protein [Arabidopsis thaliana]
527	17456_at	gb AAB80678.1 (AC002332) putative steroid dehydrogenase [Arabidopsis thaliana]
528	14895_s_at	emb CAB10562.1 (Z97344) acetylornithine deacetylase [Arabidopsis thaliana]
529	19979_at	gb AAB95235.1 (AC002130) F1N21.7 [Arabidopsis thaliana]
530	20325_s_at	emb CAA78152.1 (Z12162) protein phosphatase 1A [Arabidopsis thaliana]
531	18234_at	gb AAB61479.1 (AC000348) T7N9.3 [Arabidopsis thaliana]
532	16474_s_at	emb CAA35838.1 (X51474) kin1 [Arabidopsis thaliana]
533	18701_s_at	emb CAA38894.1 (X55053) cold regulated [Arabidopsis thaliana]
534	13785_at	gb AAD23000.1 AC007087_19 (AC007087) cold-regulated protein cor15b precursor [Arabidopsis thaliana]
535	20387_at	gb AAC23422.1 (AC004005) putative methionine aminopeptidase [Arabidopsis thaliana]
536	13178_at	gb AAB63086.1 (U93215) unknown protein [Arabidopsis thaliana]
537	12103_at	gb AAD30603.1 AC007369_13 (AC007369) Unknown protein [Arabidopsis thaliana]
538	13225_s_at	emb CAA42483.1 (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

539	17003_at	gb AAB95275.1 (AF002109) putative LIM-domain protein [Arabidopsis thaliana]
540	15878_at	emb CAA19880.1 (AL031032) putative protein [Arabidopsis thaliana]
541	13004_at	gb AAD03574.1 (AC003952) putative senescence-related protein [Arabidopsis thaliana]
542	14052_at	gb AAC34333.1 (AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]
543	15798_at	gb AAC05351.1 (AC002521) putative receptor-like protein kinase [Arabidopsis thaliana]
793	12345_at	gb AAB67985.1 (L36246) anoxia-induced protein [Arabidopsis thaliana]
544	16818_s_at	emb CAA20206.1 (AL031187) serine/threonine kinase-like protein [Arabidopsis thaliana]
545	13916_at	gb AAC62136.1 (AC005169) unknown protein [Arabidopsis thaliana]
666	20342_at	emb CAB41311.1 (AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
546	20421_at	emb CAB10242.1 (Z97336) germin precursor oxalate oxidase [Arabidopsis thaliana]
547	14250_r_at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
548	14249_i_at	emb CAB43438.1 (AL050300) putative protein [Arabidopsis thaliana]
549	17544_s_at	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
550	12879_s_at	gb AAC49282.1 (U40856) AIG1 [Arabidopsis thaliana]
551	20017_at	gb AAC16079.1 (AC004521) unknown protein [Arabidopsis thaliana]
552	13177_at	emb CAB40989.1 (AL049640) growth factor like protein [Arabidopsis thaliana]
553	19946_at	gb AAF18611.1 AC005170_1 (AC005170) similar to senescence-associated protein [Arabidopsis thaliana]
554	17894_at	gb AAD08938.1 (AC005724) unknown protein [Arabidopsis thaliana]
555	15855_at	gb AAD15572.1 (AC006340) unknown protein [Arabidopsis thaliana]
556	15558_r_at	emb CAB45807.1 (AL080253) putative protein [Arabidopsis thaliana]
557	15208_s_at	No hits found less than or equal to 1e-15.

558	16153_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
559	14636_s_at	gb AAF21072.1 AC013258_10 (AC013258) thaumatin-like protein [Arabidopsis thaliana]
560	19178_at	dbj BAA86999.1 (AB035137) blue copper binding protein [Arabidopsis thaliana]
561	17580_at	emb CAB56039.1 (AJ133786) gigantea protein [Arabidopsis thaliana]
562	14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 Cytochrome P450 family. ESTs gb N65665, gb T14112, gb T76255, gb T20906 and gb AI100027 come from this gene.
563	18946_at	emb CAA72484.1 (Y11788) peroxidase ATP24a [Arabidopsis thaliana]
564	13009_i_at	emb CAA17138.1 (AL021889) putative protein [Arabidopsis thaliana]
565	18508_s_at	gb AAA33709.1 (L16797) glutamate decarboxylase [Petunia x hybrida]
566	12556_at	emb CAB45330.1 (AL079344) nucleotide pyrophosphatase-like protein [Arabidopsis thaliana]
567	13115_at	gb AAB60774.1 (AC000375) ESTs gb U75592, gb T13956, gb T43869 come from from this gene. [Arabidopsis thaliana]
568	15046_s_at	gb AAB87120.1 (AC003000) unknown protein [Arabidopsis thaliana]
339	17303_s_at	gb AAC67339.2 (AC005499) putative WRKY-type DNA binding protein [Arabidopsis thaliana]
569	18597_at	emb CAB45881.1 (AL080282) berberine bridge enzyme-like protein [Arabidopsis thaliana]
570	13908_s_at	emb CAB42588.1 (A71590) unnamed protein product [Arabidopsis thaliana]
571	14553_at	emb CAB41103.1 (AL049655) putative protein [Arabidopsis thaliana]
572	18928_at	gb AAB64044.1 (AC002333) putative endochitinase [Arabidopsis thaliana]

573	12772_at	gb AAC72119.1 (AC005278) Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from <i>Daucus carota</i> . ESTs gb H37281, gb T44167, gb T21813, gb N38437, gb Z26470, gb R65072, gb N76373, gb F15470, gb Z35182, gb H76373, gb Z34678 and gb Z35387> emb CAA18124.1 (AL022141) putative receptor protein kinase [<i>Arabidopsis thaliana</i>]
574	16326_at	
575	20479_i_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>] gb AAD28318.1 AC006436_9 (AC006436) putative receptor-like protein kinase [<i>Arabidopsis thaliana</i>]
576	16393_s_at	
577	17413_s_at	emb CAA67551.1 (X99097) peroxidase [<i>Arabidopsis thaliana</i>] gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [<i>Arabidopsis thaliana</i>]
578	14620_s_at	
579	20480_s_at	emb CAB38908.1 (AL035708) cytochrome P450-like protein [<i>Arabidopsis thaliana</i>] gb AAC79625.1 (AC005770) unknown protein [<i>Arabidopsis thaliana</i>]
580	15866_s_at	emb CAA21214.1 (AL031804) putative protein [<i>Arabidopsis thaliana</i>] gb AAC79625.1 (AC005770) unknown protein [<i>Arabidopsis thaliana</i>]
581	19182_at	emb CAA74639.1 (Y14251) glutathione S-transferase [<i>Arabidopsis thaliana</i>]
582	18255_at	
583	16054_s_at	
584	14672_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [<i>Arabidopsis thaliana</i>]
585	20291_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>] emb CAA74639.1 (Y14251) glutathione S-transferase [<i>Arabidopsis thaliana</i>]
586	16053_i_at	
587	17083_s_at	gb AAD25838.1 AC006951_17 (AC006951) putative indole-3-glycerol phosphate synthase [<i>Arabidopsis thaliana</i>]
588	12889_s_at	gb AAA32738.1 (M92353) anthranilate synthase alpha subunit [<i>Arabidopsis thaliana</i>] gb AAD22285.1 AC006920_9 (AC006920) unknown protein [<i>Arabidopsis thaliana</i>]
589	12642_at	

590	17487_s_at	gb AAC49117.1 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana]
591	14838_s_at	gb AAA32835.1 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana]
592	17104_s_at	dbj BAA13640.1 (D88541) phosphoserine aminotransferase [Arabidopsis thaliana]
593	19892_at	gb AAC79626.1 (AC005770) putative protease inhibitor [Arabidopsis thaliana]
594	16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
664	13273_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4 [Arabidopsis thaliana]
595	12892_g_at	gb AAC63850.1 (U73786) ACC synthase [Arabidopsis thaliana]
596	15141_s_at	dbj BAA22096.1 (D85191) vegetative storage protein [Arabidopsis thaliana]
597	18231_at	emb CAA55322.1 (X78585) Di21 [Arabidopsis thaliana]
598	15629_s_at	dbj BAA24440.1 (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]
599	15978_at	emb CAA48579.1 (X68592) adenosine nucleotide translocator [Arabidopsis thaliana]
600	20269_at	gb AAB82640.1 (AC002387) putative pectinesterase [Arabidopsis thaliana]
601	14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase [Arabidopsis thaliana]
602	17930_s_at	emb CAA07352.1 (AJ006960) peroxidase [Arabidopsis thaliana]
603	16952_s_at	gb AAC78532.1 (AC005662) calmodulin-like protein [Arabidopsis thaliana]
604	12930_s_at 12842_s_at	gb AAC49679.1 (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana] No hits found less than or equal to 1e-15.
605	16063_s_at	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
228	12904_s_at	dbj BAA32418.1 (AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]
606	12908_s_at	dbj BAA32422.1 (AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

607	15937_at	emb CAA17127.1 (AL021889) hypothetical protein [Arabidopsis thaliana]
608	17843_s_at	gb AAB87109.1 (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
609	18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
610	20519_at	gb AAC80599.1 (AC005106) T25N20.20 [Arabidopsis thaliana]
611	19641_at	gb AAC95189.1 (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
612	17408_at	gb AAD32297.1 AC006533_21 (AC006533) putative glucosyltransferase [Arabidopsis thaliana]
613	15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase [Arabidopsis thaliana]
614	14731_s_at	gb AAC49988.1 (AF014960) multidrug resistance-associated protein 2; AtMRP2 [Arabidopsis thaliana]
615	20685_at	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]
616	16968_at	emb CAA17559.1 (AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]
617	18253_s_at	gb AAC78440.1 (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana] thaliana]
618	15496_at	gb AAD20156.1 (AC006282) putative glucosyl transferase [Arabidopsis thaliana]
619	19137_at	emb CAA52771.1 (X74755) ATAF1 [Arabidopsis thaliana]
620	19132_s_at	emb CAA18722.1 (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]
621	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function [Arabidopsis thaliana]
622	17024_s_at	gb AAB67854.1 (U61231) cytochrome P450 [Arabidopsis thaliana]
623	14705_i_at	emb CAB69849.1 (AL137189) anthranilate N-benzoyltransferase-like protein [Arabidopsis thaliana]
624	17500_s_at	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]

625	13217_s_at	emb CAB42906.1 (AL049862) calmodulin-like protein [Arabidopsis thaliana]
626	15196_s_at	gb AAC49573.1 (U43412) 3'-phosphoadenosine 5'-phosphosulfate reductase [Arabidopsis thaliana]
627	18590_at	emb CAA10955.1 (AJ222713) unnamed protein product [Arabidopsis thaliana]
628	14700_at	No hits found less than or equal to 1e-15.
629	14665_r_at	emb CAA69879.1 (Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
630	12630_at	gb AAF18681.1 AF024504_11 (AF024504) unknown protein [Arabidopsis thaliana]
631	18953_at	gb AAC69851.1 (AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
632	13514_s_at	emb CAA16793.1 (AL021713) putative protein [Arabidopsis thaliana]
633	12490_at	gb AAF02787.1 AF195115_7 (AF195115) weak similarity to receptor protein kinase [Arabidopsis thaliana]
634	12246_s_at	emb CAB10404.1 (Z97340) phytochrome D [Arabidopsis thaliana]
635	20536_s_at	emb CAB37488.1 (AL035539) putative protein [Arabidopsis thaliana]
636	18409_at	gb AAC72122.1 (AC005278) F15K9.14 [Arabidopsis thaliana]
637	19387_at	gb AAD21475.1 (AC007017) unknown protein [Arabidopsis thaliana]
638	16117_s_at	gb AAB70244.1 (AF016848) WD-40 repeat protein [Arabidopsis thaliana]
639	18347_s_at	emb CAA21480.1 (AL031986) putative protein [Arabidopsis thaliana]
640	15880_at	emb CAB38906.1 (AL035708) putative protein [Arabidopsis thaliana]
641	16603_s_at	gb AAC49767.1 (AF003094) AP2 domain containing protein RAP2.1 [Arabidopsis thaliana]
642	12049_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]
643	12048_at	gb AAC13598.1 (AF058914) F21E10.13 gene product [Arabidopsis thaliana]
		gb AAC78704.1 (AF001308) predicted glycosyl transferase [Arabidopsis thaliana]

		gb AAB61117.1 (AC002062) ESTs
		gb N38288,gb T43486,gb AA395242 come
644	14064_at	from this gene. [Arabidopsis thaliana]
		gb AAC04492.1 (AC003974) unknown
645	12149_at	protein [Arabidopsis thaliana]
		emb CAA91183.1 (Z54356) HD-ZIP
646	14295_s_at	[Arabidopsis thaliana]
		emb CAA16930.1 (AL021768) TMV
		resistance protein N-like [Arabidopsis
647	19034_at	thaliana]
		gb AAC27848.1 (AC004218) unknown
648	18624_at	protein [Arabidopsis thaliana]
		gb AAC97218.1 (AC005936) unknown
649	13181_at	protein [Arabidopsis thaliana]
		gb AAD10163.1 (AC005917) putative Tal1-
		like non-LTR retroelement protein
650	18866_at	[Arabidopsis thaliana]
		emb CAB44686.1 (AL078620) cytochrome
651	19502_at	P450-like protein [Arabidopsis thaliana]
		emb CAA19807.1 (AL031018) hypothetical
652	16301_s_at	protein [Arabidopsis thaliana]
		gb AAD32774.1 AC007661_11 (AC007661)
653	19411_at	unknown protein [Arabidopsis thaliana]
		emb CAA71588.1 (Y10556) CONSTANS
654	20300_g_at	[Arabidopsis thaliana]
		emb CAA71588.1 (Y10556) CONSTANS
655	20299_at	[Arabidopsis thaliana]
		gb AAB57688.1 (U96045) APS reductase
656	18696_s_at	[Arabidopsis thaliana]
		gb AAC26980.1 (AF016283) 5'-
		adenylylsulfate reductase [Arabidopsis
657	15186_s_at	thaliana] [Arabidopsis thaliana]
659	16609_s_at	AtERF2 (, BAA32419.1; AB008104)
		EREBP4-like, AtERF6 (, CAB10530.1;
660	12909_s_at	Z97343)
661	16536_s_at	AtERF5 (, BAA32422.1; AB008107)
		put. C2H2 zinc finger transcription factor (,
301	15665_s_at	AAB80922.1; AF022658)
		Myb-like (, emb CAA20567.1 (AL031394)
668	13176_at	putative protein
670	15778_at	X98676.2_at
671	20619_at	AC005896.161_at
672	12966_s_at	AL023094.197_s_at
673	20335_s_at	Y14208.2_s_at
674	18949_at	Z54136.1_at
675	13015_s_at	X98673.2 s at emb CAB41311.1

		(AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
676	19646_s_at	AC005819.55_s_at
677	19855_at	AC007260.16_at
		AC007047.101_at gb AAC49767.1
		(AF003094) AP2 domain containing protein
678	18475_at	RAP2.1 [Arabidopsis thaliana]
		unspecified t-factor gb AAC49775.1
		(AF003102) AP2 domain containing protein
679	13001_at	RAP2.9 [Arabidopsis thaliana]
		AC004665.101_at emb CAA67234.1
		(X98676) zinc finger protein [Arabidopsis thaliana]
680	15219_at	ATTHIRED4_s_at gb AAC98070.1
		(AC005896) putative C2H2-type zinc finger protein [Arabidopsis thaliana]
681	13189_s_at	hsp70_s_at emb CAA18838.1 (AL023094)
		bZIP transcription factor ATB2 [Arabidopsis thaliana]
684	13284_s_at	

Table 10

<u>Set</u>	<u>Content</u>	<u>Number of unique genes</u>
2	7 or 8 not edm1 not	55 genes
5	rps2 not pad4 or NahG	
3	edm1 not rps2 not pad4 or NahG	44 genes
4	rps2 not edm1 not pad4 or NahG	12 genes
5	pad4 or NahG not edm1 not rps2	20 genes
6	edm1 and rps2 not pad4 or NahG	17 genes
10	7	edm1 and pad4 or NahG not rps2
	8	rps2 and pad4 or NahG not edm1
	9	edm1 and rps2 and pad4 or NahG
		<u>11 genes</u>
	Total	184 genes

- 15 For engineering resistance to pathogens whose growth is restricted by RPP7 or RPP8 dependent responses, such as oomycete pathogens, all 184 genes are potentially useful. The 128 genes in sets 2, 3, 4, and 6 are more likely to be useful, as *pad4* and *NahG* do not interfere with resistance mediated by *RPP7* or *RPP8*, so genes under their control should not be important for this type of
- 20 resistance. The 99 genes in sets 2 and 3 are even more likely to be useful, because they not affected by *rps2*, and *RPP7* and *RPP8* trigger a different kind of resistance response than the one triggered by *RPS2*. The 44 genes in set 3 are

most likely to be useful, as they require *EDM1*, and *EDM1* is required for resistance.

Example 3

5 Transcriptional Responses Triggered by the RPP7 Defense Signaling Pathway

The *RPP7* defense-signaling pathway (Figure 1) mediates resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Hiks1. In contrast to conventional *R*-gene dependent defense signaling pathways in *Arabidopsis*, such as the *RPP4* pathway, the *RPP7* pathway does not essentially
10 require salicylic acid accumulation or previously described defense regulators, such as *EDS1*, *NDR1*, *NPR1*, *PAD4* and others.

A comparative analysis of transcriptional responses triggered by the *RPP7* and *RPP8* pathways was performed by gene expression profiling using Affymetrix oligonucleotide chips with roughly 8,200 different *Arabidopsis*
15 genes, representing roughly a third of the genome. For the analysis, 2 week old seedlings were harvested 0, 12 or 48 hours post infection with a particular *Peronospora* isolate (Table 11). To examine *RPP8* triggered transcriptional responses, a transgenic line Col-0 line carrying the *RPP8* resistance gene from the *Arabidopsis* ecotype Landsberg erecta was infected with the *Peronospora*
20 isolate Emco5. This interaction is incompatible. The interaction between Emco5 and Col-0 wild type plants served as compatible control. Responses triggered by the *RPP7* pathway were analyzed using the incompatible interaction between the *Peronospora* isolate Hiks1 and Col-0 wild type plants, as well as compatible interactions between Hiks1 and the susceptible mutants *rpp7*, *edm1*,
25 *edm2* and *edm3*. To compare transcriptional responses triggered by the unconventional *RPP7* and *RPP8* pathways with those triggered by the more conventional *RPP4* pathway, Col-0 wild type plants were infected with the *Peronospora* isolate Emoy2, which is avirulent on this ecotype. The interactions between Emoy2 and NahG plants, as well as the mutants *pad4*, *ndr1* and *npr1*,
30 served as compatible controls. Whereas *pad4* and NahG plants are fully Emoy2 susceptible, *ndr1* and *npr1* plants are only partly compromised in Emoy2 resistance.

Table 11

	<u>Plant</u>	<u>Peronospora isolate</u>	<u>Interaction type</u>
	Col-0 (tgRPP8)	Emco5	incompatible
	Col-0 (<i>rpp8</i>)	Emco5	compatible
5	Col-0 (<i>RPP7</i>)	Hiks1	incompatible (2x)
	Col-0 (<i>rpp7</i> ; 3929)	Hiks1	compatible
	Col-0 (<i>edm1</i>)	Hiks1	compatible
	Col-0 (<i>edm2</i>)	Hiks1	compatible
	Col-0 (<i>edm3</i>)	Hiks1	compatible
10	Col-0 (<i>RPP4</i>)	Emoy2	incompatible
	Col-0 (<i>ndr-1-1</i>)	Emoy2	intermediate
	Col-0 (<i>pad4-1</i>)	Emoy2	compatible
	Col-0 (<i>NahG</i>)	Emoy2	compatible
	Col-0 (<i>npr1-1</i>)	Emoy2	intermediate

15

ResultsIdentification of Genes Potentially Required for *RPP7* Mediated *Peronospora* Resistance

Genes that play a role in the establishment of resistance may show differences in their regulation or their expression levels between compatible and incompatible interactions (e.g., genes may show lower expression levels in “loss of Hiks-resistance mutants” as compared to Col-0 wild type plants). Thus, for each gene expression, ratios were calculated between Col-0 and each of the four Hiks response mutants (*rpp7*, *edm1*, *edm2* or *edm3*) at each time point (0, 12 and 48 hours). The resulting data set, consisting of 12 expression ratios for each of the 8,775 probe sets on the chip, was first analyzed with “CLUSTER” and “TREE VIEW”, two commonly used programs for chip and micro-array data analysis (Eisen et al., 1998). Genes that demonstrated only minor or less significant expression differences between Col-0 wild type and the mutants were excluded from analysis. Genes that showed at least one 3-fold expression difference over all 12 calculated expression ratios were first considered for further analysis.

Table 12 shows 194 probe sets corresponding to genes having SEQ ID NOs: 301-494, the expression of which is altered after infection of *Arabidopsis* with *P. parasitica* (wild-type relative to *rpp7*, *edm1*, *edm2*, or *edm3*). Table 13

depicts about 100 genes (genes comprising SEQ ID NOs: 373, 385, 242, 369, 306, 232, 346, 367, 212, 221, 307, 322, 240, 313, 270, 252, 383, 245, 377, 212, 327, 297, 375, 263, 250, 282, 358, 257, 332, 560, 284, 220, 259, 355, 248, 281, 215, 236, 309, 386, 253, 333, 336, 296, 319, 414, 354, 353, 293, 278, 324, 339, 345, 225, 249, 264, 310, 228, 214, 311, 343, 298, 384, 277, 314, 372, 331, 338, 370, 352, 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303, 274, 254, 223, 348, 318, 251, 291, 289, 361, 285, 368, 342, 290, 351, 312, 286, 287, 273, 239, 326, 226, 227, 350, 280, 317, 359, 294, 279, 382, 356, 234, 218, 217, 347, 379, 401, 378, 363, 341, 208, 268, 267, 364, 266, 337, 269, 269, 325, 793 and 224) represented by 137 probe sets that show at least one 3-fold-expression difference in comparisons between wild type *Arabidopsis* Col-0 and mutants *rrp7* or *edm1*, *edm2*, or *edm3* infected with *P. parasitica* Hiks1 (i.e., probe sets that show at least one 3-fold difference in expression levels over all 12 expression ratios calculated between Col-0 wild type and each of the 4 Hiks response mutants at each of the time points). Genes were grouped together according to similarities of their expression characteristics. Expression ratios were color encoded. Positive expression ratios were red and negative ratios were green. Black indicated no expression difference. Genes were represented in rows and infection treatments in columns. Red generally indicated that a gene at a given time point is more strongly expressed in Col-0 wild type plants as compared to the respective mutant. One cluster represented genes that are upregulated in response to Hiks1 infection by the *RPP7* pathway (Table 14; genes comprising SEQ ID NOs: 365, 261, 374, 238, 344, 241, 380, 371, 262, 258, 256, 304, 275, 303, 274, 254, 310, 228, 214, 347 and 225, which are induced by Hiks1-infection and which are *RPP7*, *EDM1*, *EDM2*, *EDM3*-dependent genes and so may encode regulators acting downstream of those genes; see probe sets 12505, 13217 and 12904 which correspond to genes that encode potential regulators of Hiks response pathway). Genes in this cluster represent genes that are more strongly expressed in Col-0 wild type than in all four mutants predominantly at the 12 hour time-point in each comparison. The expression difference is less pronounced in the case of *edm2* and *edm3*, but it is consistent over all four comparisons.

Table 12

Affy ID (Probe Set)	Reference No.
12324_i_at	AC007212
12333_at	AJ286345
12345_at	L36246
12500_s_at	AF081067
12505_s_at	AC005309
12608_i_at	S70188
12642_at	AC006920
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12911_s_at	X84229
12916_s_at	AF021244
13138_at	AL096882
13177_at	AL049640
13178_at	U93215
13187_i_at	U35829
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13273_s_at	U68017
13284_s_at	AJ002551
13604_at	AC000104
13615_at	AC002332
13617_at	AC006592
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14028_at	AF075597
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309

14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14295_s_at	Z54356
14595_at	AL022580
14608_at	AC007357
14614_at	AC004165
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14643_s_at	AC006836
14672_s_at	U18993
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
14965_at	AC002329
15057_at	AL035440
15085_s_at	AL031018
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15216_s_at	U75198
15431_at	AL030978
15496_at	AC006282
15523_s_at	AL078637
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15622_s_at	U43945

15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15950_at	AC006429
15954_at	U72155
15969_s_a	AJ133036
15978_at	X68592
15982_s_a	X98190
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16412_s_at	AL022603
16442_s_at	AJ002551
16461_I_at	AC004683
16462_s_a	AC004683
16504_s_at	Z97335
16510_at	AL034567
16514_at	AL035538
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16578_s_at	AL137080
16609_s_at	AB008104
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
16951_i_at	AC005662
16952_s_at	AC005662
16981_s_at	U35829
17014_s_at	U05206
17033_s_at	U83179
17054_s_at	AF134128
17073_s_at	AC006836
17119_s_at	AF132212
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17379_at	AC018721
17386_at	AC006264
17413_s_at	X99097

17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17549_s_a	L37126
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17917_s_at	AC004261
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18255_at	AC005770
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18591_at	X74756
18607_s_at	U78721
18635_at	AC004005
18706_s_a	X75782
18716_at	AC007396
18876_at	AF002109
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19594_i_at	X98321
19640_at	AC004561
19977_at	AL049659
20017_at	AC004521
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20297_at	AC007153
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336

20555_s_a	AL080318
20585_s_at	AC005309
20641_at	X91919

Table 13

Probe Set	Description
12324_i_at	AC007212
12345_at	L36246
12505_s_at	AC005309
12608_i_at	S70188
12746_i_at	AL096882
12748_f_at	AL096882
12761_s_at	AC006577
12773_at	AC005727
12778_r_at	AC006577
12798_at	AC003028
12802_at	AL022373
12842_s_at	
12843_s_at	AC007195
12845_s_at	AJ004810
12879_s_at	U40856
12891_at	U73786
12892_g_at	U73786
12904_s_at	AB008103
12908_s_at	AB008107
12911_s_at	X84229
13138_at	AL096882
13178_at	U93215
13189_s_at	U35829
13198_i_at	AL021749
13212_s_at	AL137080
13217_s_at	AL049862
13258_s_at	AC005309
13604_at	AC000104
13718_at	Z72152
13771_at	AC006593
13785_at	AC007087
14052_at	AC004122
14096_at	AC002291
14097_at	AC005309
14116_at	AF077407
14148_at	AF224762
14196_at	AC012563
14201_at	AL163972
14219_at	AC068667
14248_at	AC007357
14250_r_at	AL050300
14595_at	AL022580

14608_at	AC007357
14621_at	AC004747
14627_i_at	X76609
14628_r_at	X76609
14635_s_at	AC005398
14636_s_at	AC013258
14675_s_at	D85191
14691_at	AP002046
14704_s_at	AC006067
14709_at	AP002046
14711_s_at	AF085279
14731_s_at	AF014960
14784_at	AC005310
14951_at	AL049481
15057_at	AL035440
15105_s_at	Z14987
15116_f_at	AF121356
15125_f_at	D85190
15141_s_at	D85191
15145_s_at	D64155
15154_s_at	AL096860
15161_s_at	U90522
15178_s_at	U43489
15431_at	AL030978
15496_at	AC006282
15593_s_at	U54561
15611_s_at	L22567
15616_s_at	AJ009696
15846_at	AC006067
15847_g_at	AC006067
15950_at	AC006429
15954_at	U72155
16038_s_at	L04173
16063_s_at	AB008103
16105_s_at	U68017
16150_s_at	AL049730
16153_s_at	AC013258
16393_s_at	AC006436
16504_s_at	Z97335
16510_at	AL034567
16536_s_at	AB008107
16578_s_at	AL137080
16620_s_at	AF051338
16637_s_at	Z97336
16817_s_at	AL096882
16864_i_at	AL133248
17014_s_at	U05206
17033_s_at	U83179

17054_s_at	AF134128
17123_s_at	AF106087
17128_s_at	AC005398
17187_at	AF128396
17303_s_at	AC005499
17386_at	AC006264
17413_s_at	X99097
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17567_at	AL162751
17886_at	AC004484
17899_at	Z97339
17961_at	AC007323
17963_at	AL049730
18003_at	AF188334
18064_r_at	
18069_at	
18216_at	AC012375
18217_g_at	AC012375
18235_at	AC000348
18252_at	AL096882
18272_at	AF002109
18533_at	AL021684
18556_at	AC006264
18590_at	AJ222713
18607_s_at	U78721
18635_at	AC004005
18716_at	AC007396
18920_at	AC002338
18928_at	AC002338
19034_at	AL021768
19171_at	AC002335
19178_at	AB035137
19182_at	AL031804
19251_at	AL035538
19640_at	AC004561
19977_at	AL049659
20034_i_at	A71607
20201_at	AL078470
20227_s_at	AB027252
20269_at	AC002387
20314_s_at	AL096882
20335_s_at	Y14208
20429_s_at	Z97336
20585_s_at	AC005309
20641_at	X91919

Table 14

Probe Set	Description
12505_s_at	AC005309
12879_s_at	U40856
12904_s_at	AB008103
13189_s_at	U35829
13217_s_at	AL049862
14116_at	AF077407
14148_at	AF224762
14201_at	AL163972
14248_at	AC007357
14250_r_at	AL050300
14691_at	AP002046
14704_s_at	AC006067
15846_at	AC006067
15847_g_at	AC006067
16063_s_at	AB008103
17500_s_at	AL049862
17544_s_at	U40856
18716_at	AC007396
19178_at	AB035137
19640_at	AC004561
20269_at	AC002387

Thus, Hiks1 induced upregulation is compromised in all four tested “loss of Hiks1 resistance mutants” and there is a correlation between breakdown of resistance and deregulation of these genes. This may indicate that these genes play important roles in mediating Hiks1 resistance. Furthermore, these genes appear to act downstream of all four genetically defined *RPP7* pathway components, *RPP7*, *EDM1*, *EDM2* and *EDM3*. Some genes of this set may encode important regulators; whereas others may indicate metabolic processes required for Hiks1 resistance.

Seventy-eight genes (Table 15; genes comprising SEQ ID NOs:330, 292, 311, 243, 237, 302, 315, 283, 300, 372, 308, 335, 272, 305, 357, 213, 362, 331, 254, 384, 277, 343, 298, 349, 314, 265, 262, 258, 256, 303, 321, 304, 275, 274, 323, 238, 374, 241, 344, 244, 365, 261, 380, 371, 295, 255, 316, 233, 345, 225, 260, 229, 324, 301, 235, 340, 278, 320, 231, 319, 230, 354, 353, 293, 376, 247, 246, 366, 216, 214, 276, 299, 310, 334, 271, 381 and 228) that show the same, but less pronounced, expression characteristics were selected using relaxed selection criterion (at least one 2-fold expression difference over all 12 calculated expression ratios). With a lower cutoff criterion of at least one 2-fold-expression difference across all twelve expression ratios, this cluster is larger

than that shown in Table 14. Genes that are part of this less stringently defined cluster were included in further analyses so as to not exclude potentially important genes. Potential regulators in this cluster are listed in Table 16 (genes comprising SEQ ID NOs: 220, 323, 231, 319, 214, 301, 340, 243, 227, 321, 235, 5 315, 298, 314, 328, 344 and 349). Four different ERF transcription factors genes are upregulated by the *RPP7*-pathway. Genes encoding ERFs are known to be upregulated in response to several stress-related stimuli, such as wounding, pathogens or ethylene. Moreover, ERF transcription factors bind to GCC boxes, which are ethylene, wounding and pathogen-responsive *cis*-elements. This 10 cluster also contains a gene encoding an ACC synthase, a component of the ethylene biosynthetic pathway. Therefore, ethylene may play a role in the Hiks response pathway.

Table 15

Probe Set	Description
12500_s_at	AF081067
12505_s_at	AC005309
12642_at	AC006920
12879_s_at	U40856
12904_s_at	AB008103
12905_s_at	AB008104
12908_s_at	AB008107
12909_s_at	Z97343
12916_s_at	AF021244
13177_at	AL049640
13187_i_at	U35829
13189_s_at	U35829
13217_s_at	AL049862
13273_s_at	U68017
13284_s_at	AJ002551
13615_at	AC002332
13617_at	AC006592
14116_at	AF077407
14141_at	AC011437
14148_at	AF224762
14201_at	AL163972
14223_at	AL024486
14248_at	AC007357
14250_r_at	AL050300
14614_at	AC004165
14643_s_at	AC006836
14672_s_at	U18993

14691_at	AP002046
14704_s_at	AC006067
14706_r_at	AL137189
14709_at	AP002046
14711_s_at	AF085279
15085_s_at	AL031018
15216_s_at	U75198
15431_at	AL030978
15523_s_at	AL078637
15616_s_at	AL078637
15622_s_at	U43945
15629_s_at	AB010407
15665_s_at	AF022658
15680_s_at	D42061
15846_at	AC006067
15847_g_at	AC006067
15866_s_at	AC005770
15978_at	X68592
16063_s_at	AB008103
16105_s_at	U68017
16393_s_at	AB008103
16412_s_at	U68017
16442_s_at	AJ002551
16536_s_at	AB008107
16539_s_at	Z97343
16569_s_at	L23968
16609_s_at	AB008104
16620_s_at	AF051338
16952_s_at	AC005662
16981_s_at	U35829
17073_s_at	AC006836
17119_s_at	AF132212
17379_at	AC018721
17499_s_at	AF107726
17500_s_at	AL049862
17544_s_at	U40856
17917_s_at	AC004261
18070_r_at	
18216_at	AC012375
18217_g_at	AC012375
18255_at	AC005770
18591_at	X74756
18716_at	AC007396
18876_at	AF002109
19178_at	AB035137
19182_at	AL031804
19640_at	AC004561
20017_at	AC004521

20269_at	AC002387
20297_at	AC007153
20429_s_at	Z97336

Additionally, a gene encoding a lipoxygenase, a component of the jasmonic acid biosynthetic pathway, is upregulated. Other regulators potentially acting downstream of RPP7, EDM1, EDM2 and EDM3 include some putative zinc finger transcription factors and protein kinases as well as two calmodulin-like proteins and a calcium binding protein, which may point to a role of calcium in the *RPP7*-pathway.

Table 16

10 I. Transcriptional regulators:

- 1.) AtERF1 (12904_s_at, BAA32418.1; AB008103)
- 2.) AtERF2 (16609_s_at, BAA32419.1; AB008104)
- 3.) EREBP4-like (12909_s_at, CAB10530.1; Z97343)
- 4.) AtERF5 (16536_s_at, BAA32422.1; AB008107)
- 15 5.) putative CONSTANS-like zinc finger (12505_s_at, AAC63643.1; AC005309)
- 6.) putative C2H2 zinc finger transcription factor (15665_s_at, AAB80922.1; AF022658)
- 7.) putative C3H zinc finger protein (17379_at, AAF18728.1; AC018721)
- 20 8.) heat shock transcription factor 4 (13273_s_at, AAC31756.1; U68017)
- 9.) SigA binding protein (14148_s_at, AAF34713.1; AF224762)

II. Other signaling proteins

- 10.) AtACS-6 (12892_g_at, CAB51412.1, AL096882, 35400..37154)
- 11.) lipoxygenase (16569_s_at, AAA32749.1; L23968)
- 25 12.) growth factor like protein (13177_at, CAB40989.1; AL049640)
- 13.) serine/threonine protein kinase (16412_s_at, CAA18704.1; AL022603)
- 14.) wall associated kinase 1 (15616_s_at, CAB08794.1; AJ009696)
- 15.) putative receptor-like protein kinase (16393_s_at, AAD28318.1; AC006436)
- 30 16.) calmodulin-like (16951_i_at, AAC78532.1; AC005662)
- 17.) calmodulin-like (17500_s_at; CAB42906.1; AL049862)
- 18.) calcium binding protein (17917_s_at, AAD12002.1; AC004261)

Twenty-six genes (genes comprising SEQ ID NOs: 300, 308, 272, 213, 362, 265, 374, 241, 261, 380, 310, 228, 233, 330, 311, 243, 237, 254, 230, 244, 365, 216, 316, 345, 225, 301, 278, 354, 353, 293, 335, 271 and 321, also shown in Table 15), represented by 33 probe sets, were found to be commonly

5 upregulated in response to both *Peronospora* isolates, Hiks1 and Emco5, in an RPP7- or RPP8-dependent (and EDM1, EDM2 and EDM3-dependent) manner (Table 17). Elevated expression of these genes may be required for resistance against both *Peronospora* isolates or against *Peronospora parasitica* in general. Among these 26 genes are those encoding ERF1, putative zinc finger

10 transcription factors, two proteins potentially involved in calcium signaling, a lipxygenase, and a cysteine rich antifungal protein.

Table 17

15	26 <i>Peronospora</i> (Hiks1 and Emco5) induced RPP8, RPP7, EDM1,2,3-dependent genes	
	Transcription factors	
	AtERF1	
	Putative salt-tolerance zinc finger transcription factor (18217_g_at)	
20	(ZFPI) hypothetical Cys-3-His zinc finger protein	
	Putative C2H2 zinc finger transcription factor	
	Heat shock transcription factor 4	
	Other potential proteins	
25	Calmodulin-like protein	
	Similarity to centrin, <i>Marsilea vestita</i> contains EF-hand calcium-binding domain (15431_at)	
	Lipxygenase	
30	Others	
	heat shock protein 70	
	putative steroid sulfotransferase	tryptophan synthase alpha chain
	putative glucosyltransferase	similar to xyloglucan fucosyltransferase (12642_at)
35	phosphoglycerate dehydrogenase	Pad3 (Cytochrome P450)
	ATAF2	putative pectinesterase
	OPDA-reductase homolog	AIG1
	coronatine-induced protein 1	putative glutathione S-transferase
	thioredoxin h	adenosine nucleotide translocator
40	IAA-amino acid hydrolase	contains similarity to sugar transporters
		CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 PRECURSOR (AFP1) (18716_at)

Thirteen of these 26 genes (genes comprising SEQ ID NOs: 308, 300, 272, 362, 265, 242, 261, 380, 228, 243, 254, 216 and 225, *Peronospora* (Hiks1, Emco5 and Emoy2) induced and *RPP4*, *RPP8* and *RPP7* dependent) were also found to be more strongly expressed during the incompatible interaction between the *Peronospora* isolate Emoy2 and Col-0 plants as compared to Emoy2 infections of the compatible or intermediate type (see Table 18). These 13 genes may play an important role in defense against *Peronospora parasitica* in general. Among these genes is PAD3, which was previously demonstrated to be required for pathogen-induced phytoalexin production. Strikingly, Hiks1 resistance is partially compromised in the *pad1-1/pad3-1* double mutant, whereas Emoy2 resistance is reduced in the *pad3-1* single mutant (Glazebrook et al. 1997).

Table 18

13 *Peronospora* (Hiks1, Emco5 and Emoy2) induced
RRP4-pathway, RPP7-pathway, and RPP8-dependent genes

- adenosine nucleotide translocator (15978_at)
- phosphoglycerate dehydrogenase (15629_s_at)
- tryptophan synthase alpha chain (14672_s_at)
- ATAF2 (18591_at)
- putative glucosyltransferase (14614_at)
- calmodulin-like protein (13217_s_at)
- pad3 (cytochrome P450)(14248_at)
- putative pectinesterase (20269_at)
- ethylene responsive element binding factor 1 (12904_s_at)
- heat shock transcription factor 4 (13273_s_at)
- sugar transporter-like (14116_at)
- similar to xyloglucan fucosyltransferase (12642_at)
- AIG1 (12879_s_at)

Identification of promoter motifs common to *RPP7* and *RPP8* controlled genes

Sequence motifs conserved in the promoters of genes co-regulated by the *RPP7* or *RPP8* pathways may lead to information about the types of transcription factors controlling expression of these genes and may serve as starting points for isolating and/or cloning of such factors. Sub-categorization of *RPP7*-

5 upregulated genes by K-means clustering, based on the absolute expression levels of the genes, revealed the existence of only a few basic expression profiles. K-means clustering into five gene sets gave the most consistent and tight clusters. For each of the five gene sets (Table 19), the expression changes in two repetitions of the Col-0 wild type/Hiks1 interaction are shown as well as
10 in the *rpp7* mutant and *edm1*, *edm2* and *edm3*.

The first set comprises genes (genes comprising SEQ ID NOs: 292, 302, 315, 300, 308, 213, 265, 374, 241, 344, 261, 299, 365 and 276) that show early and transient upregulation. The genes peak at 12 hours and return to their ground-states at approximately the 48 hours post infection. Genes of the second
15 set (genes comprising SEQ ID NOs: 267, 305, 357, 362, 380, 310, 228, 295, 233, 329, 312, 243, 237, 283, 372, 254, 314, 323, 216, 260, 229 and 235) are also rapidly upregulated, but show a less pronounced or no decline after the peak. In both sets, the response is weaker in the mutants. Only a few genes in the first set respond almost as strongly in *edm2* and *edm3* plants as in wild type plants.

20 Genes of the third (genes comprising SEQ ID NOs: 258, 256, 303, 304, 275, 244, 316, 354 and 225) and fifth (genes comprising SEQ ID NOs: 330, 384, 277, 343, 298, 349, 262, 274, 238 and 301) set show an almost linear increase of transcript level in wild type. In the mutants, this increase is delayed and in some cases less steep. In the fourth set (genes comprising SEQ ID NOs: 432, 347,
25 370, 412, 323, 411, 322, 449, 448, 385, 471, and 339) the expression levels rise in the first repetition of the Col-0 wild type/Hiks interaction, but respond very little in the second one. In *edm3*, the transcript levels drop from a high ground state. The probe sets and genes corresponding to each of these K-means cluster sets are shown in Table 19.

30

Table 19

K-means set 1	Description	K-means set2	Description
12500_s_at	AF081067	12642_at	AC006920
13217_s_at	AL049862	12904_s_at	AB008103
14248_at	AC007357	12905_s_at	AB008104

14614_at	AC004165	12916_s_at	AF021244
14706_r_at	AL137189	13177_at	AL049640
15216_s_at	U75198	13187_i_at	U35829
15622_s_at	U43945	13273_s_at	U68017
15629_s_at	AB010407	14116_at	AF077407
15680_s_at	D42061	14223_at	AL024486
15978_at	X68592	14672_s_at	X76609
16412_s_at	U68017	15085_s_at	AL031018
17500_s_at	AL049862	15523_s_at	AL078637
18070_r_at		15866_s_at	AC005770
18716_at	AC007396	16063_s_at	AB008103
19640_at	AC004561	16105_s_at	AL049730
		16393_s_at	AC006436
		16609_s_at	AB008104
		16952_s_at	AC005662
K-means set 3	Description	18255_at	AC005770
12879_s_at	U40856	18591_at	X74756
13284_s_at	AJ002551	19182_at	AL031804
14148_at	AF224762	20269_at	AC002387
14201_at	AC068667		
14704_s_at	AC006067		
15846_at	AC006067	K-means set 5	Description
15847_g_at	AC006067	13189_s_at	U35829
16442_s_at	AJ002551	14250_r_at	AL050300
17544_s_at	U40856	14691_at	AP002046
		14709_at	AP002046
K-means set4	Description	15616_s_at	AJ009696
12908_s_at	AB008107	15665_s_at	AF022658
12909_s_at	Z97343	16981_s_at	U35829
13617_at	AC006592	17499_s_at	AF107726
14141_at	AC011437	17917_s_at	AC004261
14711_s_at	AF085279	20429_s_at	Z97336
15431_at	AL030978		
16536_s_at	AB008107		
16539_s_at	Z97343		
17379_at	AC018721		
18216_at	AC012375		
18217_g_at	AC012375		
20017_at	AC004521		

Recently, the plant specific family of WRKY transcription factors has been implicated in the regulation of defense-associated genes. Promoters of genes upregulated during systemic acquired resistance were found to be strongly enriched in potential WRKY binding sites. WRKY factors comprise a large family of 72 different members in *Arabidopsis*. Generally these factors appear to bind to sequence motifs containing the core T G A C (W box). It has not yet

been determined whether individual WRKY family members differ in their preferences for distinct W box variations. However, it is probable that a given WRKY protein has a binding preference for a certain variation of the W box motif.

5 Using the program AlignACE, three variations of potential WRKY binding sites were found to be conserved in sub-sets of *RPP7* controlled genes. Two of these motifs are highly enriched in promoters of genes from K-means cluster 3, representing genes that show a linear increase in transcript level after *Peronospora* infection (Table 20; genes comprising SEQ ID NOs: 384, 298, 349, 10 262 and 238 for W box I and genes comprising SEQ ID NOs: 384, 349, 262, 238 and 301 for W box II). These motifs are also present in promoters of K-means cluster 5, which represents a similar expression profile. Focusing on sustained up-regulated genes, that show a particularly pronounced expression difference between Col-0 wild type plants and the Hiks1 response mutants, a third variation 15 of potential WRKY binding sites was found to be significantly enriched (Table 21; genes comprising SEQ ID NOs: 397, 371, 238, 262, 256, 275, 254, 214 and 225). In all three cases, sequence conservation clearly exceeds the core motif of WRKY binding sites that appears to be recognized by all members of this family. These additionally conserved positions may confer specificity for 20 certain WRKY family members. They may provide a highly defined binding site preferentially recognized by a distinct WRKY factor or may serve as binding sites for another transcription factor binding closely adjacent to and specifically interacting with a distinct WRKY factor. In any case, the high conservation of extended potential WRKY binding motifs strongly suggests that specific 25 members of this family participate in the regulation of certain sub-sets of *RPP7*-controlled genes.

Table 20

	<u>W box I</u> MAP Score: 8.98114	
30	GTCATCTTTTAATCTCTGG	0 638 1
	GTCATCTTTTAATCGCCGG	0 932 1
	GCCTTTGCTTATTTATAGG	0 1036 1
	GTCATTTGTTACAAAGAGG	1 318 1
	GTCATTGATCATAAACTGT	1 389 0
35	GCCACTGCTGAATTGTCGG	1 494 1
	GTCCATTGTCAATAAATGG	2 689 1
	GTCCATTGTAAATAAATGT	2 949 1

5 GTCATCTTTTAATCTCTGT 3 475 0
 GTCACGTATGAATGGAAGG 4 73 1
 GTCAACGTTTAGTTCATGT 4 226 0
 GTCAAGTTTAAATTGTGG 4 352 1
 GTCAACGTTTAGTTCATGT 4 401 0
 *** * * * * **
 GTCANNTNTNANTNNNNGG

G A T

Expected frequency by chance: 0.02/1kb
 10 Observed frequency: 1.2/1kb
 Enrichment: ~60 fold
W box II MAP Score: 15.2966

15 ATTAAAAGATGAC 0 638 0
 ATTAAAAGATGAC 0 932 0
 ATTAAATGCTGTC 2 752 0
 ATTAAATGCTGTC 2 1011 0
 AGCAAAAGCTGAC 2 1092 1
 ATTAAAAGATGAC 3 481 1
 ATCAAAAGTTGTC 3 829 1
 20 ACTAAACGTTGAC 4 232 1
 ACTAAACGTTGAC 4 407 1
 ACTAAAAAGTGAC 5 755 1
 * * * * *

25 W II ANTAAANGNTGAC
 C A T

W I: CCNNNNANTNANCNNTGAC
 A T A

30 Expected frequency by chance: 0.04/1kb
 Observed frequency: 1.35/1kb
 Enrichment: ~30 fold
 Table 21

35 ATAGGTGGTCAAGT 1 106 0
 AATTGTGGTCATTT 1 823 0
 ACTTGTGGTCAATT 2 804 0
 AAAAGGGGTCATTT 2 970 1
 ATATGTCGTCTCTT 2 994 0
 AGTTGTGGTCTACC 3 502 0
 40 AAAAGTTGTCAATT 3 732 1
 AGACGTCGTAATTT 4 400 0
 ACGTGGCGTCATAT 5 179 0
 ATGTGGCGTCTCCT 6 249 1
 AGTTGGTGTACGTC 6 925 1
 45 ATTCGTGGTCAACT 7 582 1
 ATATGTCGTCACTT 7 875 1
 * * * * *
 ANNGTNGTCANNT

G

50

expected: 0.05/1kb;
 in random set: 0/1kb;
 this set: 1/1kb;
 enrichment: 10-20 fold;

5

Novel, conserved promoter motifs were also found. Genes of K-means set 1, which are early and transient *RPP7*-pathway specific genes, share two similar highly conserved promoter motifs, G G T/C C C A (SEQ ID NO:714; genes comprising SEQ ID NOs: 302, 315, 308, 265, 374, 241, 261, 299 and 365) and G N C C A A A (SEQ ID NO:715; genes comprising SEQ ID NOs: 292, 302, 308, 265, 374, 241, 261, 299, 365 and 276) (Table 22). Both motifs are almost perfectly conserved and are represented in nearly all promoters of this gene set. They are compact six- or seven-mers, which is typical for transcription factor binding sites. For the second motif, the permutations G A C C A A A and G T C C A A A are strongly represented. These permutations may constitute the preferred binding site of a so far unknown transcription factor.

15

Table 22

Two related novel motifs are highly enriched in all
 11 promoters of K-means set1

20

GGTCCA 1 232 0
 GGCCCA 1 289 1
 GGTCCA 1 597 1
 25 GGTCCA 2 517 0
 GGTCCA 3 211 1
 GGCCCA 3 360 1
 GGTCCA 4 597 1
 GGCCCA 4 681 1
 30 GGTCCA 5 352 0
 GGTCCA 5 1060 1
 GGTCCA 6 358 0
 GGCCCA 7 776 0
 GGCCCA 7 816 0
 35 GGTCCA 8 285 0
 GGTCCA 9 888 1

GGTCCA C

Expected frequency by chance: 0.22/1kb

40 Observed frequency: 1.2/1kb

Enrichment: 5.4 fold

GCCCAAA 0 601 1

GTCCAAA 10 1186 1

GTCCAAA 9 562 1

5 GACCAAA 8 640 0
 GCCCAA 7 774 0
 GTCCAA 7 717 1
 GTCCAA 6 712 1
 5 GACCAAA 5 970 1
 GTCCAA 5 350 0
 GACCAAA 4 1164 1
 GACCAAA 4 1072 1
 GTCCAA 4 784 0
 10 GACCAAA 4 714 0
 GGCCAA 4 698 0
 GCCCAA 3 361 1
 GACCAAA 1 920 0
 GTCCAA 1 230 0
 15 *****
 GNCCAA
 Expected frequency by chance: 0.32/1kb
 Observed frequency: 1.3/1kb
 Enrichment: 4 fold
 20

Following a similar approach as for the Hiks1-induced *RPP7* pathway controlled genes, a cluster of early and transiently Emco5-induced *RPP8*-dependent genes were defined (Table 23). In Col-0-*RPP8* plants these genes (genes comprising SEQ ID NOs: 364, 341, 288, 378, 363, 379 and 219) show a
 25 very pronounced upregulation 12 hours post Emco5 infection, after which they return to expression ground states. Using AlignACE, two different motifs (see Example 2) were found to be strongly enriched in the promoters of this cluster. The first motif strongly resembles the type I consensus binding site of Myb transcription factors. This motif is also almost identical to a recently identified
 30 *cis*-element conferring rapid elicitor responsive gene expression in parley cell culture (Kirsch et al., 2001). Interestingly, a gene encoding a Myb-like transcription factor (highlighted in yellow) is co-regulated with other genes of this cluster. The Myb-like transcription factor gene is the only gene of this cluster that does not contain this conserved motif in its promoter. This MYB-
 35 like factor could be a regulator of this cluster. The second motif does not resemble any known stress responsive plant *cis* element or transcription factor binding site. However, the second motif was found to be strongly represented in promoters from other defense related genes, such as SAR genes. As is typical of many transcription factor binding sites, certain permutations of its consensus

sequence may constitute palindromes. This motif was also found to be conserved by the program MEME.

Table 23

5	Glutathione-conjugate transporter AtMRP4 putative GST putative cytochrome P450 (AC002340) PAD3 (similar to cytochrome P450) CTF2B (similarity to proteins involved in Hydroxylation and oxidation of aromatic rings)	
10	Ribonuclease RNS1 Putative Myb-like protein AlignACE Motif 1:	CAACTTTGAC AA TT CAACTG T G
15	type I Myb binding site:	
	Frequency by chance: 0.05/1kb Observed frequency in control cluster: 0.13/1kb	
20	Observed frequency in this cluster: 1.10/1kb AlignACE Motif2:	TTGGGNCNAA A A
	MEME motif:	GTCTNTTGGGNCAAAA T T A G C
25	Frequency by chance: 0.13/1kb Observed frequency in control cluster: 0/1kb Observed frequency in this cluster: 1.2/1kb	

Different types of transcription factors may participate in the control of distinct *RPP7*-pathway dependent expression profiles. Promoters of genes showing a linear sustained increase of transcript are enriched in different variations of WRKY binding sites. However, no *WRKY*-pathway gene was found to be upregulated by the *RPP7* pathway. Therefore, WRKY factors involved in *RPP7* mediated up-regulation of K-means cluster 3 and 5 genes may already be pre-formed when the pathogen signal is perceived. However, only 21 *WRKY* genes out of 72 members of this family in *Arabidopsis* are represented on the oligonucleotide chip. Upregulated WRKY factors participating in *RPP7* mediated gene regulation may not be present on the chip. A novel type of transcription factor may be involved in regulation of early and transient *RPP7*-controlled genes (K-means cluster 1). Promoter stretches containing this motif may be used in yeast one hybrid screenings for novel factors. In addition, transgenic plants carrying appropriate promoter-reporter constructs could be used

as a basis for mutant screenings with the aim of identifying regulators acting on this motif.

A Myb-like transcription factor appears to be involved in the regulation of early and transient *RPP8*-controlled genes. A gene showing a similar pattern of regulation may encode a candidate factor controlling this cluster. The potential role of this factor in regulating *RPP8*-controlled genes may be examined using T-DNA insertion mutants.

Potential constitutive effects of the *RPP7*-pathway

In order to focus on genes showing multiple expression differences between Col-0 wild type plants and Hiks response mutants, all genes that showed at least four 1.8-fold expression differences across all comparisons were selected. The resulting clustergram contains the majority of *RPP7* pathway-dependent Hiks1-induced genes. Two more clusters of genes behaving consistently in all four tested Hiks1-response mutants were found. The first cluster comprises genes that show at all tested time points (including the 0 hpi time point) elevated transcript levels in Col-0 wild type plants as compared to all four mutants (Table 24; genes comprising SEQ ID NOs: 364, 288, 378, 363, 379, 219, 399, 389 and 390). In most cases, expression levels are not affected by Hiks1 infection. These elevated expression levels may be directed by constitutive (non Hiks1-triggered) signal flow via the *RPP7* pathway. This signal flow is disrupted in the *rpp7*, *edm1*, *edm2* and *edm3* mutants. Constitutive expression of these genes may be required for effective disease resistance and may be a prerequisite for induction of subsequent defense responses. A HD-ZIP transcription factor, which is included in this cluster, may act as a pre-formed regulator controlling genes responding to Hiks1-recognition. Its potential role in regulating *RPP7* pathway-dependent genes may be examined using T-DNA insertion mutants.

Table 24

The *RPP7* pathway constitutively activates a cluster of genes including a HD-ZIP transcription factor

PROBE SET	DESCRIPTION
14965 at	AC002329
18635 at	AC004005
14295 s at	Z54356
17386 at	AC006264

15145_s_at	D64155
20201_at	AL078470
18607_s_at	U78721
20227_s_at	AC007153
12761_s_at	AC006577
20555_s_a	AL080318

Genes of the second cluster show the opposite behavior (Table 25). Their transcript levels are elevated in all four Hiks1 response mutants as compared to Col-0 wild type plants. Hiks1-infection does also not affect their expression levels. Surprisingly, this cluster contains six genes encoding peroxidases. Since peroxidases are believed to play roles in conferring disease resistance, the biological significance of this phenomenon is obscure. Perhaps the mutant plants “realize” disruption of the *RPP7*-defense pathway and compensate for their reduced defense capacity by constitutively up-regulating some defense mechanisms. Alternatively, elevated expression of these peroxidases may be advantageous for invading *Peronospora* hyphae. Therefore, expression of these genes could be constitutively reduced by the *RPP7* pathway.

Table 25

Probe Set	Description
15982_s_at	X98190
15954_at	U72155
12333_at	AJ286345
19594_i_at	X98321
15969_s_at	AJ133036
16462_s_at	AC004683
16461_i_at	AC004683
12324_i_at	AC007212
12778_r_at	AC006577
16514_at	AL035538
17549_s_at	L37126
14028_at	AF075597
17054_s_at	AF134128

Predictions about *RPP7*-pathway hierarchy

Clustering of the Hiks1-infection data in the “treatment” dimension, instead of the “gene” dimension, revealed that at all three infection time points, gene expression profiles of the *rpp7* mutant resemble most those of the *edm1* mutant. Similarly, expression profiles of the *edm2* mutant resemble those of the

edm3 mutant. This may indicate that RPP7 and EDM1 closely act together at a certain level in the *RPP7* signalling cascade, whereas EDM2 and EDM3 may act closely together at a different level of the pathway. Close interaction of RPP7 and EDM1 is also suggested by a T-DNA tagged *rpp7* mutant that

5 phenotypically resembles the *edm1* mutant. In contrast to *rpp7*, *edm2* and *edm3*, which appear only to be compromised in resistance against the *Peronospora* isolate Hiks1, *edm1* is also compromised in resistance to other *Peronospora* isolates that are avirulent on Col-0 plants. Like *edm1*, the putatively T-DNA tagged *rpp7* mutant is also susceptible to a variety of normally Col-0

10 incompatible *Peronospora* isolates. This observation may indicate that the EDM1 protein requires a portion of the RPP7 protein for proper function, which is disrupted in the T- DNA tagged *rpp7* mutant. Assuming that RPP7, which appears to constitute an NBS-LRR receptor, acts at the top of the Hiks1 recognition pathway hierarchy, EDM1 could act at a high level as well and

15 EDM2 and EDM3 may act more downstream in the cascade.

Table 26



Table 27 shows the plant and fungal orthologs of the *Arabidopsis* sequences identified herein.

Table 27

Query= AIG1_s at 12879_s at /id_source genbank /description gb aac49282.1 (u40856) aig1 [arabidopsis thaliana] /blast_score 1.00e-150	
5	(1381 letters)
Database: plantfungal 661,018 sequences; 426,114,510 total letters	
10	Searching.....done
Score E Sequences producing significant alignments: (bits) Value	
15	gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ... 260 1e-68 emb AW625701 AW625701 EST319608 tomato radicle, 5 d post-imbibit... 228 6e-59 emb AW720227 AW720227 LjNEST17c4r Lotus japonicus nodule library... 219 4e-56 emb AW220184 AW220184 EST302667 tomato root during/after fruit s... 208 7e-53 emb AI774580 AI774580 EST255680 tomato resistant, Cornell Lycopersicon... 173 2e-42
20	emb AW685484 AW685484 NF030E02NR1F1000 Nodulated root Medicago t... 171 2e-41 emb AI443867 AI443867 sa44d09.y1 Gm-c1004 Glycine max cDNA clone... 170 3e-41 emb AW397252 AW397252 sg76f06.y1 Gm-c1007 Glycine max cDNA clone... 168 1e-40 emb AW033368 AW033368 EST276939 tomato callus, TAMU Lycopersicon... 162 5e-39 emb AV417858 AV417858 AV417858 Lotus japonicus young plants (two... 153 4e-36
25	emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lycopersicon... 138 9e-32 emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycopersicon... 111 2e-23 emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lycopersicon... 86 7e-16 emb AW164180 AW164180 Ljimp21-672-c8 Ljimp Lambda HybriZap ... 84 2e-15 emb AI781596 AI781596 EST262475 tomato susceptible, Cornell Lycopersicon... 75 1e-12
30	emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo... 62 7e-09 emb AW348781 AW348781 GM210003A22H11R Gm-r1021 Glycine max cDNA ... 54 2e-06 emb AI491210 AI491210 EST241919 tomato shoot, Cornell Lycopersicon... 29 0.010 emb AW651526 AW651526 EST329980 tomato germinating seedlings, TAMU ... 29 0.011 emb AW220594 AW220594 EST296979 tomato fruit mature green, TAMU ... 29 0.011
35	emb AW926585 AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis... 29 0.025 emb AW032321 AW032321 EST275775 tomato callus, TAMU Lycopersicon... 28 0.026 emb AW736598 AW736598 EST333090 KV3 Medicago truncatula cDNA clo... 37 0.39 emb AW736597 AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 37 0.39 emb AW713727 AW713727 h1f12ne.fl Neurospora crassa evening cDNA ... 35 1.0
40	emb AW711542 AW711542 f3g07ne.fl Neurospora crassa evening cDNA ... 35 1.0 emb AB009972 AB009972 Aspergillus oryzae gene for beta-1,4-xyl... 35 1.0 emb AW713709 AW713709 h1e09ne.fl Neurospora crassa evening cDNA ... 35 1.0 emb AW712721 AW712721 g3a07ne.fl Neurospora crassa evening cDNA ... 35 1.0 emb AW709185 AW709185 d3e02ne.fl Neurospora crassa evening cDNA ... 35 1.0
45	emb Y09354 SPABC1 S.pombe ABC1 gene. 35 1.4 emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9. 35 1.4 emb AJ225108 STA225108 Solanum tuberosum (cultivar Bintje) mitoc... 35 1.4 emb AW933326 AW933326 EST359169 tomato fruit mature green, TAMU ... 26 1.5 emb Z25870 CACDC10G C.albicans CDC10 gene for cell division cycl... 31 1.5
50	emb AC008368 AC008368 Trypanosoma brucei chromosome II clone RPC... 35 1.9 emb AQ942780 AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso... 35 1.9 emb AQ953508 AQ953508 Sheared DNA-33G8.TR Sheared DNA Trypanosom... 35 1.9 emb AC009463 AC009463 Trypanosoma brucei chromosome II clone RPC... 35 1.9 emb AQ950237 AQ950237 Sheared DNA-39C11.TF Sheared DNA Trypanoso... 35 1.9
55	emb AQ643883 AQ643883 RPCI93-DpnII-26C13.TV RPCI93-DpnII Trypano... 35 1.9 emb AQ948491 AQ948491 Sheared DNA-49H2.TF Sheared DNA Trypanosom... 35 1.9 emb AW727289 AW727289 GA_Ea0011H24 Gossypium arboreum 7-10 dpa ... 35 1.9 emb AW729536 AW729536 GA_Ea0025E24 Gossypium arboreum 7-10 dpa ... 35 1.9 gb L36856 PEAIAP34A Pisum sativum GTP-binding protein (IAP34) mR... 28 2.1
60	emb Z28341 PSCLOEP P.sativum (miranda) mRNA for chloroplast oute... 28 2.1

- emb|AW776020|AW776020 EST335085 DSIL Medicago truncatula cDNA cl... 28 2.2
 emb|AW685649|AW685649 NF032G04NR1F1000 Nodulated root Medicago t... 28 2.2
 emb|AW690755|AW690755 NF037H10ST1F1000 Developing stem Medicago ... 28 2.2
 emb|AW256896|AW256896 EST305033 KV2 Medicago truncatula cDNA clo... 28 2.3
 5 emb|AV422565|AV422565 AV422565 Lotus japonicus young plants (two... 28 2.3
 emb|AW832303|AW832303 sm07c04.y1 Gm-cl027 Glycine max cDNA clone... 27 2.3
 emb|AL136538|SPAC30 S.pombe chromosome I cosmid c30. 34 2.6
 emb|AI724721|AI724721 RHIZ1_26_C05.y2_A001 Rhizome1 Sorghum hale... 34 2.6
 emb|AW256609|AW256609 EST304746 KV2 Medicago truncatula cDNA clo... 34 2.6
 10 emb|AI775696|AI775696 EST256796 tomato resistant, Cornell Lycopersicon... 28 3.1
 emb|Z71682|SCYNR067C S.cerevisiae chromosome XIV reading frame O... 34 3.6
 emb|AI776315|AI776315 EST257415 tomato resistant, Cornell Lycopersicon... 34 3.6
 emb|AF230371|AF230371 Lycopersicon esculentum allene oxide synth... 34 3.6
 emb|AA741645|AA741645 LmLv39p3/255A Leishmania major promastigot... 34 3.6
 15 gb|U08843|PPU08843 Porphyra purpurea putative polysaccharide bin... 34 3.6
 emb|AF124792|AF124792 Sporothrix schenckii protein kinase C (PCK... 29 4.7
 emb|AQ399149|AQ399149 mgxb0019C01f CUGI Rice Blast BAC Library P... 33 5.0
 emb|AW615911|AW615911 EST325409 tomato flower buds 0-3 mm, Corne... 33 5.0
 emb|AW035453|AW035453 EST281191 tomato callus, TAMU Lycopersicon... 33 5.0
 20 emb|AF051695|AF051695 Trypanosoma cruzi sialidase homolog (P85.1... 33 5.0
 emb|Z37538|LTGRR4 L.tarentolae mRNA encoding putative NADH subun... 28 5.5
 emb|X85021|SCXLTORFS S.cerevisiae DNA from left arm of chromosom... 33 6.8
 gb|L25088|YSCMEF2MIT Saccharomyces cerevisiae nuclear-encoded mi... 33 6.8
 emb|AQ443826|AQ443826 GSSTc01287 Trypanosoma cruzi random genom... 33 6.8
 25 emb|AQ502942|AQ502942 V47H4 mTn-3xHA/lacZ Insertion Library Sacc... 33 6.8
 emb|Z85962|MSZ85962 Musa sp. DNA for sequence tagged microsatell... 33 6.8
 emb|Z49377|SCYJL102W S.cerevisiae chromosome X reading frame ORF... 33 6.8
 emb|AW224537|AW224537 EST302980 tomato root, plants pre-anthesis... 31 7.5
 emb|AW257183|AW257183 EST305320 KV2 Medicago truncatula cDNA clo... 32 9.4
 30 emb|AQ642922|AQ642922 RPCI93-DpnII-27E7.TV RPCI93-DpnII Trypanos... 32 9.4
 emb|AW738509|AW738509 EST339936 tomato flower buds, anthesis, Co... 32 9.4
 emb|AW217351|AW217351 EST296174 tomato flower buds 0-3 mm, Corne... 32 9.4
 emb|AW219255|AW219255 EST301737 tomato root during/after fruit s... 32 9.4
 emb|AC007865|AC007865 Trypanosoma brucei chromosome II clone RPC... 32 9.4
 35 emb|AW684118|AW684118 NF012F02NR1F1000 Nodulated root Medicago t... 32 9.4
 emb|AW622239|AW622239 EST313037 tomato root during/after fruit s... 32 9.4
 emb|AQ651543|AQ651543 Sheared DNA-7C22.TF Sheared DNA Trypanosom... 32 9.4
 emb|Y11565|NC11565 N.crassa acu-15 gene. 32 9.4
 emb|AW775944|AW775944 EST335009 DSIL Medicago truncatula cDNA cl... 32 9.4
 40 emb|AB014493|AB014493 Gibberella zeae gene for reductase, partia... 32 9.4

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- 45 gb|aaa32738.1|(m92353) anthranilate synthase alpha subunit
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 /gb_link /ncgi
 (1788 letters)

Database: plantfungal

- 50 661,018 sequences; 426,114,510 total letters

Searching.....done

- 55 Score E
 Sequences producing significant alignments: (bits) Value

- gb|L34344|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 772 0.0
 gb|L34343|RTAANTSYNB Ruta graveolens anthranilate synthase alpha... 467 0.0
 emb|AF079168|AF079168 Nicotiana tabacum feedback-insensitive ant... 365 0.0
 60 emb|AW931942|AW931942 EST357785 tomato fruit mature green, TAMU ... 356 3e-97
 emb|AW218352|AW218352 EST303535 tomato radicle, 5 d post-imbibit... 210 1e-73

- emb|AL031966|SPCC1442 *S.pombe* chromosome III cosmid c1442. 209 6e-69
- emb|AW651095|AW651095 EST329549 tomato germinating seedlings, TA... 222 2e-64
- dbj|D89256|D89256 *Schizosaccharomyces pombe* mRNA, partial cds, c... 205 5e-64
- emb|AW982499|AW982499 HVSMEg0003G22f *Hordeum vulgare* pre-anthesi... 215 2e-58
- 5 emb|AW460005|AW460005 si07d11.y1 *Gm-c1029 Glycine max* cDNA clone... 116 1e-57
- gb|U18839|SCE9747 *Saccharomyces cerevisiae* chromosome V cosmids ... 123 4e-48
- emb|X68327|SCTRP2 *S.cerevisiae* TRP2 gene for anthranilate syntha... 123 4e-48
- emb|AW719463|AW719463 LjNEST5b1r *Lotus japonicus* nodule library,... 184 1e-45
- emb|AI736775|AI736775 sb33d01.y1 *Gm-c1012 Glycine max* cDNA clone... 104 2e-40
- 10 gb|K01388|YSCTRP2 Yeast (*S.cerevisiae*) TRP2 gene coding for anth... 122 4e-38
- emb|AL032684|SPBP8B7 *S.pombe* chromosome II pl p8B7. 95 6e-25
- emb|AW509018|AW509018 si39b01.y1 *Gm-r1030 Glycine max* cDNA clone... 113 5e-24
- gb|T14852|T14852 crs299 lambdaZAPST *Ricinus communis* cDNA clone ... 107 2e-22
- emb|AW223881|AW223881 EST300692 tomato fruit red ripe, TAMU Lyco... 103 4e-21
- 15 emb|AF119554|AF119554 *Plasmodium falciparum* para-aminobenzoic ac... 67 6e-10
- emb|AL111470|CNS019CM *Botrytis cinerea* strain T4 cDNA library un... 45 2e-05
- emb|AI329873|AI329873 b9g02ne.r1 *Neurospora crassa* evening cDNA ... 48 3e-04
- emb|AW224247|AW224247 EST300974 tomato fruit red ripe, TAMU Lyco... 46 7e-04
- emb|AF149719|AF149719 *Aspergillus fumigatus* para aminobenzoic ac... 42 0.012
- 20 emb|AQ448372|AQ448372 mgxb0020C12f CUGI Rice Blast BAC Library P... 39 0.15
- emb|AQ324360|AQ324360 mgxb0018K01r CUGI Rice Blast BAC Library P... 39 0.15
- emb|AQ160089|AQ160089 mgxb0003G09r CUGI Rice Blast BAC Library P... 39 0.15
- emb|AW599019|AW599019 gb01b03.y1 Moss EST library PPN Physcomitr... 37 0.38
- emb|AW599000|AW599000 ga99h03.y1 Moss EST library PPN Physcomitr... 37 0.38
- 25 emb|AW678847|AW678847 WS1_1_A04.g1_A002 Water-stressed 1 (WS1) S... 35 0.88
- emb|AW680390|AW680390 WS1_52_D12.g1_A002 Water-stressed 1 (WS1) ... 35 0.89
- emb|AW678385|AW678385 WS1_15_H06.g1_A002 Water-stressed 1 (WS1) ... 35 0.89
- emb|AW747146|AW747146 WS1_66_E07.b1_A002 Water-stressed 1 (WS1) ... 35 0.89
- emb|AW678361|AW678361 WS1_15_H06.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
- 30 emb|AW745749|AW745749 WS1_37_D12.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
- emb|AW747427|AW747427 WS1_68_B09.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
- emb|AW678071|AW678071 WS1_13_E01.b1_A002 Water-stressed 1 (WS1) ... 35 0.90
- emb|AW747468|AW747468 WS1_68_B09.g1_A002 Water-stressed 1 (WS1) ... 35 0.90
- emb|AW672427|AW672427 LG1_359_A06.g1_A002 Light Grown 1 (LG1) So... 35 0.90
- 35 emb|AW744836|AW744836 LG1_384_E07.g1_A002 Light Grown 1 (LG1) So... 35 0.90
- emb|AW746170|AW746170 WS1_39_B05.g1_A002 Water-stressed 1 (WS1) ... 35 0.90
- emb|AW922317|AW922317 DG1_17_E06.g1_A002 Dark Grown 1 (DG1) Sorg... 35 0.91
- emb|AQ648582|AQ648582 RPCI93-EcoRI-IM22.TP RPCI93-EcoRI Trypanos... 36 0.99
- emb|AQ643551|AQ643551 RPCI93-EcoRI-3I24.TJ RPCI93-EcoRI Trypanos... 36 0.99
- 40 emb|AI443370|AI443370 sa31b05.x1 *Gm-c1004 Glycine max* cDNA clone... 35 1.4
- emb|AW101313|AW101313 sd77d08.y1 *Gm-c1009 Glycine max* cDNA clone... 35 1.4
- emb|AW678030|AW678030 WS1_12_B10.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
- emb|AW349006|AW349006 GM210004A12H10R *Gm-r1021 Glycine max* cDNA ... 35 1.4
- emb|AW309961|AW309961 sf27b12.x1 *Gm-c1028 Glycine max* cDNA clone... 35 1.4
- 45 emb|AW678582|AW678582 WS1_16_E09.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
- emb|AW317198|AW317198 sf38f03.x1 *Gm-c1028 Glycine max* cDNA clone... 35 1.4
- emb|AW678305|AW678305 WS1_14_G05.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
- emb|AW680905|AW680905 WS1_8_A08.b1_A002 Water-stressed 1 (WS1) S... 35 1.4
- emb|AW679666|AW679666 WS1_30_B11.g1_A002 Water-stressed 1 (WS1) ... 35 1.4
- 50 emb|AL031746|PFMAL1P3 *Plasmodium falciparum* MAL1P3, complete seq... 35 1.9
- emb|AI959816|AI959816 sc94f02.y1 *Gm-c1019 Glycine max* cDNA clone... 35 1.9
- emb|AW924277|AW924277 WS1_52_D12.b1_A002 Water-stressed 1 (WS1) ... 35 1.9
- gb|J03998|PFAGAR *Plasmodium falciparum* glutamic acid-rich protei... 35 1.9
- emb|AW696796|AW696796 NF109A07ST1F1052 Developing stem Medicago ... 35 1.9
- 55 emb|AW396753|AW396753 sf37c11.x1 *Gm-c1028 Glycine max* cDNA clone... 35 2.6
- gb|M98871|SOYCHS7A *Glycine max* chalcone synthase (chs7) gene, co... 35 2.6
- emb|AI460797|AI460797 sa69d02.y1 *Gm-c1004 Glycine max* cDNA clone... 35 2.6
- emb|AW348617|AW348617 GM210002B22G1R *Gm-r1021 Glycine max* cDNA 3... 35 2.6
- emb|AW310362|AW310362 sf35a09.x1 *Gm-c1028 Glycine max* cDNA clone... 35 2.6
- 60 emb|AI437832|AI437832 sa40c07.y1 *Gm-c1004 Glycine max* cDNA clone... 35 2.6
- gb|BE023927|BE023927 sm94c05.y1 *Gm-c1015 Glycine max* cDNA clone ... 35 2.6

- emb|AW424189|AW424189 sh62b04.y1 Gm-c1015 Glycine max cDNA clone... 35 2.6
 emb|AW101907|AW101907 sd72d01.y1 Gm-c1008 Glycine max cDNA clone... 35 2.6
 emb|AW102370|AW102370 sd86h01.y1 Gm-c1009 Glycine max cDNA clone... 35 2.6
 emb|AW309356|AW309356 sf16d02.x1 Gm-c1028 Glycine max cDNA clone... 35 2.6
 5 emb|AL355932|NCB5022 Neurospora crassa DNA linkage group II BAC ... 34 3.5
 emb|AQ652663|AQ652663 Sheared DNA-20A9.TR Sheared DNA Trypanosom... 34 3.5
 emb|Z98056|SPAC5D6 S.pombe chromosome I cosmid c5D6. 34 3.5
 emb|AW348286|AW348286 GM210001B23B6R Gm-r1021 Glycine max cDNA 3... 34 4.9
 emb|AB018422|AB018422 Pisum sativum mRNA for DNA binding zinc fi... 34 4.9
 10 emb|AW734949|AW734949 sk93b10.y1 Gm-c1035 Glycine max cDNA clone... 34 4.9
 emb|AW679089|AW679089 WS1_22_A07.g1_A002 Water-stressed 1 (WS1) ... 34 4.9
 emb|AW306776|AW306776 sf48c12.y1 Gm-c1009 Glycine max cDNA clone... 34 4.9
 gb|M36941|BLYHORDCA Hordeum vulgare C-hordein gene, complete cds. 29 5.3
 gb|BE034677|BE034677 ML01H08 ML Mesembryanthemum crystallinum cD... 33 6.7
 15 emb|Z26877|SCDCHR11 S.cerevisiae (S288C) 36.2kb DNA fragment fro... 33 6.7
 emb|AW267708|AW267708 EST305836 DSIR Medicago truncatula cDNA cl... 33 6.7
 emb|Z28162|SCYKL162C S.cerevisiae chromosome XI reading frame OR... 33 6.7
 emb|AW980990|AW980990 EST392143 GVN Medicago truncatula cDNA clo... 33 6.7
 gb|BE037412|BE037412 MP20G03 MP Mesembryanthemum crystallinum cD... 33 6.7
 20 emb|Z28161|SCYKL161C S.cerevisiae chromosome XI reading frame OR... 33 6.7
 emb|AI726247|AI726247 BNLGHi5399 Six-day Cotton fiber Gossypium ... 33 6.7
 emb|AE001401|AE001401 Plasmodium falciparum chromosome 2, sectio... 33 6.7
 emb|AW573801|AW573801 EST316392 GVN Medicago truncatula cDNA clo... 33 6.7
 emb|Z98547|PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque... 33 9.2
 25 emb|AQ659747|AQ659747 Sheared DNA-16J5.TR Sheared DNA Trypanosom... 33 9.2
 gb|BE021269|BE021269 sm56h04.y1 Gm-c1028 Glycine max cDNA clone ... 33 9.2
 emb|AW222457|AW222457 EST299268 tomato fruit red ripe, TAMU Lyco... 33 9.2
 emb|AB012116|AB012116 Vigna mungo UFGlyT mRNA for UDP-glycose:fl... 33 9.2
 emb|AW725836|AW725836 GA_Ea0019N24 Gossypium arboreum 7-10 dpa ... 33 9.2
 30 emb|AQ324451|AQ324451 mgxb0018L23r CUGI Rice Blast BAC Library P... 33 9.2
 gb|M73492|LEIHSP90 Leishmania donovani heat shock protein 90 mRN... 33 9.2
 emb|AW132634|AW132634 se06h07.y1 Gm-c1013 Glycine max cDNA clone... 33 9.2
 emb|AI166186|AI166186 a032p32u Hybrid aspen plasmid library Popu... 33 9.2
 gb|BE053953|BE053953 GA_Ea0031D23f Gossypium arboreum 7-10 dpa ... 33 9.2
 35

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 gb|aac63850.1| (u73786) acc synthase [arabidopsis thaliana]
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<http://www.ncgr.org/cgi-bin/ff?atacs6>
 (1567 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

50

Score E
 Sequences producing significant alignments: (bits) Value

- emb|X82273|BOACCS B.oleracea mRNA for ACC synthase. 944 0.0
 55 emb|X72676|BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo... 833 0.0
 emb|AB034992|AB034992 Malus domestica MdACS-5A mRNA for 1-aminoc... 725 0.0
 emb|AF057563|AF057563 Nicotiana glutinosa 1-aminocyclopropane-1-... 729 0.0
 emb|AJ005002|NTAJ5002 Nicotiana tabacum mRNA for 1-aminocyclopro... 726 0.0
 emb|AB034993|AB034993 Malus domestica MdACS-5B mRNA for 1-aminoc... 723 0.0
 60 gb|U72389|LEU72389 Lycopersicon esculentum 1-aminocyclopropane-1... 724 0.0
 gb|U72390|LEU72390 Lycopersicon esculentum 1-aminocyclopropane-1... 720 0.0

- gb|U68216|CPU68216 *Carica papaya* ACC synthase mRNA, complete cds. 435 0.0
 emb|AB033503|AB033503 *Populus euramericana* peacs-2 mRNA for 1-am... 713 0.0
 emb|AF061605|AF061605 *Nicotiana glutinosa* ACC synthase mRNA, com... 712 0.0
 emb|AJ012551|CSI012551 *Citrus sinensis* mRNA for ACC synthase. 420 0.0
 5 emb|AB033502|AB033502 *Populus euphratica* peacs-1 mRNA for 1-amin... 591 0.0
 emb|AB013100|AB013100 *Lycopersicon esculentum* LE-ACS6 mRNA for 1... 706 0.0
 emb|AB013346|AB013346 *Lycopersicon esculentum* mRNA for 1-aminocy... 704 0.0
 gb|U88971|PHU88971 *Pelargonium hortorum* 1-aminocyclopropane-1-ca... 423 0.0
 emb|Z11613|VRACCSYNM *V.radiata* mRNA for ACC synthase. 428 0.0
 10 emb|X98492|NTACCS *Nicotiana tabacum* mRNA for ACC-synthase (clone... 425 0.0
 emb|X67100|GMCACCS1 *G.max* mRNA for ACC synthase. 429 0.0
 emb|AJ012696|CSI012696 *Citrus sinensis* mRNA for ACC synthase (AC... 422 0.0
 emb|Z18953|PHAMCRBSY *P.hybrida* mRNA for 1-aminocyclopropane 1-ca... 424 0.0
 emb|AJ011095|CSI011095 *Citrus sinensis* mRNA for ACC synthase (ac... 424 0.0
 15 emb|Z18952|DCAMCRBSY *D.caryophyllus* mRNA for 1-aminocyclopropane... 686 0.0
 emb|AB006804|AB006804 *Cucumis sativus* CS-ACS2 mRNA for ACC synth... 423 0.0
 emb|AF080258|AF080258 *Musa acuminata* 1-aminocyclopropane-1-carbo... 680 0.0
 emb|AF016459|AF016459 *Pisum sativum* 1-aminocyclopropane-1-carbox... 415 0.0
 dbj|D30805|CUS1A1CS *Melon* mRNA for 1-aminocyclopropane-1-carboxy... 678 0.0
 20 emb|X65982|NTXACCSYN *N.tabacum* mRNA for 1-aminocyclopropane-1-ca... 417 0.0
 emb|AF109927|AF109927 *Musa acuminata* 1-aminocyclopropane-1-carbo... 676 0.0
 emb|AB006803|AB006803 *Cucumis sativus* CS-ACS1 mRNA for ACC synth... 676 0.0
 gb|U17231|PHU17231 *Pelargonium hortorum* clone pGAC-2 1-aminocycl... 423 0.0
 emb|AB021906|AB021906 *Musa acuminata* MA-ACS1 mRNA for ACC syntha... 671 0.0
 25 emb|AF129508|AF129508 *Musa acuminata* 1-aminocyclopropane-1-carbo... 671 0.0
 emb|AB015625|AB015625 *Pyrus pyrifolia* pPPACS3 mRNA for 1-aminocy... 393 0.0
 emb|AB031026|AB031026 *Prunus mume* PM-ACS1 mRNA for ACC synthase,... 405 0.0
 emb|Y11357|CP1A1CS *C.papaya* mRNA for 1-aminocyclopropane-1-carbo... 404 0.0
 dbj|D01032|CUCACCW *Cucurbita maxima* mRNA for 1-aminocyclopropane... 666 0.0
 30 dbj|E03724|E03724 cDNA encoding detriment induced type 1-aminocy... 666 0.0
 emb|X62536|LEACC *L.esculentum* mRNA for ACC synthase. 327 0.0
 gb|L20634|POTACCSYN *Solanum tuberosum* 1-aminocyclopropane-1-carb... 403 0.0
 emb|X59145|LEACC2MR *Lycopersicon esculentum* LE-ASCC2 mRNA (ptACC... 326 0.0
 gb|M58323|CUCACCSYN *Cucurbita pepo* 1-aminocyclopropane-1-carboxy... 663 0.0
 35 emb|AF057562|AF057562 *Nicotiana glutinosa* 1-aminocyclopropane-1-... 412 0.0
 emb|AF239987|AF239987 *Prunus persica* ACC synthase ACS1 mRNA, par... 662 0.0
 gb|M34289|TOMACS *Tomato* 1-aminocyclopropane-1-carboxylate syntha... 327 0.0
 gb|M63490|TOMACCS *Tomato* 1-aminocyclopropane-1-carboxylate synth... 657 0.0
 emb|X59146|LEACC4MR *Lycopersicon esculentum* LE-ACC4 mRNA (ptACC4... 656 0.0
 40 emb|Y15739|MAACSYNTH *Musa acuminata* mRNA for 1-aminocyclopropane... 655 0.0
 gb|U79999|MAU79999 *Musa acuminata* ACC synthase (acs3) mRNA, comp... 655 0.0
 emb|AF178076|AF178076 *Carica papaya* 1-aminocyclopropane-1-carbox... 395 0.0
 gb|U17229|PHU17229 *Pelargonium hortorum* clone pGAC-1 1-aminocycl... 407 0.0
 emb|X82265|CAACCI *C.anuum* mRNA for 1-aminocyclopropane-1-carboxyl... 639 0.0
 45 gb|U70842|STU70842 *Solanum tuberosum* 1-aminocyclopropane-1-carbo... 637 0.0
 emb|AF144746|AF144746 *Solanum melongena* 1-aminocyclopropane-1-ca... 636 0.0
 emb|AJ276295|CSI276295 *Citrus sinensis* partial mRNA for ACC synt... 418 0.0
 emb|AJ012577|CPA012577 *Carica papaya* mRNA for 1-aminocyclopropan... 387 e-180
 emb|AF038945|AF038945 *Rumex palustris* 1-aminocyclopropane-1-carb... 372 e-179
 50 gb|U73815|MDU73815 *Malus domestica* ACC synthase (MdACS-2) mRNA, ... 623 e-178
 dbj|D37937|D37937 *Cucumis melo* mRNA for 1-aminocyclopropane-1-ca... 380 e-177
 emb|Z11562|VRACCSYN *V.radiata* mRNA for 1-aminocyclopropane-1-car... 375 e-176
 emb|AF177769|AF177769 *Carica papaya* 1-aminocyclopropane-1-carbox... 369 e-175
 emb|AF083814|AF083814 *Antirrhinum majus* ACC synthase 1 (ACS1) mR... 605 e-172
 55 emb|AF178077|AF178077 *Carica papaya* 1-aminocyclopropane-1-carbox... 316 e-171
 emb|AF239989|AF239989 *Prunus persica* ACC synthase ACS25 mRNA, pa... 597 e-170
 gb|U22523|MIU22523 *Mangifera indica* 1-aminocyclopropane-carboxyl... 359 e-169
 emb|X66605|DCACCS *D.caryophyllus* mRNA for 1-aminocyclopropane-1-... 396 e-168
 emb|AF049137|AF049137 *Dianthus caryophyllus* 1-aminocyclopropane-... 338 e-167
 60 emb|AF170705|AF170705 *Mangifera indica* 1-aminocyclopropane-1-car... 290 e-167
 emb|AJ277160|CPA277160 *Carica papaya* partial paccs1A gene for 1-... 266 e-165

- emb|AB015624|AB015624 *Pyrus pyrifolia* mRNA for 1-aminocyclopropa... 359 e-163
 gb|U03294|MSU03294 *Malus sylvestris* 1-aminocyclopropane-1-carbox... 359 e-163
 gb|L31347|MAUACCSYN *Malus domestica* 1-aminocyclopropane-1-carbox... 357 e-162
 emb|AB015495|AB015495 *Passiflora edulis* PE-ACS2 mRNA for ACC syn... 368 e-162
 5 emb|Z77854|PSPACS1 *Phalaenopsis* species mRNA for 1-aminocyclopro... 514 e-161
 dbj|D01033|CUCACCA *Cucurbita maxima* mRNA for 1-aminocyclopropane... 349 e-159
 emb|X87112|PCPCACS1G *P. communis* mRNA for 1-aminocyclopropane-1-c... 346 e-159
 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclop... 336 e-159
 gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 504 e-158
 10 gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1... 343 e-157
 emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropa... 502 e-157
 gb|M66619|DINCARACC *D. caryophyllus* 1-aminocyclopropane-1-carboxy... 495 e-156
 emb|AB006805|AB006805 *Cucumis sativus* CS-ACS3 mRNA for ACC synth... 342 e-156
 gb|U34987|VRU34987 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 305 e-151
 15 emb|AB000679|AB000679 *Vigna radiata* mRNA for 1-aminocyclopropane... 340 e-151
 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 340 e-149
 gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, comp... 259 e-149
 emb|AF016458|AF016458 *Pisum sativum* 1-aminocyclopropane-1-carbox... 336 e-148
 emb|Z27233|STACCAS1 *S. tuberosum* (STAC1) gene for amino cycloprop... 238 e-147
 20 emb|Z27234|STACCAS2 *S. tuberosum* STACS2 gene for 1-Aminocycloprop... 234 e-146
 gb|U37774|CMU37774 *Cucurbita maxima* 1-aminocyclopropane-1-carbox... 235 e-145
 emb|AF043122|AF043122 *Lycopersicon esculentum* ACC synthase (LE-A... 237 e-145
 emb|Z12135|VRACCSYN4 *V. radiata* gene for ACC synthase (pMAC-4). 376 e-145
 gb|L34171|TOMACS3A *Lycopersicon esculentum* 1-aminocyclopropane-1... 236 e-143
 25 gb|U18055|LEU18055 *Lycopersicon esculentum* 1-aminocyclopropane-1... 236 e-143
 emb|AF074927|AF074927 *Sinapis arvensis* 1-aminocyclopropane-1-car... 330 e-142
 emb|AF083815|AF083815 *Antirrhinum majus* ACC synthase 2 (ACS2) mR... 482 e-141
 emb|AF151961|AF151961 *Vigna radiata* 1-aminocyclopropane-1-carbox... 234 e-141
 emb|AB021907|AB021907 *Musa acuminata* MA-ACS2 mRNA for ACC syntha... 310 e-140
 30 gb|L07883|DORAMICARB *Moth orchid* 1-aminocyclopropane-1-carboxyla... 243 e-139
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- 35 Query= AtACS6_g_at 12892_g_at/id_source genbank /description
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- emb|X82273|BOACCS *B. oleracea* mRNA for ACC synthase. 944 0.0
 emb|X72676|BJMACC *B. juncea* mRNA for 1-Aminocyclopropane-1-carbo... 833 0.0
 50 emb|AB034992|AB034992 *Malus domestica* MdACS-5A mRNA for 1-aminoc... 725 0.0
 emb|AF057563|AF057563 *Nicotiana glutinosa* 1-aminocyclopropane-1-... 729 0.0
 emb|AJ005002|NTAJ5002 *Nicotiana tabacum* mRNA for 1-aminocyclopro... 726 0.0
 emb|AB034993|AB034993 *Malus domestica* MdACS-5B mRNA for 1-aminoc... 723 0.0
 gb|U72389|LEU72389 *Lycopersicon esculentum* 1-aminocyclopropane-1... 724 0.0
 55 gb|U72390|LEU72390 *Lycopersicon esculentum* 1-aminocyclopropane-1... 720 0.0
 gb|U68216|CPU68216 *Carica papaya* ACC synthase mRNA, complete cds. 435 0.0
 emb|AB033503|AB033503 *Populus euramericana* peacs-2 mRNA for 1-am... 713 0.0
 emb|AF061605|AF061605 *Nicotiana glutinosa* ACC synthase mRNA, com... 712 0.0
 emb|AJ012551|CSI012551 *Citrus sinensis* mRNA for ACC synthase. 420 0.0
 60 emb|AB033502|AB033502 *Populus euphratica* peacs-1 mRNA for 1-amin... 591 0.0
 emb|AB013100|AB013100 *Lycopersicon esculentum* LE-ACS6 mRNA for 1... 706 0.0

	emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy...	704	0.0
	gb U88971 PHU88971 <i>Pelargonium hortorum</i> 1-aminocyclopropane-1-ca...	423	0.0
	emb Z11613 VRACCSYNM <i>V.radiata</i> mRNA for ACC synthase.	428	0.0
	emb X98492 NTACCS <i>Nicotiana tabacum</i> mRNA for ACC-synthase (clone...	425	0.0
5	emb X67100 GMCACCS1 <i>G.max</i> mRNA for ACC synthase.	429	0.0
	emb AJ012696 CSIO12696 <i>Citrus sinensis</i> mRNA for ACC synthase (AC...	422	0.0
	emb Z18953 PHAMCRBSY <i>P.hybrida</i> mRNA for 1-aminocyclopropane 1-ca...	424	0.0
	emb AJ011095 CSIO11095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac...	424	0.0
	emb Z18952 DCAMCRBSY <i>D.caryophyllus</i> mRNA for 1-aminocyclopropane...	686	0.0
10	emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth...	423	0.0
	emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	680	0.0
	emb AF016459 AF016459 <i>Pisum sativum</i> 1-aminocyclopropane-1-carbox...	415	0.0
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	emb X65982 NTXACCSYN <i>N.tabacum</i> mRNA for 1-aminocyclopropane-1-ca...	417	0.0
15	emb AF109927 AF109927 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo...	676	0.0
	emb AB006803 AB006803 <i>Cucumis sativus</i> CS-ACS1 mRNA for ACC synth...	676	0.0
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	emb AB021906 AB021906 <i>Musa acuminata</i> MA-ACS1 mRNA for ACC syntha...	671	0.0
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25	emb X62536 LEACC <i>L.esculentum</i> mRNA for ACC synthase.	327	0.0
	gb L20634 POTACCSYN <i>Solanum tuberosum</i> 1-aminocyclopropane-1-carb...	403	0.0
	emb X59145 LEACC2MR <i>Lycopersicon esculentum</i> LE-ASCC2 mRNA (ptACC...	326	0.0
	gb M58323 CUCACCSYN <i>Cucurbita pepo</i> 1-aminocyclopropane-1-carboxy...	663	0.0
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	gb M34289 TOMACS <i>Tomato</i> 1-aminocyclopropane-1-carboxylate synth...	327	0.0
	gb M63490 TOMACCS <i>Tomato</i> 1-aminocyclopropane-1-carboxylate synth...	657	0.0
	emb X59146 LEACC4MR <i>Lycopersicon esculentum</i> LE-ACC4 mRNA (ptACC4...	656	0.0
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35	gb U79999 MAU79999 <i>Musa acuminata</i> ACC synthase (acs3) mRNA, comp...	655	0.0
	emb AF178076 AF178076 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	395	0.0
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40	emb AF144746 AF144746 <i>Solanum melongena</i> 1-aminocyclopropane-1-ca...	636	0.0
	emb AJ276295 CS1276295 <i>Citrus sinensis</i> partial mRNA for ACC synt...	418	0.0
	emb AJ012577 CPA012577 <i>Carica papaya</i> mRNA for 1-aminocyclopropan...	387	e-180
	emb AF038945 AF038945 <i>Rumex palustris</i> 1-aminocyclopropane-1-carb...	372	e-179
	gb U73815 MDU73815 <i>Malus domestica</i> ACC synthase (MdACS-2) mRNA, ...	623	e-178
45	dbj D37937 D37937 <i>Cucumis melo</i> mRNA for 1-aminocyclopropane-1-ca...	380	e-177
	emb Z11562 VRACCSYN <i>V.radiata</i> mRNA for 1-aminocyclopropane-1-car...	375	e-176
	emb AF177769 AF177769 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	369	e-175
	emb AF083814 AF083814 <i>Antirrhinum majus</i> ACC synthase I (ACS1) mR...	605	e-172
	emb AF178077 AF178077 <i>Carica papaya</i> 1-aminocyclopropane-1-carbox...	316	e-171
50	emb AF239989 AF239989 <i>Prunus persica</i> ACC synthase ACS25 mRNA, pa...	597	e-170
	gb U22523 MIU22523 <i>Mangifera indica</i> 1-aminocyclopropane-carboxyl...	359	e-169
	emb X66605 DCACCS <i>D.caryophyllus</i> mRNA for 1-aminocyclopropane-1-...	396	e-168
	emb AF049137 AF049137 <i>Dianthus caryophyllus</i> 1-aminocyclopropane-...	338	e-167
	emb AF170705 AF170705 <i>Mangifera indica</i> 1-aminocyclopropane-1-car...	290	e-167
55	emb AJ277160 CPA277160 <i>Carica papaya</i> partial paccs1A gene for 1-...	266	e-165
	emb AB015624 AB015624 <i>Pyrus pyrifolia</i> mRNA for 1-aminocyclopropa...	359	e-163
	gb U03294 MSU03294 <i>Malus sylvestris</i> 1-aminocyclopropane-1-carbox...	359	e-163
	gb L31347 MAUACCSYN <i>Malus domestica</i> 1-aminocyclopropane-1-carbox...	357	e-162
	emb AB015495 AB015495 <i>Passiflora edulis</i> PE-ACS2 mRNA for ACC syn...	368	e-162
60	emb Z77854 PSPACS1 <i>Phalaenopsis species</i> mRNA for 1-aminocyclopro...	514	e-161
	dbj D01033 CUCACCA <i>Cucurbita maxima</i> mRNA for 1-aminocyclopropane...	349	e-159

- emb|X87112|PCPCACS1G *P. communis* mRNA for 1-aminocyclopropane-1-c... 346 e-159
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 5 emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropana... 502 e-157
 gb|M66619|DINCARACC *D. caryophyllus* 1-aminocyclopropane-1-carboxy... 495 e-156
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 10 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 340 e-149
 gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, comp... 259 e-149
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 15 gb|U37774|CMU37774 *Cucurbita maxima* 1-aminocyclopropane-1-carbox... 235 e-145
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 gb|L34171|TOMACS3A *Lycopersicon esculentum* 1-aminocyclopropane-1... 236 e-143
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 20 emb|AF074927|AF074927 *Sinapis arvensis* 1-aminocyclopropane-1-car... 330 e-142
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 gb|L07883|DORAMICARB *Moth orchid* 1-aminocyclopropane-1-carboxyla... 243 e-139
 25 emb|AB021908|AB021908 *Musa acuminata* MA-ACS3 mRNA for ACC syntha... 298 e-138

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- 40 Score E
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- dbj|D38126|TOBBY4D Tobacco mRNA for EREBP-2, complete cds. 144 7e-44
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 55 emb|AW396250|AW396250 sh26c01.y1 *Gm-c1016 Glycine max* cDNA clone... 116 2e-25
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(1059 letters)

30 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
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40 emb|AW200919|AW200919 se95c12.y1 Gm-c1027 Glycine max cDNA clone... 149 5e-35
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50 emb|AI486689|AI486689 EST245011 tomato ovary, TAMU Lycopersicon ... 127 2e-28
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 5 emb|AW443265|AW443265 EST308195 tomato mixed elicitor, BTI Lycopersicon... 89 5e-17
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Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

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	emb AB025025 AB025025 Chenopodium album mRNA for chlorophyllase,...	89	4e-57
	emb AF160869 AF160869 Citrus sinensis chlorophyllase mRNA, compl...	84	4e-54
40	emb AW039135 AW039135 EST281108 tomato mixed elicitor, BTI Lycopersicon...	127	2e-38
	gb BE037470 BE037470 MP21E05 MP Mesembryanthemum crystallinum cD...	81	4e-35
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	emb AW616099 AW616099 EST296862 L. hirsutum trichome, Cornell Un...	67	1e-29
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	emb AW037417 AW037417 EST278919 tomato mixed elicitor, BTI Lycop...	34	2.2
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15

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 (2616 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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30 Score E
 Sequences producing significant alignments: (bits) Value

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20 Database: plantfungal
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(528 letters)

Database: plantfungal
20 661,018 sequences; 426,114,510 total letters

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Score E
25 Sequences producing significant alignments: (bits) Value

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 emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 2e-39
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 50 emb|AW680784|AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S... 161 4e-39
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 60 emb|AW684766|AW684766 NF021G12NRIF1000 Nodulated root Medicago t... 124 1e-37
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emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154 4e-37
5 emb|AW754729|AW754729 PC07B04 Pine TriplEx pollen cone library P... 154 4e-37
emb|AW923038|AW923038 DG1_48_B02.g1_A002 Dark Grown 1 (DG1) Sorg... 154 4e-37

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/blast_score 2.00e-63 /ec_number /family /chip nova /gb_link /ncgi
(528 letters)

Database: plantfungal
15 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
20 Sequences producing significant alignments: (bits) Value

gb|U59379|BNU59379 Brassica napus thioredoxin-h-like-1 (THL-1) m... 194 4e-49
emb|X89759|BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen... 194 4e-49
emb|AB010434|AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ... 192 2e-48
25 emb|AW255457|AW255457 ML480 peppermint glandular trichome Mentha... 191 4e-48
emb|AW569018|AW569018 si74e02.y1 Gm-c1031 Glycine max cDNA clone... 186 1e-46
emb|AI988470|AI988470 sd02f07.y1 Gm-c1020 Glycine max cDNA clone... 186 1e-46
emb|AI161830|AI161830 A007P52U Hybrid aspen plasmid library Popu... 184 3e-46
emb|Z70677|RCTHIORXN R.communis mRNA for thioredoxin. 183 9e-46
30 gb|BE053835|BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ... 182 2e-45
emb|AW565750|AW565750 LG1_349_G02.g1_A002 Light Grown 1 (LG1) So... 181 3e-45
emb|AW677651|AW677651 WS1_10_F03.b1_A002 Water-stressed 1 (WS1) ... 181 3e-45
emb|AW671668|AW671668 LG1_349_G02.b1_A002 Light Grown 1 (LG1) So... 181 3e-45
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40 emb|AW164730|AW164730 se77a02.y1 Gm-c1023 Glycine max cDNA clone... 180 8e-45
emb|AJ009762|TAE9762 Triticum aestivum mRNA for thioredoxin H. 179 2e-44
emb|AW255195|AW255195 ML185 peppermint glandular trichome Mentha... 178 2e-44
emb|AI165128|AI165128 A076P57U Hybrid aspen plasmid library Popu... 177 5e-44
gb|T24347|T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone... 177 5e-44
45 dbj|D87984|D87984 Fagopyrum esculentum mRNA for thioredoxin, com... 177 8e-44
gb|BE054543|BE054543 GA_Ea0026K15f Gossypium arboreum 7-10 dpa ... 177 8e-44
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55 emb|AJ001903|TDAJ1903 Triticum durum mRNA for thioredoxin H. 175 3e-43
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emb|X69915|TATHIORDH T.aestivum mRNA for thioredoxine H. 175 3e-43
emb|A48514|A48514 Sequence 2 from Patent WO9603505. 175 3e-43
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emb|AW329764|AW329764 N201033e rootphos(-) Medicago truncatula c... 174 4e-43

- emb|AW982237|AW982237 HVSMEg0002G18f Hordeum vulgare pre-anthesi... 174 5e-43
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- 5 gb|U59380|BNU59380 Brassica napus thioredoxin-h-like-2 (THL-2) m... 101 8e-43
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- 10 emb|AI441505|AI441505 sa87c03.y1 Gm-c1004 Glycine max cDNA clone... 171 2e-42
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 emb|AW650009|AW650009 EST328463 tomato germinating seedlings, TA... 171 5e-42
- 15 emb|AW041395|AW041395 EST284259 tomato mixed elicitor, BTI Lycop... 171 5e-42
 emb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 5e-42
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- 20 emb|AI773303|AI773303 EST254403 tomato resistant, Cornell Lycop... 171 5e-42
 emb|AW094525|AW094525 EST287705 tomato mixed elicitor, BTI Lycop... 171 5e-42
 emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycop... 171 5e-42
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- 35 emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 4e-40
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- 40 emb|AF051206|AF051206 Picea mariana probable thioredoxin H (Sb09... 162 2e-39
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- 45 emb|AW680784|AW680784 WS1_7_D07.b1_A002 Water-stressed 1 (WS1) S... 161 4e-39
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- 55 emb|AW684766|AW684766 NF021G12NR1F1000 Nodulated root Medicago t... 124 1e-37
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/chip nova /gb_link
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10 http://www.ncgr.org/cgi-bin/ff?atts0190
(433 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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	Score	E
Sequences producing significant alignments:	(bits)	Value
20 emb X62120 BNCRU1 B.napus cru1 gene for cruciferin subunit.	169	4e-48
gb J05233 BNACRUCA B.napus cruciferin mRNA, 3' end.	169	9e-48
emb X59808 RSCRUG R.sativus pgCruRsE5 gene for cruciferin.	168	4e-43
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25 emb X59804 RSCRU3 R.sativus pAC2 mRNA for cruciferin.	123	1e-41
emb X57850 BNCRU4RN B.napus cru4 mRNA for cruciferin cru4 subunit.	138	2e-32
emb X57848 BNCRU4RNA B.napus cru4 mRNA for cruciferin cru4 subunit.	137	6e-32
gb M16860 BNACRUC Rapeseed cruciferin mRNA, complete cds.	132	1e-30
emb X59294 BNC1G B.napus BnC1 gene for cruciferin storage protein.	132	1e-30
30 emb X14555 BNCRUA Brassica napus cruA gene for cruciferin.	132	1e-30
emb X57849 BNCRU23 B.napus cru2/3 mRNA for cruciferin cru2/3 sub...	132	1e-30
emb X59807 RSCRU6 R.sativus pAE10 mRNA for cruciferin.	131	3e-30
emb X59806 RSCRU5 R.sativus pBB6 mRNA for cruciferin.	131	3e-30
emb X59295 BNC2G B.napus BnC2 gene for cruciferin storage protein.	130	5e-30
35 emb X82121 AHGLOBLN A.hypochondriacus mRNA for globulin.	118	3e-26
gb U38914 CSU38914 Citrus sinensis seed storage protein citrin m...	108	3e-23
emb X59803 RSCRU2 R.sativus pAG4 mRNA for cruciferin.	81	3e-22
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gb U43727 GHU43727 Gossypium hirsutum legumin B (LegB-C134) gene...	92	2e-18
gb M16936 COTSPB G.hirsutum (cotton) storage protein (beta-globu...	92	2e-18
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55 emb Y16976 CAR16976 Coffea arabica mRNA for 11S storage protein.	92	3e-18
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gb|T24336|T24336 crs1452 lambdaZAPST Ricinus communis cDNA clone... 87 8e-17
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gb|M16905|COTSPD G.hirsutum (cotton) storage protein (beta-globu... 86 1e-16
emb|X74741|ASGLAV3G A.sativa GLAV 3 gene for 11S globulin. 86 1e-16
emb|AF091842|AF091842 Sesamum indicum strain Tainan 1 11S globul... 86 2e-16
15 gb|J05485|ASTSSP12S A.sativa 12S globulin seed storage protein g... 85 2e-16
emb|X17637|AS12SSP Oat gene for 12S seed storage protein. 85 2e-16
gb|T24158|T24158 crs141 lambdaZAPST Ricinus communis cDNA clone ... 85 3e-16
emb|X15121|GMY1 Soybean Gyl gene for glycinin subunit G1. 84 4e-16
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20 gb|M36686|SOYGLYBSU Soybean glycinin A-1a-B-x subunit mRNA, comp... 84 4e-16
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dbj|E08573|E08573 cDNA encoding 12S globulin A2B of oats. 84 6e-16
emb|X76738|AS12SGLOB A.sativa (L) mRNA for 12S globulin (1685 bp). 84 6e-16
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emb|AW036121|AW036121 EST274497 tomato seed, TAMU Lycopersicon e... 83 1e-15
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50 emb|AI748727|AI748727 sb61b06.y1 Gm-c1010 Glycine max cDNA clone... 81 4e-15
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55 gb|M16868|ASTGLOB Oat storage protein 12S globulin mRNA, partial... 81 5e-15
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emb|AF180392|AF180392 Perilla frutescens legumin-like protein mR... 80 7e-15
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 3-o-methyltransferase [arabidopsis thaliana] /blast_score 1.00e-121
 5 /ec_number /family /chip nova /gb_link /ncgi
 (965 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	Score	E	
			(bits) Value
15	Sequences producing significant alignments:		
	emb AB000408 AB000408	Populus kitakamiensis mRNA for caffeoyl-Co...	215 3e-73
	gb U20736 MSU20736	Medicago sativa S-adenosyl-L-methionine:trans...	142 2e-68
	emb AW624860 AW624860	EST313689 tomato radicle, 5 d post-imbibit...	139 2e-67
	emb AF022775 AF022775	Nicotiana tabacum caffeoyl-CoA 3-O-methyl...	138 2e-67
20	emb Z54233 VVCCOAOMT	V.vinifera mRNA for caffeoyl-CoA O-methyltr...	136 9e-67
	gb M69184 PUMCCOAMT	Petroselinum crispum caffeoyl-CoA 3-O-methyl...	133 2e-66
	gb U27116 PTU27116	Populus tremuloides caffeoyl-CoA 3-O-methyltr...	135 3e-66
	emb AJ224894 PBT AJ4894	Populus balsamifera subsp. trichocarpa mR...	135 3e-66
	gb U13151 ZEU13151	Zinnia elegans S-adenosyl-L-methionine:trans-...	136 4e-66
25	emb AI489305 AI489305	EST247644 tomato ovary, TAMU Lycopersicon ...	139 4e-66
	emb AJ224895 PBT AJ4895	Populus balsamifera subsp. trichocarpa mR...	136 6e-66
	emb AJ224896 PBT AJ4896	Populus balsamifera subsp. trichocarpa mR...	136 6e-66
	emb AF168780 AF168780	Eucalyptus globulus caffeoyl-CoA O-methyl...	133 8e-66
	emb AF053553 AF053553	Mesembryanthemum crystallinum caffeoyl-CoA...	132 1e-65
30	emb AF240466 AF240466	Populus tomentosa caffeoyl-CoA O-methyltra...	135 1e-65
	emb A22706 A22706	Caffeoyl-CoA-3-O-Methyltransferase gene.	129 3e-65
	gb U62734 NTU62734	Nicotiana tabacum caffeoyl-CoA O-methyltransf...	134 5e-65
	emb Z56282 NTCCOAOMT	N.tabacum mRNA for caffeoyl-CoA O-methyltra...	132 5e-65
	gb U62736 NTU62736	Nicotiana tabacum caffeoyl-CoA O-methyltransf...	136 5e-65
35	gb U38612 NTU38612	Nicotiana tabacum caffeoyl-coenzymeA O-methyl...	136 5e-65
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	emb AF046122 AF046122	Eucalyptus globulus caffeoyl-CoA 3-O-methy...	133 9e-65
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 10 emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51
 emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50
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 35 emb|AI166314|AI166314 xylem.est.159 Poplar xylem Lambda ZAPII li... 136 4e-44
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 40 emb|AW831448|AW831448 sm23c03.y1 Gm-c1028 Glycine max cDNA clone... 140 6e-43
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 emb|AW695899|AW695899 NF100E02ST1F1017 Developing stem Medicago ... 125 5e-42
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 45 emb|AW683492|AW683492 NF012H09LF1F1079 Developing leaf Medicago ... 134 2e-41
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 50 emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
 emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40
 emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
 emb|AI960196|AI960196 sc80a08.y1 Gm-c1018 Glycine max cDNA clone... 132 5e-40
 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
 55 emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

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(827 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

5

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	emb AW350323 AW350323	GM210007B20E12R Gm-r1021 Glycine max cDNA ...	80 2e-27
	emb AW509006 AW509006	si38h07.y1 Gm-r1030 Glycine max cDNA clone...	79 2e-26
	emb AW685404 AW685404	NF028H10NR1F1000 Nodulated root Medicago t...	74 2e-24
15	emb AW781320 AW781320	sk68d07.y1 Gm-c1016 Glycine max cDNA clone...	86 2e-24
	emb AI897832 AI897832	EST267275 tomato ovary, TAMU Lycopersicon ...	78 1e-23
	emb AW102460 AW102460	sd88d10.y1 Gm-c1009 Glycine max cDNA clone...	70 2e-22
	emb AI490284 AI490284	EST248610 tomato ovary, TAMU Lycopersicon ...	103 2e-22
	emb AI487362 AI487362	EST245684 tomato ovary, TAMU Lycopersicon ...	72 3e-20
20	gb BE125690 BE125690	DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh...	96 3e-19
	emb X80231 LTCAMA	L.tarentolae CAM A gene for calmodulin.	73 1e-18
	emb AL115248 CNS01C9K	Botrytis cinerea strain T4 cDNA library un...	65 4e-18
	dbj D10521 TETCALW	T.pyriformis mRNA for calmodulin.	73 7e-18
	gb M76407 SLECALMODU	Stylonychia lemnae calmodulin gene, complet...	74 9e-18
25	emb AF007889 AF007889	Symbiodinium microadriaticum calmodulin (S...	74 1e-17
	emb AF078679 AF078679	Olea europaea calcium-binding protein (PCA...	57 2e-17
	emb X56511 TBCALUBG	T. brucei genes for calmodulin, EFH5 and ubi...	77 2e-17
	emb X52096 TCCALB2	Trypanosoma cruzi CalA2 calmodulin gene.	77 2e-17
	emb AF030033 AF030033	Phascolus vulgaris calmodulin (CaM) mRNA, ...	75 2e-17
30	emb X90560 PPCAMPROT	Physcomitrella patens mRNA for calmodulin.	71 2e-17
	gb U91642 POU91642	Pleurotus ostreatus calmodulin mRNA, complete...	75 2e-17
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	emb X85091 MPCAM	M.pyriferi mRNA for calmodulin.	74 2e-17
	gb M83535 PHTCALPIA	P.infestans calmodulin (calA) gene, complete...	75 2e-17
35	emb Y08373 TGCM	T.gondii mRNA for calmodulin.	74 2e-17
	gb C96396 C96396	C96396 Marchantia polymorpha immature sex organ...	73 3e-17
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	emb AB044286 AB044286	Chara corallina ccam mRNA for calmodulin, ...	75 4e-17
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	gb J05116 ACKCAL	A.klebsiana calmodulin gene, complete cds.	75 4e-17
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45	gb U12505 HCCMD	Histoplasma capsulatum 186AS calmodulin mRNA, co...	74 8e-17
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	emb AW164773 AW164773	se77e12.y1 Gm-c1023 Glycine max cDNA clone...	64 8e-17
	emb AW719875 AW719875	LjNEST11d4r Lotus japonicus nodule library...	57 8e-17
50	emb AW830090 AW830090	sm22a12.y1 Gm-c1028 Glycine max cDNA clone...	64 8e-17
	emb AW126204 AW126204	N100049e rootphos(-) Medicago truncatula c...	57 8e-17
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55	gb K02944 TRBCMRSG	Trypanosoma brucei gambiense calmodulin genes...	73 2e-16
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	gb U10150 BNU10150	Brassica napus Naehan calmodulin (bcml) mRNA...	73 2e-16
	emb X89890 BPCALMG	B.pilosa mRNA for calmodulin.	73 2e-16
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60	emb AW101324 AW101324	sd77e09.y1 Gm-c1009 Glycine max cDNA clone...	59 2e-16
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 emb|AL115056|CNS01C48 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
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 15 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16
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 20 gb|BE036340|BE036340 MO23E04 MO Mesembryanthemum crystallinum cD... 73 4e-16
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 25 gb|U49104|TAU49104 Triticum aestivum calmodulin TaCaM3-3 mRNA, c... 73 4e-16
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 30 gb|U48242|TAU48242 Triticum aestivum calmodulin TaCaM1-1 mRNA, c... 73 4e-16
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 35 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
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 gb|L18912|LILCALMODU Lilium longiflorum calmodulin mRNA, complet... 73 4e-16
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 (1408 letters)

55

Database: plantfungal

661,018 sequences; 426,114,510 total letters

60

Searching.....done

Score E

	Sequences producing significant alignments:	(bits) Value
	emb AB014483 AB014483 <i>Nicotiana tabacum</i> NtHSF1 mRNA for heat sho...	213 2e-62
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5	emb AI900223 AI900223 sc02f05.y1 Gm-c1012 Glycine max cDNA clone...	205 3e-53
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	emb AI055366 AI055366 coau0003M17 Cotton Boll Abscission Zone cD...	191 1e-47
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15	emb AW931781 AW931781 EST357624 tomato fruit mature green, TAMU ...	189 3e-47
	emb AW686121 AW686121 NF033H01NR1F1000 Nodulated root <i>Medicago</i> t...	188 1e-46
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	gb C95479 C95479 C95479 Citrus unshiu Miyagawa-wase maturation s...	166 5e-40
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	emb AW030725 AW030725 EST273980 tomato callus, TAMU <i>Lycopersicon</i> ...	165 1e-39
	emb AW041695 AW041695 EST284559 tomato mixed elicitor, BTI <i>Lycop</i> ...	165 1e-39
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	emb X67600 LPHSF8 L.peruvianum Lp-hsf8 mRNA for heat stress tran...	161 1e-38
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35	emb AI729182 AI729182 BNLGH12855 Six-day Cotton fiber <i>Gossypium</i> ...	149 5e-35
	emb AI489721 AI489721 EST248060 tomato ovary, TAMU <i>Lycopersicon</i> ...	149 5e-35
	emb AW034402 AW034402 EST277973 tomato callus, TAMU <i>Lycopersicon</i> ...	148 7e-35
	emb X67601 LPHSF30 L.peruvianum Lp-hsf30 mRNA for heat stress tr...	148 9e-35
	emb AW906822 AW906822 EST342945 potato stolon, Cornell Universit...	147 2e-34
40	emb AW164509 AW164509 se74f12.y1 Gm-c1023 Glycine max cDNA clone...	147 2e-34
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45	emb AW222011 AW222011 EST298822 tomato fruit red ripe, TAMU <i>Lyc</i> ...	144 2e-33
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	emb AB014484 AB014484 <i>Nicotiana tabacum</i> NtHSF2 mRNA for heat sho...	140 3e-32
	emb AF208544 AF208544 <i>Lycopersicon peruvianum</i> heat stress transc...	139 4e-32
50	emb AW738534 AW738534 EST339961 tomato flower buds, anthesis, Co...	139 5e-32
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	emb AW874988 AW874988 00109 leafy spurge Lambda HybriZAP 2.1 two...	138 1e-31
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	emb AV415736 AV415736 AV415736 <i>Lotus japonicus</i> young plants (two...	138 1e-31
55	emb AW979619 AW979619 EST341218 tomato root deficiency, Cornell ...	137 2e-31
	emb AW932142 AW932142 EST357985 tomato fruit mature green, TAMU ...	136 3e-31
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	emb AW569138 AW569138 si63g09.y1 Gm-r1030 Glycine max cDNA clone...	134 1e-30
	emb AW569256 AW569256 si64g09.y1 Gm-r1030 Glycine max cDNA clone...	134 1e-30
60	emb AW203851 AW203851 sf38h11.y1 Gm-c1028 Glycine max cDNA clone...	133 3e-30
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 10 emb|AW931892|AW931892 EST357735 tomato fruit mature green, TAMU ... 104 2e-21
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 20 emb|AI895834|AI895834 EST265277 tomato callus, TAMU Lycopersicon... 95 9e-19
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 gb|M94683|YSPHSF Schizosaccharomyces pombe heat shock transcript... 93 6e-18
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 25 emb|AW933448|AW933448 EST359387 tomato fruit mature green, TAMU ... 89 8e-17
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 emb|AZ045432|AZ045432 T234030b shotgun sub-library of BAC clone ... 84 2e-15
 emb|X83031|SCPOS9 S.cerevisiae POS9 gene. 83 5e-15
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 30 gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 83 5e-15
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 gb|M22040|YSCHSF1A S.cerevisiae heat shock transcription factor ... 81 2e-14
 emb|Z72596|SCYGL074C S.cerevisiae chromosome VII reading frame O... 81 2e-14
 gb|J03139|YSCHSF S.cerevisiae heat shock factor gene (HSF), comp... 81 2e-14
 35 emb|AI212342|AI212342 x3c12a1.r1 Aspergillus nidulans 24hr asexu... 73 8e-14
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 40 emb|AW307441|AW307441 sf57a06.y1 Gm-c1009 Glycine max cDNA clone... 70 5e-11
 emb|AW620962|AW620962 sj98b03.y1 Gm-c1023 Glycine max cDNA clone... 70 5e-11

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 thaliana] /blast_score 2.00e-75 /ec_number /family /chip nova
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 http://www.ncgr.org/cgi-bin/ff?hsp176a
 50 (613 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

55 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- 60 gb|M33901|PEAHSP177A Pisum sativum 17.7 kDa heat shock protein (... 126 3e-44
 gb|M99429|PHNSHSPA Ipomoea nil small heat shock protein, complet... 171 4e-42

- emb|X98617|MSSHPI7KD M.sativa mRNA for 17kD heat shock protein. 171 6e-42
 emb|AF159562|AF159562 Prunus dulcis cytosolic class II low molec... 105 7e-42
 gb|L47740|PIAEMB29R Picea glauca class II cytoplasmic small mole... 169 2e-41
 emb|AW569703|AW569703 si79c12.yl Gm-c1031 Glycine max cDNA clone... 107 6e-41
 5 emb|X99346|PASHSP P.abies mRNA for small heat shock protein. 166 1e-40
 emb|AW667877|AW667877 GA_Ea0011C02 Gossypium arboreum 7-10 dpa ... 110 2e-40
 emb|AW725392|AW725392 GA_Ea0017J18 Gossypium arboreum 7-10 dpa ... 110 2e-40
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 10 gb|BE053976|BE053976 GA_Ea0002N06f Gossypium arboreum 7-10 dpa ... 110 3e-39
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 20 emb|AI812703|AI812703 18B10 Pine Lambda Zap Xylem library Pinus ... 145 3e-34
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 emb|X95716|PCSHSPGEN P.crispum mRNA for 17.9kDa heat shock prote... 105 3e-28
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 emb|AB027500|AB027500 Daucus carota Dchsp-1 mRNA, complete cds. 98 2e-26
 25 emb|AJ225049|LPAJ5049 Lycopersicon peruvianum mRNA for Hsp20.2 p... 105 8e-26
 emb|AF090115|AF090115 Lycopersicon esculentum cytosolic class II... 106 3e-25
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 40 gb|L47717|PIAEMB27R Picea glauca heat shock protein 17.0 (EMB27)... 110 1e-23
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 emb|X92983|PMLMWHSPA P.menziesii mRNA for low molecular weight h... 104 6e-22
 50 emb|AW569996|AW569996 si85c11.yl Gm-c1031 Glycine max cDNA clone... 104 6e-22
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 emb|X58279|TAHSP173 T.aestivum mRNA for heat shock protein 17.3. 102 1e-21
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 55 gb|M33899|PEAHSP181A Pisum sativum 18.1 kDa heat shock protein (... 65 5e-21
 emb|AF089843|AF089843 Funaria hygrometrica cytosolic I small hea... 64 9e-21
 gb|U63631|FXU63631 Fragaria x ananassa LMW heat shock protein mR... 63 2e-20
 gb|U46545|HAU46545 Helianthus annuus 17.7 kDa heat-shock protein... 63 2e-20
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 60 emb|AF123255|AF123255 Lycopersicon esculentum 17.7 kD class I sm... 61 3e-20
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- emb|AW929084|AW929084 EST337788 tomato flower buds 8 mm to pre-a... 61 3e-20
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 emb|X07160|GMHSP185 Soybean gene for heat shock protein Gmhsp18... 61 1e-19
 10 emb|AF161179|AF161179 Malus domestica low molecular weight heat ... 60 1e-19
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 20 emb|AW221905|AW221905 EST298716 tomato fruit red ripe, TAMU Lyco... 62 4e-19
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 35 emb|AF089845|AF089845 Funaria hygrometrica cytosolic II small he... 94 1e-18
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 emb|AW223810|AW223810 EST300621 tomato fruit red ripe, TAMU Lyco... 57 1e-18

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45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

50 Score E
 Sequences producing significant alignments: (bits) Value

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 60 emb|AF042329|AF042329 Eimeria tenella heat shock protein 90 (hsp... 514 0.0
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- emb|Z29667|PFHESHP R. P. falciparum (7) mRNA for heat-shock protein. 507 0.0
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5 gb|M15346|TRBHSC T. cruzi tandemly repeated gene encoding an 85 k... 457 0.0
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gb|M73492|LEIHSP90 Leishmania donovani heat shock protein 90 mRNA... 456 0.0
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10 gb|U92465|AFU92465 Aspergillus fumigatus heat shock protein (Hsp... 458 e-165
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15 emb|Z67751|SC38KCXVI S. cerevisiae DNA (chromosome XVI; 38 kb). 448 e-159
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emb|AF251005|AF251005 Candida tropicalis heat shock protein 90 g... 444 e-158
20 emb|Z49808|SC8010 S. cerevisiae chromosome XIII cosmid 8010. 447 e-158
emb|AF221856|AF221856 Euphorbia esula heat-shock protein 80 mRNA... 292 e-158
gb|M26044|YSC HSC82 S. cerevisiae HSC82 gene encoding hsc82, the ... 447 e-157
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25 emb|AI489832|AI489832 EST248171 tomato ovary, TAMU Lycopersicon ... 471 e-132
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emb|AW218188|AW218188 EST303369 tomato radicle, 5 d post-imbibit... 452 e-126
35 emb|AW731352|AW731352 GA_Ea0030E22 Gossypium arboreum 7-10 dpa ... 449 e-125
emb|AW621485|AW621485 EST312283 tomato root during/after fruit s... 445 e-124
emb|AW905909|AW905909 EST342082 potato stolon, Cornell Universit... 331 e-124
emb|AW618647|AW618647 EST320633 L. pennellii trichome, Cornell U... 439 e-122
emb|AI730385|AI730385 BNLGH16770 Six-day Cotton fiber Gossypium ... 439 e-122
40 emb|AW931002|AW931002 EST356845 tomato fruit mature green, TAMU ... 436 e-121
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emb|AW217359|AW217359 EST296010 tomato flower buds 0-3 mm, Corne... 427 e-118
emb|AW216642|AW216642 EST295356 tomato callus, TAMU Lycopersicon... 423 e-117
45 emb|AW217696|AW217696 EST296410 tomato flower buds 8 mm to pre-a... 422 e-117
emb|AW011081|AW011081 ST16E03 Pine TriplEx shoot tip library Pin... 421 e-116
emb|AI730419|AI730419 BNLGH17100 Six-day Cotton fiber Gossypium ... 417 e-115
emb|AW907064|AW907064 EST343096 potato stolon, Cornell Universit... 413 e-114
emb|AW696590|AW696590 NF108G11ST1F1087 Developing stem Medicago ... 413 e-114
50 emb|AW738699|AW738699 EST340126 tomato flower buds, anthesis, Co... 412 e-114
emb|AI442468|AI442468 sa27d08.y1 Gm-c1004 Glycine max cDNA clone... 412 e-114
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- emb|AW735801|AW735801 EST336569 tomato flower buds 0-3 mm, Corne... 402 e-111
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 5 emb|AW218948|AW218948 EST301430 tomato root during/after fruit s... 396 e-110
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 emb|AW616417|AW616417 EST322828 L. hirsutum trichome, Cornell Un... 397 e-109
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 15 emb|AI781620|AI781620 EST262499 tomato susceptible, Cornell Lyco... 389 e-107
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 20 emb|AW651194|AW651194 EST329648 tomato germinating seedlings, TA... 266 e-106
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Database: plantfungal
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55	emb AI779924 AI779924 EST260803 tomato susceptible, Cornell Lyco...	228	8e-59
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	emb AI729603 AI729603 BNLGHi13760 Six-day Cotton fiber Gossypium...	202	8e-51
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60	emb AV426381 AV426381 AV426381 Lotus japonicus young plants (two...	145	3e-43
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	emb Y14573 HVCH4H Hordeum vulgare DNA for chromosome 4H.	107 7e-41
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	emb AI440563 AI440563 sa84c07.y1 Gm-c1004 Glycine max cDNA clone...	155 1e-36
5	emb AI166945 AI166945 xylem.est.727 Poplar xylem Lambda ZAPII li...	149 4e-35
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10	emb AI778500 AI778500 EST259379 tomato susceptible, Cornell Lyco...	76 3e-30
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30	emb AW569990 AW569990 si85c05.y1 Gm-c1031 Glycine max cDNA clone...	75 1e-12
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40	emb AZ221382 AZ221382 Gm_UMb001_002_A13R UMN Soybean BAC Library...	33 0.65
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50	emb X05498 SCSNR17B Yeast SNR17B gene for U3 small nuclear RNA.	35 1.8
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35 Database: plantfungal
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 10 emb|AW923451|AW923451 DG1_52_H09.b1_A002 Dark Grown 1 (DG1) Sorg... 31 7.1
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| 50 | emb Z49705 SC8520X <i>S. cerevisiae</i> chromosome XIII cosmid 8520. | 32 | 3.8 |
| | emb AB001684 AB001684 <i>Chlorella vulgaris</i> C-27 chloroplast DNA, c... | 32 | 3.8 |
| | emb AL049185 PFMAL13P2 <i>Plasmodium falciparum</i> chromosome 13 strai... | 32 | 3.8 |
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| 55 | emb AW991095 AW991095 SsS0129 Suaeda salsa ZAP cDNA library Suae... | 28 | 5.9 |
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| | emb AF057379 AF057379 <i>Nicotiana tabacum</i> clone G8-1 unknown mRNA. | 31 | 6.5 |
| | emb AB005455 AB005455 <i>Antirrhinum majus</i> DNA, genomic survey sequ... | 31 | 7.3 |
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Database: plantfungal
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	emb AW625258 AW625258 EST319261 tomato radicle, 5 d post-imbibit...	47	4e-05	
40	emb AI779024 AI779024 EST259903 tomato susceptible, Cornell Lyco...	46	1e-04	
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	emb AW278224 AW278224 sf41c11.y1 Gm-cl009 Glycine max cDNA clone...	45	3e-04	
	gb BE059759 BE059759 sn36g02.y1 Gm-cl016 Glycine max cDNA clone ...	45	3e-04	
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	emb AW661378 AW661378 833004H08.y1 C. reinhardtii CC-125 -S, Lam...	38	0.033	
	emb AW625785 AW625785 EST319692 tomato radicle, 5 d post-imbibit...	37	0.045	
55	emb AQ639212 AQ639212 927P1-10E7.TP 927P1 Trypanosoma brucei gen...	30	0.055	
	emb X02873 DCEXTG Carrot gene for extensin.	37	0.062	
	emb AW926428 AW926428 HVSMEg0007D04 Hordeum vulgare pre-anthesis...	35	0.063	
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	emb X55685 LEEXTEN5 Tomato extensin mRNA (clone uG-18).	36	0.12	
	emb X55682 LEEXTEN2 Tomato extensin mRNA (clone wY).	35	0.16	
60	emb X55681 LEEXTEN1 Tomato extensin mRNA (clone w17-1).	35	0.16	
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 5 emb|AI779223|AI779223 EST260102 tomato susceptible, Cornell Lyco... 35 0.22
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 10 emb|AF163953|AF163953 *Saccharomyces cerevisiae* isolate wt-2 telo... 29 0.26
 emb|X59720|SCCHRIII *S.cerevisiae* chromosome III complete DNA seq... 28 0.30
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 emb|X91836|VUEXT26GN *V.unguiculata* Ext26G gene. 34 0.58
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 emb|X86030|VURNEXT26 *V.unguiculata* mRNA for extensin-like prote... 34 0.58
 emb|AF163960|AF163960 *Saccharomyces cerevisiae* isolate wt-21 tel... 31 0.58
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 emb|Y15372|MTY15372 *Medicago truncatula* mRNA for MtN4 gene, part... 33 0.79
 emb|AV393340|AV393340 AV393340 *Chlamydomonas reinhardtii* C9 Chla... 33 0.79
 30 emb|AL117324|LMFL2719 *Leishmania major* Friedlin chromosome 23 co... 33 0.79
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 40 emb|AW696703|AW696703 NF109H07ST1F1063 Developing stem *Medicago* ... 33 1.1
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 emb|X74106|NTGRPR *N.tabacum* gene for glycine-rich protein. 33 1.1
 45 emb|AW725658|AW725658 GA_Ea0019C15 *Gossypium arboreum* 7-10 dpa ... 27 1.5
 emb|AA660327|AA660327 00198 MtrHE *Medicago truncatula* cDNA 5', m... 32 1.5
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 50 emb|AW686104|AW686104 NF034D07NR1F1000 Nodulated root *Medicago t...* 32 1.5
 gb|M76670|TOMEXTENA *L.esculentum* extensin (class I) gene, comple... 32 1.5
 gb|BE034655|BE034655 ML01E08 ML *Mesembryanthemum crystallinum* cD... 32 1.5
 emb|AL161025|L3320Y *Leishmania major* Friedlin cosmid L3320 t7 en... 32 1.5
 emb|AW329194|AW329194 N200406e rootphos(-) *Medicago truncatula* c... 32 1.5
 55 emb|AF163952|AF163952 *Saccharomyces cerevisiae* isolate wt-1 telo... 27 1.5
 emb|Z98532|SPAC1B1 *S.pombe* chromosome I cosmid c1B1. 28 1.6
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 gb|U66179|SCU66179 *Skeletonema costatum* fucoxanthin-chlorophyll ... 32 2.0
 emb|AC006280|AC006280 *Plasmodium falciparum* chromosome 12 clone ... 32 2.0
 60 emb|AW277958|AW277958 sf88a11.y1 Gm-c1019 Glycine max cDNA clone... 32 2.0

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AJ245479 BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,...	260	e-121
	emb AI495914 AI495914 sb17g06.y1 Gm-c1004 Glycine max cDNA clone...	57	4e-10
	emb AW217278 AW217278 EST295992 tomato callus, TAMU Lycopersicon...	50	6e-10
	emb AF179222 AF179222 Brassica rapa subsp. pekinensis floral nec...	43	2e-08
20	emb AW737522 AW737522 EST338949 tomato flower buds, anthesis, Co...	52	5e-06
	emb AW650581 AW650581 EST329035 tomato germinating seedlings, TA...	49	6e-06
	emb AW200887 AW200887 se94g08.y1 Gm-c1027 Glycine max cDNA clone...	50	3e-05
	emb AW774361 AW774361 EST333512 KV3 Medicago truncatula cDNA clo...	48	1e-04
	emb AW033701 AW033701 EST277272 tomato callus, TAMU Lycopersicon...	47	2e-04
25	emb AW738253 AW738253 EST339680 tomato flower buds, anthesis, Co...	46	5e-04
	emb AW285102 AW285102 LG1_300_F04.g1_A002 Light Grown 1 (LG1) So...	40	6e-04
	emb AI896626 AI896626 EST266069 tomato callus, TAMU Lycopersicon...	46	6e-04
	emb AW563740 AW563740 LG1_248_A08.g1_A002 Light Grown 1 (LG1) So...	43	0.004
	emb AW256640 AW256640 EST304777 KV2 Medicago truncatula cDNA clo...	42	0.006
30	emb AF133053 AF133053 Clarkia breweri S-adenosyl-L-methionine:sa...	42	0.006
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35	emb AW595921 AW595921 si95b09.y1 Gm-c1032 Glycine max cDNA clone...	35	0.94
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	emb AQ875548 AQ875548 V126F8 mTn-3xHA/lacZ Insertion Library, st...	35	1.3
	emb AI069155 AI069155 mgae0005dA02f Magnaporthe grisea Appressor...	34	1.8
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	emb AC005507 AC005507 Plasmodium falciparum chromosome 12 clone ...	34	2.4
	emb AF134688 AF134688 Plasmodium falciparum strain MAI5 from Mal...	34	2.4
	emb AF134683 AF134683 Plasmodium falciparum strain UNK1 CG2 omeg...	34	2.4
	emb AB009111 AB009111 AB009111 Chlamydomonas W80 lambda ZAP II C...	34	2.4
45	emb AL109814 PFMAL13PB Plasmodium falciparum chromosome 13 strai...	34	2.4
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50	emb AF134698 AF134698 Plasmodium falciparum strain COM1 from Com...	33	3.3
	gb U60200 STU60200 Solanum tuberosum lipoxxygenase (POTLX-1) mRNA...	33	4.6
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60	emb X95516 STLIPOT13 S.tuberosum mRNA for lipoxxygenase (clone T13).	33	4.6
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10	emb AA786508 AA786508 m3a04a1.r1 Aspergillus nidulans 24hr asexu...	32	6.3
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	emb Y14007 TAY14007 Triticum aestivum mRNA for gibberellin 20-ox...	32	6.3
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15	emb AA273033 AA273033 T4296 MVAT4 bloodstream form of serodeme W...	32	8.6
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	emb AA495648 AA495648 c078 Zhou and Ragan 1993 Gracilaria gracil...	32	8.6
	emb AL049182 PFMAL13P5 Plasmodium falciparum chromosome 13 strai...	32	8.6
	emb X56775 HVGLB1 H.vulgare Glb 1 gene for 1-3,1-4-beta-D-glucan...	32	8.6
20	emb Z72916 SCYGR131W S.cerevisiae chromosome VII reading frame O...	32	8.6
	emb Z72915 SCYGR130C S.cerevisiae chromosome VII reading frame O...	32	8.6
	gb U10083 TGU10083 Toxoplasma gondii RH hypoxanthine-guanine pho...	32	8.6
	emb AB026835 AB026835 Toxoplasma gondii mRNA for hypoxanthine-gu...	32	8.6
	gb U09219 TGU09219 Toxoplasma gondii RH hypoxanthine-guanine pho...	32	8.6
25	gb U10247 TGU10247 Toxoplasma gondii RH hypoxanthine-xanthine-gu...	32	8.6
	emb AB012774 AB012774 AB012774 Toxoplasma gondii mRNA (T.Koyama)...	32	8.6
	gb S73865 S73865 linoleate:oxygen oxidoreductase [Solanum tubero...	32	8.6
	emb AW761275 AW761275 sl65d12.y1 Gm-cl027 Glycine max cDNA clone...	32	8.6
	emb AL112245 CNS019Y5 Botrytis cinerea strain T4 cDNA library un...	32	8.6
30	emb X56260 HVGLUEND Barley DNA for (1,3;1,4)-beta-glucanase.(EC ...	32	8.6
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Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters

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55	emb AF030694 AF030694 Plasmodium falciparum strain Dd2 heat shoc...	31	3.3
	emb X12493 SCADR6 Yeast ADR6 gene for transcription factor.	30	4.5
	gb U14726 SCU14726 Saccharomyces cerevisiae Syg1p (SYG1) gene, c...	30	4.5
	emb Z46861 SC9905 S.cerevisiae chromosome IX cosmid 9905 and lam...	30	4.5
	gb L29456 TOBHIC12X Nicotiana tabacum histone H1 (H1C12) mRNA, c...	30	4.5
60	gb U33335 U33335 Saccharomyces cerevisiae chromosome XVI, left a...	30	4.5
	emb AJ290663 PAB290663 Picea abies copia like retroelement parti...	30	6.2

emb|AL115708|CNS01CMC Botrytis cinerea strain T4 cDNA library un... 30 6.2
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 emb|AQ875584|AQ875584 V127B11 mTn-3xHA/lacZ Insertion Library, s... 29 8.5
 5 gb|L16451|YSAAPRP Candida albicans acid proteinase-related prote... 29 8.5
 emb|AW981797|AW981797 PC18H02 Pine TriplEx pollen cone library P... 29 8.5
 emb|AQ644958|AQ644958 RPCI93-DpnII-30N9.TJ RPCI93-DpnII Trypanos... 29 8.5
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 emb|AW564851|AW564851 LG1_310_D10.b1_A002 Light Grown 1 (LG1) So... 29 8.5
 10 emb|AI895394|AI895394 EST264837 tomato callus, TAMU Lycopersicon... 27 9.6

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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30	emb AI489151 AI489151 EST247490 tomato ovary, TAMU Lycopersicon ...	152	4e-54	
	emb AI483907 AI483907 EST249778 tomato ovary, TAMU Lycopersicon ...	152	1e-52	
	emb AW931514 AW931514 EST357357 tomato fruit mature green, TAMU ...	145	4e-52	
	emb AI771546 AI771546 EST252646 tomato ovary, TAMU Lycopersicon ...	144	2e-49	
	emb AW736637 AW736637 EST333129 KV3 Medicago truncatula cDNA clo...	142	6e-48	
	emb AI166286 AI166286 xylem.est.133 Poplar xylem Lambda ZAPII li...	151	6e-40	
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	emb AW559446 AW559446 EST314494 DSIR Medicago truncatula cDNA cl...	143	1e-38	
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40	emb AW692307 AW692307 NF049H04ST1F1043 Developing stem Medicago ...	143	1e-36	
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	emb AW932074 AW932074 EST357917 tomato fruit mature green, TAMU ...	116	3e-26	
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	emb AW221352 AW221352 EST297821 tomato fruit mature green, TAMU ...	63	2e-21	
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5 gb|BE033948|BE033948 MG02E01 MG Mesembryanthemum crystallinum cD... 68 2e-18
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10 emb|AI726953|AI726953 BNLGHi6948 Six-day Cotton fiber Gossypium ... 66 5e-17
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15 emb|AW726749|AW726749 GA_Ea0022J22 Gossypium arboreum 7-10 dpa ... 64 6e-16
emb|AW689509|AW689509 NF021E09ST1F1000 Developing stem Medicago ... 63 6e-16
emb|AV411180|AV411180 AV411180 Lotus japonicus young plants (two... 75 9e-16
emb|AW697936|AW697936 NXNV_072_C04_F Nsf Xylem Normal wood Verti... 42 1e-15
20 emb|AW692507|AW692507 NF052C09ST1F1000 Developing stem Medicago ... 60 2e-15
emb|AW685394|AW685394 NF028G11NR1F1000 Nodulated root Medicago t... 60 2e-15
emb|AI725103|AI725103 1002 PtIFG2 Pinus taeda cDNA clone 8942r, ... 54 3e-15
emb|AW133056|AW133056 se13g09.y1 Gm-c1013 Glycine max cDNA clone... 69 4e-15
emb|AW695422|AW695422 NF094F05ST1F1046 Developing stem Medicago ... 52 5e-15
emb|AW693273|AW693273 NF064A06ST1F1000 Developing stem Medicago ... 60 7e-15
25 emb|AI727564|AI727564 BNLGHi8414 Six-day Cotton fiber Gossypium ... 66 1e-14
emb|AW254916|AW254916 ML134 peppermint glandular trichome Mentha... 67 3e-14
emb|AI166906|AI166906 xylem.est.692 Poplar xylem Lambda ZAPII li... 59 5e-14
emb|AW648535|AW648535 EST326989 tomato germinating seedlings, TA... 64 7e-14
30 emb|AW691201|AW691201 NF038H04ST1F1000 Developing stem Medicago ... 45 2e-13
emb|AW691254|AW691254 NF042G01ST1F1000 Developing stem Medicago ... 71 6e-13
emb|AI771903|AI771903 EST253003 tomato ovary, TAMU Lycopersicon ... 58 2e-12
emb|AW755537|AW755537 sl05b09.y1 Gm-c1036 Glycine max cDNA clone... 43 2e-12
emb|AW690391|AW690391 NF030B07ST1F1000 Developing stem Medicago ... 49 3e-12
gb|BE125956|BE125956 DG1_60_B12.b1_A002 Dark Grown 1 (DG1) Sorgh... 56 2e-11
35 emb|AW933549|AW933549 EST359308 tomato fruit mature green, TAMU ... 46 3e-11
emb|AW573921|AW573921 EST316512 GVN Medicago truncatula cDNA clo... 59 6e-11
emb|AV425214|AV425214 AV425214 Lotus japonicus young plants (two... 54 6e-11
emb|AW621185|AW621185 EST311983 tomato root during/after fruit s... 62 1e-10
emb|AW720132|AW720132 LjNEST14h12r Lotus japonicus nodule librar... 57 1e-10
40 emb|AW697024|AW697024 NF111E05ST1F1038 Developing stem Medicago ... 43 1e-10
emb|AI727398|AI727398 BNLGHi7916 Six-day Cotton fiber Gossypium ... 66 2e-10
emb|AW317889|AW317889 sg58e01.y1 Gm-c1007 Glycine max cDNA clone... 64 2e-10
emb|AI773497|AI773497 EST254597 tomato resistant, Cornell Lycope... 66 6e-10
emb|AI779047|AI779047 EST259926 tomato susceptible, Cornell Lyco... 66 6e-10
45 emb|AW160290|AW160290 EST290148 L. pennellii trichome, Cornell U... 66 6e-10
emb|AW690159|AW690159 NF028E04ST1F1000 Developing stem Medicago ... 40 9e-10
emb|AW697130|AW697130 NF112E12ST1F1098 Developing stem Medicago ... 40 9e-10
emb|AA739537|AA739537 302 PtIFG2 Pinus taeda cDNA clone 8497M 3'... 57 9e-10
emb|AW934683|AW934683 EST353575 tomato flower buds 0-3 mm, Corne... 44 1e-09
50 emb|AW217676|AW217676 EST296390 tomato flower buds 8 mm to pre-a... 44 1e-09
gb|L47871|L47871 BNAF1521 Mustard flower buds Brassica rapa cDNA... 47 1e-09
emb|AI163871|AI163871 A050p31u Hybrid aspen plasmid library Popu... 59 1e-09
emb|AW728602|AW728602 GA_Ea0017E06 Gossypium arboreum 7-10 dpa ... 64 1e-09
emb|AW617945|AW617945 EST314019 L. pennellii trichome, Cornell U... 46 2e-09
55 emb|AW647996|AW647996 EST326450 tomato germinating seedlings, TA... 64 2e-09
emb|AW218271|AW218271 EST303452 tomato radicle, 5 d post-imbibit... 64 2e-09
emb|AI776062|AI776062 EST257162 tomato resistant, Cornell Lycope... 64 2e-09
emb|AW036254|AW036254 EST278333 tomato seed, TAMU Lycopersicon e... 64 2e-09
emb|AW650814|AW650814 EST329268 tomato germinating seedlings, TA... 64 2e-09
60 emb|AI443133|AI443133 sa84g05.y1 Gm-c1004 Glycine max cDNA clone... 63 3e-09
emb|AW906997|AW906997 EST343224 potato stolon, Cornell Universit... 63 3e-09

emb|AI495275|AI495275 sb02h04.y1 Gm-c1004 Glycine max cDNA clone... 50 3e-09
 gb|BE053949|BE053949 GA__Ea0031D21f Gossypium arboreum 7-10 dpa ... 48 4e-09
 emb|AW730655|AW730655 GA__Ea0018A01 Gossypium arboreum 7-10 dpa ... 48 4e-09

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

20 emb|AV427887|AV427887 AV427887 Lotus japonicus young plants (two... 61 6e-17
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 emb|AI967590|AI967590 Ljimpest06-480-c9 Ljirnp Lambda HybriZap ... 68 2e-14
 emb|AW684644|AW684644 NF019C10NR1F1000 Nodulated root Medicago t... 62 9e-12
 gb|BE036389|BE036389 MO24B03 MO Mesembryanthemum crystallinum cD... 44 2e-06
 25 gb|BE034652|BE034652 ML01E04 ML Mesembryanthemum crystallinum cD... 35 0.57
 emb|AC005308|AC005308 Plasmodium falciparum chromosome 12 clone ... 35 0.57
 gb|N60116|N60116 TgESTzy01b10.r1 TgRH Tachyzoite cDNA Toxoplasma... 34 0.78
 emb|AF161334|AF161334 Raphanus raphanistrum subsp. raphanistrum ... 33 1.5
 gb|L37356|PUMPAL3A Petroselinum crispum phenylalanine ammonia-ly... 33 2.0
 30 emb|AI974840|AI974840 T113322e KV2 Medicago truncatula cDNA clon... 32 2.8
 gb|U36470|NCU36470 Neurospora crassa vacuolar ATPase 41 kDa subu... 32 2.8
 emb|AI938788|AI938788 sc60a05.y1 Gm-c1016 Glycine max cDNA clone... 32 2.8
 emb|AF114794|AF114794 Porphyra purpurea mitochondrion, complete ... 32 3.8
 emb|AI374339|AI374339 T6652 MVAT4 bloodstream form of serodeme W... 32 3.8
 35 emb|AI374387|AI374387 T6725 MVAT4 bloodstream form of serodeme W... 32 3.8
 emb|AI374381|AI374381 T6716 MVAT4 bloodstream form of serodeme W... 32 3.8
 emb|AI894927|AI894927 EST264370 tomato callus, TAMU Lycopersicon... 31 5.2
 emb|AA550548|AA550548 1711m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 31 5.2
 emb|AJ223459|ANAJ3459 Aspergillus nidulans prnA gene. 31 5.2
 40 emb|AJ390536|CAL390536 Candida albicans DNA, clone 222g9. 31 5.2
 emb|AW119888|AW119888 sd54b09.y1 Gm-c1016 Glycine max cDNA clone... 31 5.2
 emb|AI431203|AI431203 sa22f12.y2 Gm-c1006 Glycine max cDNA clone... 31 5.2
 emb|AF161331|AF161331 Sinapis arvensis S-locus related 1 (SLR1) ... 31 7.2
 emb|AF137311|AF137311 Miscanthus sinensis phytochrome B (PHYB) g... 31 7.2
 45 gb|T36711|T36711 EST101701 S. cerevisiae strain X2180-1A Sacchar... 31 7.2
 emb|AW781868|AW781868 sl97g02.y1 Gm-c1027 Glycine max cDNA clone... 31 7.2
 emb|AW755482|AW755482 sl04e07.y1 Gm-c1036 Glycine max cDNA clone... 30 9.9
 emb|AW694935|AW694935 NF081F05ST1F1046 Developing stem Medicago ... 30 9.9
 emb|AZ215370|AZ215370 Sheared DNA-56C1.TF Sheared DNA Trypanosom... 30 9.9
 50 emb|AQ945786|AQ945786 Sheared DNA-30C5.TR Sheared DNA Trypanosom... 30 9.9
 emb|AA739646|AA739646 411 PtIFG2 Pinus taeda cDNA clone 8694M 3'... 30 9.9
 emb|AL034353|SPBC1271 S.pombe chromosome II cosmid c1271. 30 9.9
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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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10	emb AI776331 AI776331 EST257431 tomato resistant, Cornell Lycopersicon...	51	8e-06
	emb AI938454 AI938454 sc45e10.y1 Gm-c1015 Glycine max cDNA clone...	44	0.001
	emb AF086822 AF086822 Candida boidinii dihydroxyacetone synthase...	36	0.38
	emb AV406828 AV406828 Lotus japonicus young plants (two...)	31	0.49
	emb AI731942 AI731942 BNLGH11450 Six-day Cotton fiber Gossypium...	35	0.71
15	emb AQ255443 AQ255443 mgxb0014121r CUGI Rice Blast BAC Library P...	35	0.71
	emb AQ940346 AQ940346 Sheared DNA-33M2.TF Sheared DNA Trypanosom...	34	1.3
	emb AI210373 AI210373 i0e05a1.r1 Aspergillus nidulans 24hr asexu...	34	1.8
	emb AQ935542 AQ935542 CpG2525A CplOWAgDNA1 Cryptosporidium parvu...	33	2.5
	gb T18147 T18147 0722c3 czapPFDd2.1, Debopam Chakrabarti Plasmod...	33	2.5
20	emb AW651276 AW651276 EST329730 tomato germinating seedlings, TA...	33	3.5
	emb AI392128 AI392128 NCSM1B1T7 Subtracted Mycelial Neurospora c...	32	4.8
	emb AW330094 AW330094 TENU4840 T.cruzi epimastigote normalized c...	32	4.8
	emb AF055296 AF055296 Zantedeschia aethiopica geranylgeranyl red...	32	4.8
	emb AI725804 AI725804 BNLGH113200 Six-day Cotton fiber Gossypium...	32	4.8
25	emb AW686984 AW686984 NF004F11RT1F1094 Developing root Medicago ...	32	6.6
	emb AJ273808 AJ273808 AJ273808 Metarhizium anisopliae ARSEF 2575...	32	6.6
	emb AQ943530 AQ943530 Sheared DNA-42D24.TR Sheared DNA Trypanoso...	31	9.0
	emb AQ941987 AQ941987 Sheared DNA-42F7.TR Sheared DNA Trypanosom...	31	9.0
	emb AW620371 AW620371 sj04d01.y1 Gm-c1032 Glycine max cDNA clone...	31	9.0
30	emb AI973930 AI973930 sd13g08.y1 Gm-c1020 Glycine max cDNA clone...	31	9.0
	emb AF069470 AF069470 Phleum pratense group V allergen Phl p 5.0...	31	9.0
	emb AL160716 P406R Leishmania major Friedlin PAC P406 right end...	31	9.0
	emb AQ851400 AQ851400 LMAJFV1_lm40b04.y1 Leishmania major FV1 ra...	31	9.0
	emb AF061068 AF061068 Phleum pratense clone 10029 major allergen...	31	9.0
35	emb AQ953188 AQ953188 Sheared DNA-50B12.TF Sheared DNA Trypanoso...	31	9.0
	emb AW719942 AW719942 LjNEST12c6r Lotus japonicus nodule library...	31	9.0
	emb X74735 PPHLP5 P. pratense mRNA for PhlpV.	31	9.0
	emb AW396374 AW396374 sh27d05.y1 Gm-c1016 Glycine max cDNA clone...	31	9.0
	gb N60997 N60997 TgESTzy23f10.r1 TgRH Tachyzoite cDNA Toxoplasma...	31	9.0
40	emb AI164737 AI164737 A068P10U Hybrid aspen plasmid library Popu...	31	9.0
	emb AW348348 AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3...	26	9.5
	emb AW309665 AW309665 sf22g06.x1 Gm-c1028 Glycine max cDNA clone...	26	9.5
	emb AW310247 AW310247 sf33d01.x1 Gm-c1028 Glycine max cDNA clone...	26	9.5
	emb AW508196 AW508196 si50d10.y1 Gm-r1030 Glycine max cDNA clone...	27	9.6
45	emb AW102012 AW102012 sd81h10.y1 Gm-c1009 Glycine max cDNA clone...	26	9.8
	emb AW309166 AW309166 sg05b01.y1 Gm-c1019 Glycine max cDNA clone...	26	9.8
	emb AW598779 AW598779 sj46h06.y1 Gm-c1033 Glycine max cDNA clone...	26	9.8
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Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

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	emb AW698685 AW698685 R125 non-glandular-haired subtracted cDNA ...	32	1.4
5	emb AF061282 AF061282 Sorghum bicolor 22 kDa kafirin cluster.	31	5.6
	emb AL031854 SPBC337 S.pombe chromosome II cosmid c337.	31	5.6
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	31	5.6
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone ...	31	5.6
	gb M74062 YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl...	31	5.6
10	emb AQ947500 AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso...	31	5.6
	gb M83307 YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl...	31	5.6
	emb AL031856 SPBC1734 S.pombe chromosome II cosmid c1734.	31	5.6
	emb AC073246 AC073246 Trypanosoma brucei chromosome II clone RPC...	30	7.7
	emb AL031535 SPCC16C4 S.pombe chromosome III cosmid c16C4.	30	7.7
15	emb AC012647 AC012647 Trypanosoma brucei chromosome II clone RPC...	30	7.7
	gb L28038 TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc...	30	7.7
	emb AB004322 AB004322 Nicotiana sylvestris NsPMT1 gene for putre...	30	7.7
	emb AQ941496 AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso...	30	7.7
	emb AQ946940 AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom...	30	7.7
20	emb AQ942433 AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom...	30	7.7
	emb AF133529 AF133529 Candida albicans mRNA cap methyltransferas...	30	7.7

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Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

Searching.....done

	Sequences producing significant alignments:	Score	E	(bits)	Value
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	emb AF061282 AF061282 Sorghum bicolor 22 kDa kafirin cluster.	31	5.6		
40	emb AL031854 SPBC337 S.pombe chromosome II cosmid c337.	31	5.6		
	emb AC004709 AC004709 Plasmodium falciparum chromosome 12, *** S...	31	5.6		
	emb AC006280 AC006280 Plasmodium falciparum chromosome 12 clone ...	31	5.6		
	gb M74062 YSPCDC27A Schizosaccharomyces pombe cdc27+ gene, compl...	31	5.6		
	emb AQ947500 AQ947500 Sheared DNA-39L12.TF Sheared DNA Trypanoso...	31	5.6		
45	gb M83307 YSPCDC27B Schizosaccharomyces pombe cdc27+ mRNA, compl...	31	5.6		
	emb AL031856 SPBC1734 S.pombe chromosome II cosmid c1734.	31	5.6		
	emb AC073246 AC073246 Trypanosoma brucei chromosome II clone RPC...	30	7.7		
	emb AL031535 SPCC16C4 S.pombe chromosome III cosmid c16C4.	30	7.7		
	emb AC012647 AC012647 Trypanosoma brucei chromosome II clone RPC...	30	7.7		
50	gb L28038 TRBKINCSBA Trypanosoma rangeli kinetoplast DNA sequenc...	30	7.7		
	emb AB004322 AB004322 Nicotiana sylvestris NsPMT1 gene for putre...	30	7.7		
	emb AQ941496 AQ941496 Sheared DNA-44O18.TF Sheared DNA Trypanoso...	30	7.7		
	emb AQ946940 AQ946940 Sheared DNA-36C7.TF Sheared DNA Trypanosom...	30	7.7		
	emb AQ942433 AQ942433 Sheared DNA-45G7.TR Sheared DNA Trypanosom...	30	7.7		
55	emb AF133529 AF133529 Candida albicans mRNA cap methyltransferas...	30	7.7		

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Database: plantfungal
661,018 sequences; 426,114,510 total letters

5 Searching.....done

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emb AW399343 AW399343 EST309843 L. pennellii trichome, Cornell U...	234	2e-60	
emb AW618318 AW618318 EST320304 L. pennellii trichome, Cornell U...	177	1e-53	
emb AW310982 AW310982 sg31b02.x1 Gm-c1024 Glycine max cDNA clone...	97	1e-51	
15 emb AI442277 AI442277 sa66a04.y1 Gm-c1004 Glycine max cDNA clone...	200	2e-50	
emb AW687759 AW687759 NF013B05RT1F1044 Developing root Medicago ...	160	1e-46	
emb AW684122 AW684122 NF012F06NR1F1000 Nodulated root Medicago t...	83	2e-44	
emb AW309867 AW309867 sf25g10.x1 Gm-c1028 Glycine max cDNA clone...	89	5e-43	
gb BE020423 BE020423 sm40e08.y1 Gm-c1028 Glycine max cDNA clone ...	88	2e-39	
20 emb AW691118 AW691118 NF041D08ST1F1000 Developing stem Medicago ...	78	2e-35	
emb AW160235 AW160235 EST290093 L. pennellii trichome, Cornell U...	120	6e-32	
emb AI960862 AI960862 sc91f07.y1 Gm-c1019 Glycine max cDNA clone...	74	5e-30	
emb AW349633 AW349633 GM210006A11B3R Gm-r1021 Glycine max cDNA 3...	89	8e-29	
emb AW775076 AW775076 EST334227 KV3 Medicago truncatula cDNA clo...	81	6e-26	
25 gb BE020331 BE020331 sm40d08.y1 Gm-c1028 Glycine max cDNA clone ...	69	4e-23	
emb AW746031 AW746031 WS1_39_A03.b1_A002 Water-stressed I (WS1) ...	74	8e-23	
emb AW621546 AW621546 EST312344 tomato root during/after fruit s...	64	1e-13	
emb AW622846 AW622846 EST306916 tomato flower buds 3-8 mm, Come...	54	2e-12	
gb L43984 BLYBD Hordeum vulgare (clone ABG377) chromosome 3H STS...	69	8e-11	
30 emb AW774216 AW774216 EST333367 KV3 Medicago truncatula cDNA clo...	69	1e-10	
emb AW774324 AW774324 EST333475 KV3 Medicago truncatula cDNA clo...	69	1e-10	
emb AW686169 AW686169 NF038H07NR1F1000 Nodulated root Medicago t...	68	2e-10	
emb AW160234 AW160234 EST290092 L. pennellii trichome, Cornell U...	46	2e-08	
emb AW685496 AW685496 NF030G02NR1F1000 Nodulated root Medicago t...	45	2e-07	
35 emb AW684082 AW684082 NF011H08NR1F1000 Nodulated root Medicago t...	55	2e-06	
emb AW693839 AW693839 NF069F08ST1F1074 Developing stem Medicago ...	53	6e-06	
emb AI163659 AI163659 A046p04u Hybrid aspen plasmid library Popu...	53	6e-06	
emb AW033404 AW033404 EST276975 tomato callus, TAMU Lycopersicon...	49	1e-04	
emb AI054662 AI054662 coau0001K11 Cotton Boll Abscission Zone cD...	37	2e-04	
40 emb AW758414 AW758414 874008A01.y1 C. reinhardtii CC-1690, Lambd...	41	0.022	
emb AW746188 AW746188 WS1_39_A03.g1_A002 Water-stressed I (WS1) ...	41	0.022	
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emb AI488725 AI488725 EST247064 tomato ovary, TAMU Lycopersicon ...	38	0.20	
45 emb Z69731 SPAC6C3 S.pombe chromosome I cosmid c6C3.	36	0.71	
emb Z38061 SC9168 S.cerevisiae chromosome IX cosmid 9168.	36	0.71	
emb AW925349 AW925349 HVSMEg0001B12 Hordeum vulgare pre-anthesis...	36	0.71	
emb AW671585 AW671585 LG1_348_H11.b1_A002 Light Grown I (LG1) So...	36	0.97	
gb BE024935 BE024935 894007A03.x1 C. reinhardtii CC-1690, normal...	36	0.97	
50 emb AW216501 AW216501 EST295215 tomato callus, TAMU Lycopersicon...	36	0.97	
emb AW680841 AW680841 WS1_7_E11.g1_A002 Water-stressed I (WS1) S...	35	1.3	
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emb AW100578 AW100578 sd57b08.y1 Gm-c1008 Glycine max cDNA clone...	35	1.3	
emb AW010724 AW010724 ST11E02 Pine TriplEx shoot tip library Pin...	35	1.8	
55 emb AL138854 SPAC23G3 S.pombe chromosome I cosmid c23G3.	35	2.5	
emb AW934681 AW934681 EST353573 tomato flower buds 0-3 mm, Come...	34	3.5	
emb Z98975 SPAC19E9 S.pombe chromosome I cosmid c19E9.	34	3.5	
emb AW690479 AW690479 NF035A03ST1F1000 Developing stem Medicago ...	34	3.5	
emb Z50142 SPAC2F7 S.pombe chromosome I cosmid c2F7.	34	3.5	
60 emb AA728334 AA728334 LmLv39p7/70M Leishmania major promastigote...	34	4.8	
emb AI779448 AI779448 EST260327 tomato susceptible, Cornell Lyco...	34	4.8	

	emb AQ639314 AQ639314 927P1-2A10.TV 927P1 Trypanosoma brucei gen...	34 4.8
	emb AW725460 AW725460 GA__Ea0018B02 Gossypium arboreum 7-10 dpa ...	34 4.8
	emb AW256577 AW256577 EST304714 KV2 Medicago truncatula cDNA clo...	34 4.8
	emb AW234006 AW234006 sf33a07.y1 Gm-c1028 Glycine max cDNA clone...	34 4.8
5	emb AW727061 AW727061 GA__Ea0011B08 Gossypium arboreum 7-10 dpa ...	34 4.8
	emb AZ221057 AZ221057 Sheared DNA-64F1.TR Sheared DNA Trypanosom...	34 4.8
	emb AI781303 AI781303 EST262182 tomato susceptible, Cornell Lyco...	34 4.8
	emb AA898817 AA898817 NCP3G4T7 Perithecial Neurospora crassa cDN...	34 4.8
	emb AI329539 AI329539 b6b04ne.fl Neurospora crassa evening cDNA ...	33 6.6
10	emb AW754602 AW754602 PC04B10 Pine TriplEx pollen cone library P...	33 6.6
	emb AL049181 PFMAL13P4 Plasmodium falciparum chromosome 13 strai...	33 6.6
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	emb AZ215288 AZ215288 Sheared DNA-83F7.TR Sheared DNA Trypanosom...	33 9.0
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Database: plantfungal
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	emb AW618112 AW618112 EST314162 L. pennellii trichome, Cornell U...	28	0.72
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	emb AW040234 AW040234 EST282740 tomato mixed elicitor, BTI Lycop...	28	3.0
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| | gb BE054146 BE054146 GA_Ea0034H12f <i>Gossypium arboreum</i> 7-10 dpa ... | 167 | 7e-50 | |
| | gb L24438 THLCYP450A <i>Thlaspi arvense</i> germline cytochrome P450 mR... | 144 | 2e-48 | |
| | emb Z22545 PHFLAHYDB <i>P.hybrida</i> flavonoid 3',5'-hydroxylase mRNA. | 77 | 9e-47 | |
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| | emb Z22544 PHFLAHYDA <i>P.hybrida</i> flavonoid 3',5'-hydroxylase mRNA. | 71 | 2e-44 | |
| | dbj D85184 D85184 <i>Gentiana triflora</i> mRNA for flavonoid 3',5'-hyd... | 85 | 8e-44 | |
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| | emb Y09423 NRCYP71A5 <i>Nepeta racemosa</i> mRNA for cytochrome P450, C... | 126 | 8e-40 | |
| 45 | emb AF122821 AF122821 <i>Capsicum annuum</i> cytochrome P450 (PepCYP) m... | 127 | 2e-39 | |
| | gb U48435 SCU48435 <i>Solanum chacoense</i> putative cytochrome P450 ge... | 136 | 3e-39 | |
| | emb AJ238612 CRO238612 <i>Catharanthus roseus</i> mRNA for cytochrome P... | 135 | 3e-39 | |
| | emb AF124815 AF124815 <i>Mentha spicata</i> cytochrome p450 mRNA, compl... | 134 | 4e-39 | |
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| 50 | gb U48434 SCU48434 <i>Solanum chacoense</i> cytochrome P450 mRNA, compl... | 124 | 2e-38 | |
| | emb AW255799 AW255799 ML868 peppermint glandular trichome <i>Mentha</i> ... | 116 | 2e-38 | |
| | emb AF124816 AF124816 <i>Mentha x piperita</i> cytochrome p450 isoform ... | 123 | 1e-37 | |
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| 55 | emb X71658 SMCYPEG8 <i>S.melongena</i> CYP76A1 mRNA. | 130 | 2e-36 | |
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| | emb AW668053 AW668053 GA_Ea0012G23 <i>Gossypium arboreum</i> 7-10 dpa ... | 129 | 3e-36 | |
| | emb Z33875 CYMPCP450 <i>M.piperita</i> gene for cytochrome P-450 oxidase. | 126 | 3e-36 | |
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emb|AW218579|AW218579 EST303762 tomato radicle, 5 d post-imbibit... 133 4e-30
emb|AB028152|AB028152 *Torenia hybrida* TFNS5 mRNA for cytochrome ... 64 4e-30
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20 http://www.ncgr.org/cgi-bin/ff?pad4
(1732 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

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emb|AW707128|AW707128 sk10a03.y1 Gm-c1023 Glycine max cDNA clone... 58 4e-17
emb|AW560897|AW560897 EST315945 DSIR Medicago truncatula cDNA cl... 73 1e-16
emb|AW257406|AW257406 EST305543 KV2 Medicago truncatula cDNA clo... 73 1e-16
45 emb|AW685948|AW685948 NF036G07NR1F1000 Nodulated root Medicago t... 73 1e-16
emb|AW698315|AW698315 NXNV_071_G01_F Nsf Xylem Normal wood Verti... 75 3e-16
emb|AZ051219|AZ051219 Gm_UMB001_062_F16R UMN Soybean BAC Library... 55 2e-15
emb|AW587665|AW587665 ST63B10 Pine TriplEx shoot tip library Pin... 78 2e-15
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50 emb|AW888098|AW888098 NXNV_108_F09_F Nsf Xylem Normal wood Verti... 72 1e-14
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60 emb|AW870069|AW870069 NXNV_123_G03_F Nsf Xylem Normal wood Verti... 58 2e-10
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- emb|AW349142|AW349142 GM210003B22H5R Gm-r1021 Glycine max cDNA 3... 57 3e-09
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 5 emb|AW031593|AW031593 EST275047 tomato callus, TAMU Lycopersicon... 35 2e-07
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 10 emb|AW349364|AW349364 GM210004B12G1R Gm-r1021 Glycine max cDNA 3... 56 1e-06
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 20 emb|AZ214023|AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso... 46 9e-04
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 emb|AW933515|AW933515 EST359274 tomato fruit mature green, TAMU ... 32 0.003
 emb|AZ213147|AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso... 36 0.003
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 25 emb|AW870252|AW870252 NXNV_128_C06_F Nsf Xylem Normal wood Vertic... 44 0.004
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 gb|BE123796|BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic... 31 0.006
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 35 emb|AW687805|AW687805 NF013F08RT1F1074 Developing root Medicago ... 32 0.14
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 40 emb|AW685575|AW685575 NF029B05NR1F1000 Nodulated root Medicago t... 39 0.14
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 emb|AW934555|AW934555 EST353447 tomato flower buds 0-3 mm, Corne... 38 0.27
 45 emb|AW307176|AW307176 sf53g04.y1 Gm-c1009 Glycine max cDNA clone... 31 0.36
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 50 emb|AW686305|AW686305 NF036D07NR1F1000 Nodulated root Medicago t... 36 0.96
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 emb|AF127256|AF127256 Laureliopsis philippiana rpl16 gene, chlor... 35 1.8
 emb|AF127255|AF127255 Laurelia sempervirens rpl16 gene, chloropl... 35 1.8
 55 emb|AF127257|AF127257 Nemuaron vieillardii rpl16 gene, chloropla... 35 1.8
 emb|AW508953|AW508953 si38d01.y1 Gm-r1030 Glycine max cDNA clone... 28 2.1
 emb|AW719424|AW719424 LjNEST4d11r Lotus japonicus nodule library... 28 2.1
 emb|AW032864|AW032864 EST276423 tomato callus, TAMU Lycopersicon... 29 2.1
 emb|AW306559|AW306559 se52d10.y1 Gm-c1017 Glycine max cDNA clone... 35 2.5
 60 emb|AI399344|AI399344 NCW01D11T7 Westergaards Neurospora crassa ... 35 2.5
 emb|AI485040|AI485040 EST243320 tomato ovary, TAMU Lycopersicon ... 34 3.4

	emb Z49212 SC9952X <i>S.cerevisiae</i> chromosome XIII cosmid 9952.	34	3.4
	emb AA741585 AA741585 <i>LmLv39p3/132B</i> <i>Leishmania major</i> promastigot...	34	3.4
	emb X81715 SCMDYGENE <i>S.cerevisiae</i> partial MDY gene.	34	3.4
	emb X73956 TBMAP292 <i>T.brucei</i> Tb-292 mRNA for membrane associated...	34	3.4
5	emb AZ212769 AZ212769 Sheared DNA-66C3.TR Sheared DNA Trypanosom...	34	3.4
	emb X82612 SCATM1 <i>S.cerevisiae</i> ATM1 gene.	34	3.4
	emb AC005139 AC005139 <i>Plasmodium falciparum</i> chromosome 12, *** S...	34	4.7
	emb AA649446 AA649446 T4369 MVAT4 bloodstream form of serodeme W...	34	4.7
10	Query= PAD4_r_at 14250_r_at /id_source genbank /description emb cab43438.1 (al050300) putative protein [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link http://www3.ncbi.nlm.nih.gov/htbin- post/entrez/query?db=n&form=6&dopt=g&uid=gb pad4 /ncgi http://www.ncgr.org/cgi-bin/ff?pad4 (1732 letters)		
15	Database: plantfungal 661,018 sequences; 426,114,510 total letters		
20	Searching.....done		
	Score E	(bits)	Value
25	Sequences producing significant alignments:		
	emb AW981483 AW981483 EST392636 <i>DSIL</i> <i>Medicago truncatula</i> cDNA cl...	126	8e-59
	emb AW684289 AW684289 NF015A11NR1F1000 <i>Nodulated root</i> <i>Medicago t...</i>	124	5e-37
	emb AW032082 AW032082 EST275536 tomato callus, TAMU <i>Lycopersicon...</i>	112	2e-29
30	emb AI781175 AI781175 EST262054 tomato susceptible, Cornell Lyco...	62	4e-24
	emb AW011208 AW011208 ST18A05 Pine TriplEx shoot tip library Pin...	107	2e-23
	emb AW225676 AW225676 ST70B12 Pine TriplEx shoot tip library Pin...	95	2e-20
	emb AV423915 AV423915 AV423915 <i>Lotus japonicus</i> young plants (two...	98	6e-20
	emb AI778594 AI778594 EST259473 tomato susceptible, Cornell Lyco...	95	2e-19
35	emb AW032676 AW032676 EST276235 tomato callus, TAMU <i>Lycopersicon...</i>	95	2e-19
	emb AW559251 AW559251 EST306087 <i>DSIR</i> <i>Medicago truncatula</i> cDNA cl...	97	4e-19
	emb AW774727 AW774727 EST333878 KV3 <i>Medicago truncatula</i> cDNA clo...	97	4e-19
	emb AW707128 AW707128 sk10a03.y1 Gm-c1023 <i>Glycine max</i> cDNA clone...	58	4e-17
	emb AW560897 AW560897 EST315945 <i>DSIR</i> <i>Medicago truncatula</i> cDNA cl...	73	1e-16
40	emb AW257406 AW257406 EST305543 KV2 <i>Medicago truncatula</i> cDNA clo...	73	1e-16
	emb AW685948 AW685948 NF036G07NR1F1000 <i>Nodulated root</i> <i>Medicago t...</i>	73	1e-16
	emb AW698315 AW698315 NXNV_071_G01_F Nsf Xylem Normal wood Verti...	75	3e-16
	emb AZ051219 AZ051219 Gm_UMB001_062_F16R UMN Soybean BAC Library...	55	2e-15
	emb AW587665 AW587665 ST63B10 Pine TriplEx shoot tip library Pin...	78	2e-15
45	emb AW217058 AW217058 EST295772 tomato callus, TAMU <i>Lycopersicon...</i>	71	2e-15
	emb AW888098 AW888098 NXNV_108_F09_F Nsf Xylem Normal wood Verti...	72	1e-14
	emb AW560122 AW560122 EST315170 <i>DSIR</i> <i>Medicago truncatula</i> cDNA cl...	51	4e-14
	emb AW980840 AW980840 EST391993 GVN <i>Medicago truncatula</i> cDNA clo...	51	4e-14
	emb AW560121 AW560121 EST315169 <i>DSIR</i> <i>Medicago truncatula</i> cDNA cl...	51	7e-14
50	emb AI920196 AI920196 1726 Pine Lambda Zap Xylem library Pinus t...	59	1e-13
	emb AW559836 AW559836 EST314884 <i>DSIR</i> <i>Medicago truncatula</i> cDNA cl...	78	2e-13
	emb AW290408 AW290408 NXNV019H08F Nsf Xylem Normal wood Vertical...	73	3e-13
	gb BE049795 BE049795 NXNV_144_C08_F Nsf Xylem Normal wood Vertic...	52	7e-13
	emb AW687647 AW687647 NF011F10RT1F1090 Developing root <i>Medicago ...</i>	51	9e-13
55	emb AW687408 AW687408 NF009C08RT1F1065 Developing root <i>Medicago ...</i>	49	2e-10
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	emb AI855891 AI855891 sc30h08.y1 Gm-c1014 <i>Glycine max</i> cDNA clone...	58	1e-09
	emb AW349142 AW349142 GM210003B22H5R Gm-r1021 <i>Glycine max</i> cDNA 3...	57	3e-09
	emb AW065112 AW065112 ST39G09 Pine TriplEx shoot tip library Pin...	62	1e-08
60	emb AW736866 AW736866 NXNV_083_H05_F Nsf Xylem Normal wood Verti...	52	2e-08
	emb AW685287 AW685287 NF027B11NR1F1000 <i>Nodulated root</i> <i>Medicago t...</i>	46	4e-08

	emb AW031593 AW031593 EST275047 tomato callus, TAMU Lycopersicon...	35	2e-07
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	emb AW773999 AW773999 EST332985 KV3 Medicago truncatula cDNA clo...	51	5e-07
	emb AW704685 AW704685 sk39c02.y1 Gm-c1028 Glycine max cDNA clone...	39	5e-07
5	gb BE123705 BE123705 NXNV_151_H02_F Nsf Xylem Normal wood Vertic...	53	1e-06
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10	emb AW694970 AW694970 NF082B02ST1F1015 Developing stem Medicago ...	37	8e-06
	emb AW687653 AW687653 NF011G04RT1F1035 Developing root Medicago ...	49	1e-04
	emb AI416889 AI416889 sa19d09.x1 Gm-c1005 Glycine max cDNA clone...	49	1e-04
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	emb AI780239 AI780239 EST261118 tomato susceptible, Cornell Lyco...	34	4e-04
15	emb AW985058 AW985058 NXNV_130_D03_F Nsf Xylem Normal wood Verti...	31	7e-04
	emb AZ214023 AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso...	46	9e-04
	emb AZ214029 AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso...	46	0.001
	emb AW933515 AW933515 EST359274 tomato fruit mature green, TAMU ...	32	0.003
	emb AZ213147 AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso...	36	0.003
20	emb AW616497 AW616497 EST322908 L. hirsutum trichome, Cornell Un...	35	0.004
	emb AW870252 AW870252 NXNV_128_C06_F Nsf Xylem Normal wood Verti...	44	0.004
	emb AW687535 AW687535 NF010F08RT1F1074 Developing root Medicago ...	43	0.006
	gb BE123796 BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic...	31	0.006
	emb AW618666 AW618666 EST320652 L. pennellii trichome, Cornell U...	33	0.009
25	emb AW317531 AW317531 sg51e11.y1 Gm-c1025 Glycine max cDNA clone...	41	0.013
	emb AW686129 AW686129 NF033H12NR1F1000 Nodulated root Medicago t...	32	0.023
	emb AV417662 AV417662 AV417662 Lotus japonicus young plants (two...	30	0.025
	emb AW010126 AW010126 ST02C06 Pine TriplEx shoot tip library Pin...	41	0.029
	emb AW686977 AW686977 NF004F04RT1F1042 Developing root Medicago ...	33	0.031
30	emb AW329638 AW329638 N200899e rootphos(-) Medicago truncatula c...	40	0.075
	emb AW687805 AW687805 NF013F08RT1F1074 Developing root Medicago ...	32	0.14
	emb AW775153 AW775153 EST334304 KV3 Medicago truncatula cDNA clo...	29	0.14
	emb AI812757 AI812757 18G10 Pine Lambda Zap Xylem library Pinus ...	39	0.14
	emb AW774485 AW774485 EST333636 KV3 Medicago truncatula cDNA clo...	39	0.14
35	emb AW693919 AW693919 NF070E05ST1F1038 Developing stem Medicago ...	39	0.14
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	emb AF127257 AF127257 Nemuaron vieillardii rpl16 gene, chloropla...	35	1.8
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	emb AI485040 AI485040 EST243320 tomato ovary, TAMU Lycopersicon ...	34	3.4
	emb Z49212 SC9952X S.cerevisiae chromosome XIII cosmid 9952.	34	3.4
	emb AA741585 AA741585 LmLv39p3/132B Leishmania major promastigot...	34	3.4
60	emb X81715 SCMDYGENE S.cerevisiae partial MDY gene.	34	3.4
	emb X73956 TBMAP292 T.brucei Tb-292 mRNA for membrane associated...	34	3.4

emb|AZ212769|AZ212769 Sheared DNA-66C3.TR Sheared DNA Trypanosom... 34 3.4
 emb|X82612|SCATM1 *S.cerevisiae* ATM1 gene. 34 3.4
 emb|AC005139|AC005139 *Plasmodium falciparum* chromosome 12, *** S... 34 4.7
 emb|AA649446|AA649446 T4369 MVAT4 bloodstream form of serodeme W... 34 4.7

5

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 [arabidopsis /blast_score 1.00e-134 /ec_number /family /chip nova
 /gb_link /ncgi
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10

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15

Searching.....done

	Score	E	(bits)	Value
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	emb AJ002221 DLJ002221	<i>Digitalis lanata</i>	mRNA for phenylalanine a...	412 e-113
	dbj D83076 D83076	<i>Lithospermum erythrorhizon</i>	mRNA for phenylalan...	411 e-113
	dbj D83075 D83075	<i>Lithospermum erythrorhizon</i>	mRNA for phenylalan...	408 e-112
25	emb Y12461 HAPHAMLY	<i>Helianthus annuus</i>	mRNA for phenylalanine amm...	331 e-112
	emb AF237955 AF237955	<i>Rubus idaeus</i>	phenylalanine ammonia-lyase 2...	407 e-112
	gb M29232 IPBPAL	Sweet potato	phenylalanine ammonia-lyase mRNA (...	407 e-112
	emb AB042520 AB042520	<i>Catharanthus roseus</i>	mRNA for phenylalanine...	328 e-111
	gb L36822 SSNPAL	<i>Stylosanthes humilis</i>	phenylalanine ammonia-lyas...	403 e-111
30	dbj D26596 CMEPAL	<i>Camellia sinensis</i>	mRNA for phenylalanine ammon...	403 e-111
	emb X58180 MSPAL	<i>M.sativa</i>	PAL mRNA for phenylalanine ammonia-lyase.	398 e-109
	gb L11747 POPPALGA	<i>Populus tricarpha</i> X <i>Populus deltoides</i>	(hybri...	318 e-109
	gb U43338 CLU43338	<i>Citrus limon</i>	phenylalanine ammonia-lyase (pal...	396 e-109
	emb AF237954 AF237954	<i>Rubus idaeus</i>	phenylalanine ammonia-lyase 1...	395 e-108
35	emb X17462 PCPAL4	<i>P.crispum</i>	RNA for PAL4, phenylalanine ammonia...	319 e-108
	emb X78269 NTPHEAL	<i>N.tabacum</i> (Samsun NN)	mRNA for phenylalanine ...	312 e-106
	dbj D17467 TOBPAL1	Tobacco	mRNA for phenylalanine ammonia-lyase,...	312 e-105
	emb AJ250836 CAR250836	<i>Cicer arietinum</i>	mRNA for phenylalanine am...	373 e-102
	emb X81159 PCPAL3	<i>P.crispum</i>	mRNA for phenylalanine ammonia-lyase 3.	174 e-102
40	emb X81158 PCPAL2	<i>P.crispum</i>	mRNA for phenylalanine ammonia-lyase 2.	173 e-101
	emb X99997 BFPAL	<i>B.finlaysoniana</i>	mRNA for phenylalanine ammonia...	214 2e-95
	emb AW667320 AW667320	GA_Ea0008P06	<i>Gossypium arboreum</i> 7-10 dpa ...	349 8e-95
	dbj E04042 E04042	cDNA sequence coding for pea	phenylalanine amm...	347 3e-94
	dbj D10001 PEAPAL	<i>P.sativum</i>	mRNA for phenylalanine ammonia-lyase...	347 3e-94
45	dbj D78640 IPBPALA	<i>Ipomoea batatas</i>	mRNA for phenylalanine ammoni...	291 3e-94
	emb AJ238754 CCL238754	<i>Citrus clementina</i> X <i>Citrus reticulata</i>	mRN...	314 3e-91
	emb AW220322 AW220322	EST302805	tomato root during/after fruit s...	326 6e-88
	emb AW725857 AW725857	GA_Ea0019O22	<i>Gossypium arboreum</i> 7-10 dpa ...	319 9e-86
	emb AJ238753 CCL238753	<i>Citrus clementina</i> X <i>Citrus reticulata</i>	mRN...	319 1e-85
50	dbj D10003 PEAPAL2	<i>P.sativum</i>	gene for phenylalanine ammonia-lyas...	220 2e-85
	emb Z49147 HVPAL7RM	<i>H.vulgare</i>	partial PAL mRNA for phenylalanine...	154 5e-85
	gb U16130 PAU16130	<i>Persea americana</i>	phenylalanine ammonia lyase ...	296 9e-81
	emb AW774460 AW774460	EST333611	KV3 <i>Medicago truncatula</i> cDNA clo...	302 1e-80
	emb X63103 STPAL1	<i>S.tuberosum</i>	PAL-1 gene for phenylalanine ammon...	196 6e-79
55	emb AW685111 AW685111	NF026A05NR1F1000	Nodulated root <i>Medicago t...</i>	292 8e-78
	emb AF165998 AF165998	<i>Vigna unguiculata</i>	phenylalanine ammonia-ly...	292 1e-77
	emb AI899906 AI899906	sb96a02.y1	Gm-cl012 <i>Glycine max</i> cDNA clone...	287 3e-76
	emb AW691458 AW691458	NF045B11ST1F1000	Developing stem <i>Medicago ...</i>	286 6e-76
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60	emb AW688208 AW688208	NF004F12ST1F1000	Developing stem <i>Medicago ...</i>	278 1e-73
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- emb|AF218454|AF218454 *Coffea arabica* clone 430.4 phenylalanine a... 275 2e-72
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emb|AW686498|AW686498 NF042A10NR1F1000 Nodulated root *Medicago* t... 168 2e-60
gb|U39792|PTU39792 *Pinus taeda* phenylalanine ammonia-lyase (lpPA... 129 5e-60
15 dbj|D10002|PEAPAL1 *P.sativum* gene for phenylalanine ammonia-lyas... 231 2e-59
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emb|AI563248|AI563248 EST00372 watermelon lambda zap library Cit... 222 7e-57
emb|AJ289609|BPE289609 *Betula pendula* partial pal gene for pheny... 133 3e-56
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20 emb|AJ278116|BPE278116 *Betula pendula* partial pal gene for phen... 131 9e-56
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30 dbj|D30656|POPPALA *Populus kitakamiensis* gene for phenylalanine ... 208 1e-52
dbj|D43802|POPPALG2BA *Populus kitakamiensis* gene for phenylalani... 208 2e-52
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gb|M91192|TFRPAL1X *Trifolium subterraneum* phenylalanine ammonia-... 197 3e-52
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35 emb|AB008200|AB008200 *Nicotiana tabacum* palB gene for phenylalan... 204 2e-51
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dbj|D43803|POPPALG4B *Populus kitakamiensis* gene for phenylalanin... 201 2e-50
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45 emb|AB008199|AB008199 *Nicotiana tabacum* palA gene for phenylalan... 195 6e-49
emb|X15473|PCPAL1GN *P.crispum* PAL-1 gene for phenylalanine ammon... 120 6e-49
emb|X63104|STPAL2 *S.tuberosum* PAL-2 gene for phenylalanine ammon... 193 5e-48
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50 emb|AF019965|AF019965 *Pinus monticola* phenylalanine ammonia lyas... 130 4e-45
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emb|AW031859|AW031859 EST275313 tomato callus, TAMU *Lycopersicon*... 165 4e-44
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60 emb|AV409143|AV409143 AV409143 *Lotus japonicus* young plants (two... 166 3e-40

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(3115 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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20	emb AW694081 AW694081 NF072E06ST1F1050 Developing stem Medicago ...	225	1e-57
	emb AW684895 AW684895 NF022G07NR1F1000 Nodulated root Medicago t...	222	9e-57
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	emb AF237955 AF237955 Rubus idaeus phenylalanine ammonia-lyase 2...	220	6e-56
25	dbj D10003 PEAPAL2 P.sativum gene for phenylalanine ammonia-lyas...	219	9e-56
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 emb|X17462|PCPAL4 P.crispum RNA for PAL4, phenylalanine ammonia-... 199 4e-50
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 20 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanin... 196 7e-49
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 35 emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 181 3e-44
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60

(1602 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

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25	emb AQ874893 AQ874893 V118C3 mTn-3xHA/lacZ Insertion Library, st...	49	1e-07
	emb AJ228925 AJ228925 AJ228925 Barley leaf, 8 day old seedling H...	57	4e-07
	emb AW220409 AW220409 EST302892 tomato root during/after fruit s...	53	5e-06
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 20 emb|AW171746|AW171746 N100640e rootphos(-) Medicago truncatula c... 33 8.1
 emb|AI960269|AI960269 sc81b07.y1 Gm-c1018 Glycine max cDNA clone... 27 9.1

- Query= PDF1.2_at 14621_at /id_source genbank /description
 25 gb|aac31244.1| (ac004747) putative antifungal protein [arabidopsis
 thaliana] /blast_score 1.00e-31 /ec_number /family /chip nova
 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|pdf1|/ncgi)
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 http://www.ncgr.org/cgi-bin/ff?pdf1
 30 (400 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

- 35 Searching.....done

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| | Sequences producing significant alignments: | (bits) | Value |
| 40 | emb A26875 A26875 R.sativus AFP1 gene. | 160 | 5e-39 |
| | gb U18557 RSU18557 Raphanus sativus antifungal protein 1 preprot... | 159 | 1e-38 |
| | gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl... | 127 | 6e-37 |
| | gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot... | 138 | 1e-35 |
| | emb X97318 RSAFP4 R.sativus mRNA for antifungal protein 4. | 145 | 3e-34 |
| 45 | emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3. | 127 | 2e-31 |
| | emb A26963 A26963 D.merkii AMP1 sequence. | 76 | 2e-13 |
| | emb X53375 HASF18 Sunflower anther-specific mRNA SF18. | 75 | 3e-13 |
| | emb A27062 A27062 C.benedictus AMP2 sequence. | 74 | 4e-13 |
| | emb A26906 A26906 C.benedictus AMP1 sequence. | 73 | 7e-13 |
| 50 | gb L47901 L47901 BNAF1712 Mustard flower buds Brassica rapa cDNA... | 65 | 2e-10 |
| | emb AT001728 AT001728 AT001728 Flower bud cDNA Brassica rapa sub... | 65 | 3e-10 |
| | emb A27064 A27064 C.ternatea AMP1 sequence. | 58 | 7e-09 |
| | emb AT001738 AT001738 AT001738 Flower bud cDNA Brassica rapa sub... | 52 | 2e-06 |
| | emb AW870017 AW870017 NXNV_122_A10_F Nsf Xylem Normal wood Verti... | 35 | 7e-06 |
| 55 | emb AW064751 AW064751 ST35D04 Pine, TriPLEx shoot tip library Pin... | 36 | 7e-06 |
| | emb X91487 PASPI1GEN P.abies mRNA for gamma-thionin protein (put... | 40 | 1e-05 |
| | emb AW621708 AW621708 EST312506 tomato root during/after fruit s... | 43 | 9e-05 |
| | emb AW220215 AW220215 EST302698 tomato root during/after fruit s... | 43 | 1e-04 |
| | emb AW220231 AW220231 EST302714 tomato root during/after fruit s... | 43 | 1e-04 |
| 60 | emb AW219164 AW219164 EST301646 tomato root during/after fruit s... | 43 | 1e-04 |
| | emb AW219793 AW219793 EST302275 tomato root during/after fruit s... | 43 | 1e-04 |

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	emb AW622375 AW622375 EST313174 tomato root during/after fruit s...	41	4e-04
	emb AW622390 AW622390 EST313189 tomato root during/after fruit s...	41	4e-04
	emb AW621171 AW621171 EST311969 tomato root during/after fruit s...	40	7e-04
5	dbj D29679 TOBPIT1A Tobacco pit1 mRNA (which expression is induc...	44	7e-04
	emb AW622051 AW622051 EST312849 tomato root during/after fruit s...	40	7e-04
	emb AW622079 AW622079 EST312877 tomato root during/after fruit s...	40	9e-04
	emb AW621330 AW621330 EST312128 tomato root during/after fruit s...	40	9e-04
	emb AW219347 AW219347 EST301829 tomato root during/after fruit s...	40	0.001
10	emb AW220086 AW220086 EST302569 tomato root during/after fruit s...	40	0.001
	emb AW621962 AW621962 EST312760 tomato root during/after fruit s...	40	0.001
	emb AW621634 AW621634 EST312432 tomato root during/after fruit s...	37	0.005
	emb AW623112 AW623112 EST321057 tomato flower buds 3-8 mm, Come...	40	0.006
	emb AW683448 AW683448 NF012D04LF1F1041 Developing leaf Medicago ...	40	0.006
15	emb AI487824 AI487824 EST246146 tomato ovary, TAMU Lycopersicon ...	40	0.006
	emb AI483999 AI483999 EST249870 tomato ovary, TAMU Lycopersicon ...	40	0.007
	gb U20591 SLU20591 Solanum lycopersicum flower-specific gamma-th...	40	0.007
	emb AW622923 AW622923 EST306993 tomato flower buds 3-8 mm, Come...	40	0.007
	emb AW929929 AW929929 EST354199 tomato flower buds 8 mm to pre-a...	40	0.007
20	emb AW929939 AW929939 EST354209 tomato flower buds 8 mm to pre-a...	40	0.007
	emb AI897392 AI897392 EST266835 tomato ovary, TAMU Lycopersicon ...	40	0.008
	emb AI490243 AI490243 EST248569 tomato ovary, TAMU Lycopersicon ...	40	0.008
	emb AI487859 AI487859 EST246181 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AW217552 AW217552 EST296266 tomato flower buds 3-8 mm, Come...	40	0.009
25	emb AI489818 AI489818 EST248157 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AI487398 AI487398 EST245720 tomato ovary, TAMU Lycopersicon ...	40	0.009
	emb AW217379 AW217379 EST296063 tomato flower buds 0-3 mm, Come...	40	0.010
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30	emb AI483612 AI483612 EST249462 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI485550 AI485550 EST243871 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI484887 AI484887 EST243150 tomato ovary, TAMU Lycopersicon ...	40	0.010
	emb AI484497 AI484497 EST242507 tomato ovary, TAMU Lycopersicon ...	40	0.012
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35	emb AW775186 AW775186 EST331908 GVN Medicago truncatula cDNA clo...	39	0.016
	emb AI486656 AI486656 EST244977 tomato ovary, TAMU Lycopersicon ...	38	0.024
	emb AI485044 AI485044 EST243324 tomato ovary, TAMU Lycopersicon ...	37	0.041
	emb AW399651 AW399651 EST310151 L. pennellii trichome, Cornell U...	38	0.042
	emb A26964 A26964 D.merkii AMP2 sequence.	37	0.080
40	emb X77993 HASF18A H.annuus SF18 gene.	31	0.14
	emb A27063 A27063 L.cicera AFP sequence.	34	0.74
	emb AI757757 AI757757 EtESTea34d02.y1 Eimeria S5-2 Sporozoite st...	34	0.74
	emb AW217119 AW217119 EST295833 tomato callus, TAMU Lycopersicon...	27	0.90
	emb X95363 CAGT C.annuum gamma thionin gene.	33	1.0
45	emb X95730 CAGTHIOGN Capsicum annuum defensin gene.	33	1.0
	emb AL035477 PFMAL4P4 Plasmodium falciparum chromosome 4 strain ...	33	1.0
	emb AL117384 LMFL5883 Leishmania major Friedlin chromosome 23 co...	29	1.3
	emb Z74387 SCYDR262W S.cerevisiae chromosome IV reading frame OR...	33	1.4
	emb Z68329 SC9320A S.cerevisiae chromosome IV cosmid 9320A.	33	1.4
50	emb Z70202 SC9320X S.cerevisiae chromosome IV cosmid 9320X.	33	1.4
	emb AQ846121 AQ846121 LMAJFV1_lm14f01.y1 Leishmania major FV1 ra...	29	1.7
	emb AW725876 AW725876 GA_Ea0020A08 Gossypium arboreum 7-10 dpa ...	32	1.9
	emb AV387503 AV387503 AV387503 Chlamydomonas reinhardtii C9 Chla...	32	2.6
	emb AQ947439 AQ947439 Sheared DNA-50L12.TF Sheared DNA Trypanoso...	31	3.6
55	emb AA836739 AA836739 L30-187T3 Ice plant Lambda Uni-Zap XR expr...	31	3.6
	gb M65164 PAR51C P.tetraulera 51C surface protein gene, complet...	31	3.6
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60	emb AQ642382 AQ642382 RPCI93-DpnII-29C10.TV RPCI93-DpnII Trypano...	31	5.0
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5 emb|AI728815|AI728815 BNLGHi11757 Six-day Cotton fiber Gossypium... 31 5.0
emb|AI726605|AI726605 BNLGHi6250 Six-day Cotton fiber Gossypium ... 31 5.0
gb|BE033595|BE033595 MF04D10 MF Mesembryanthemum crystallinum cD... 30 6.8
emb|AW508408|AW508408 si40e08.y1 Gm-r1030 Glycine max cDNA clone... 30 6.8
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emb|AW093819|AW093819 EST286999 tomato mixed elicitor, BTI Lycop... 30 6.8
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15 emb|AL034557|PFMAL4P1 Plasmodium falciparum chromosome 4 strain ... 30 6.8
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/chip nova /gb_link /ncgi
(738 letters)

25 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

30 Score E
Sequences producing significant alignments: (bits) Value

gb|U70666|BNU70666 Brassica napus pathogenesis-related protein P... 323 3e-88
35 gb|U21849|BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds. 323 3e-88
gb|U64806|BNU64806 Brassica napus pathogenesis-related protein P... 209 4e-85
emb|AI352851|AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl... 311 4e-84
emb|AI352893|AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl... 165 3e-62
emb|AW217013|AW217013 EST295727 tomato callus, TAMU Lycopersicon... 152 4e-60
40 emb|AW219671|AW219671 EST302153 tomato root during/after fruit s... 151 1e-59
emb|AW092403|AW092403 EST285583 tomato mixed elicitor, BTI Lycop... 151 1e-59
emb|AI895090|AI895090 EST264533 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW625930|AW625930 EST319825 tomato radicle, 5 d post-imbibit... 151 1e-59
emb|AW032514|AW032514 EST276073 tomato callus, TAMU Lycopersicon... 151 1e-59
45 emb|AW034260|AW034260 EST277831 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW040983|AW040983 EST283847 tomato mixed elicitor, BTI Lycop... 151 1e-59
emb|AW034206|AW034206 EST277777 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW219480|AW219480 EST301878 tomato root during/after fruit s... 151 1e-59
emb|AW092623|AW092623 EST285803 tomato mixed elicitor, BTI Lycop... 151 1e-59
50 emb|AW040954|AW040954 EST283818 tomato mixed elicitor, BTI Lycop... 151 1e-59
emb|AW034454|AW034454 EST278025 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW032723|AW032723 EST276282 tomato callus, TAMU Lycopersicon... 151 1e-59
emb|AW033873|AW033873 EST277444 tomato callus, TAMU Lycopersicon... 151 1e-59
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55 emb|AW033593|AW033593 EST277164 tomato callus, TAMU Lycopersicon... 151 3e-59
emb|AW034724|AW034724 EST278526 tomato callus, TAMU Lycopersicon... 148 7e-59
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60 emb|AW329241|AW329241 N200453e rootphos(-) Medicago truncatula c... 160 1e-58
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- emb|AW035820|AW035820 EST281974 tomato callus, TAMU Lycopersicon... 145 6e-58
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 emb|AW622143|AW622143 EST312941 tomato root during/after fruit s... 149 2e-57
 5 emb|AI352771|AI352771 MB58-5G PZ204.BNlib Brassica napus cDNA cl... 220 2e-57
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 emb|AI782621|AI782621 EST263500 tomato susceptible, Cornell Lyco... 144 7e-57
 10 emb|AW126362|AW126362 N100469e rootphos(-) Medicago truncatula c... 160 3e-56
 emb|AW981257|AW981257 EST392410 DSIL Medicago truncatula cDNA cl... 128 9e-56
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 emb|AI352783|AI352783 MB59-12D PZ204.BNlib Brassica napus cDNA c... 198 3e-55
 emb|X14065|NTPRP1 Nicotiana tabacum gene for basic form of patho... 140 4e-55
 15 emb|AW625666|AW625666 EST319573 tomato radicle, 5 d post-imbibit... 135 6e-55
 emb|AW032727|AW032727 EST276286 tomato callus, TAMU Lycopersicon... 147 1e-53
 emb|X52555|NTW381 Tobacco W38/1 gene for PR-1 pathogenesis-relat... 116 1e-52
 gb|BE034214|BE034214 MH01C07 MH Mesembryanthemum crystallinum cD... 112 4e-52
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 20 emb|AW559969|AW559969 EST315017 DSIR Medicago truncatula cDNA cl... 81 4e-52
 emb|AI352801|AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl... 194 1e-51
 emb|X17681|NTPR1CA Tobacco gene for pathogenesis-related protein... 111 2e-51
 emb|X05454|NTPR1CR Nicotiana tabacum mRNA for PR-1c protein. 111 2e-51
 emb|X12487|NTPR1C Tobacco mRNA fragment for pathogenesis-related... 111 2e-51
 25 emb|AJ011520|LES011520 Lycopersicon esculentum pr1a (P4) gene. 98 1e-50
 gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
 emb|A22634|LEPI4GENE L.esculentum P14 gene. 98 1e-50
 emb|AJ250136|STU250136 Solanum tuberosum mRNA for pathogenesis r... 99 2e-50
 emb|AW218808|AW218808 EST301288 tomato root during/after fruit s... 116 3e-50
 30 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
 emb|AW094536|AW094536 EST287716 tomato mixed elicitor, BTI Lycop... 116 3e-50
 emb|AW038553|AW038553 EST280236 tomato mixed elicitor, BTI Lycop... 116 3e-50
 dbj|D90196|TOBPR1A Nicotiana tabacum mRNA for PR1a protein precu... 104 3e-50
 emb|X05959|NTPR1AG Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
 35 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
 emb|X06361|NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 104 4e-50
 emb|X12485|NTPR1A Tobacco mRNA fragment for pathogenesis-related... 104 4e-50
 emb|AW033469|AW033469 EST277040 tomato callus, TAMU Lycopersicon... 116 5e-50
 emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 104 7e-50
 40 emb|AI352858|AI352858 MB70-10D PZ204.BNlib Brassica napus cDNA c... 197 7e-50
 emb|AI782416|AI782416 EST263295 tomato susceptible, Cornell Lyco... 95 7e-50
 emb|AW034882|AW034882 EST279111 tomato callus, TAMU Lycopersicon... 95 1e-49
 emb|AW031086|AW031086 EST274393 tomato callus, TAMU Lycopersicon... 116 1e-49
 emb|X74939|HVPRIAR H.vulgare HvPR-1a mRNA for a basic PR-1-type... 114 2e-49
 45 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
 emb|AW034167|AW034167 EST277738 tomato callus, TAMU Lycopersicon... 94 2e-49
 emb|X17680|NTPR1BA Tobacco gene for pathogenesis-related protein... 103 3e-49
 emb|X03465|NTPRPR Nicotiana tabacum mRNA for pathogenesis-relate... 103 3e-49
 dbj|D90197|TOBPR1B1 Nicotiana tabacum mRNA for PR1b protein. 103 3e-49
 50 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 6e-49
 gb|M69248|TOMPRP6 Lycopersicon esculentum PR (pathogenesis relat... 92 6e-49
 emb|X68738|LEP1P14A L.esculentum mRNA for ethylene-induced P1(p1... 92 6e-49
 emb|AI781499|AI781499 EST262378 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI779424|AI779424 EST260303 tomato susceptible, Cornell Lyco... 92 6e-49
 55 emb|AW031093|AW031093 EST274400 tomato callus, TAMU Lycopersicon... 92 6e-49
 emb|AI779425|AI779425 EST260304 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI782545|AI782545 EST263424 tomato susceptible, Cornell Lyco... 92 6e-49
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 60 emb|AI778680|AI778680 EST259559 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI899514|AI899514 EST268957 tomato susceptible, Cornell Lyco... 92 6e-49

- emb|AI779287|AI779287 EST260166 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI773130|AI773130 EST254230 tomato resistant, Cornell Lycope... 92 6e-49
 emb|AI778790|AI778790 EST259669 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI778791|AI778791 EST259670 tomato susceptible, Cornell Lyco... 92 6e-49
 5 emb|AI778985|AI778985 EST259864 tomato susceptible, Cornell Lyco... 92 6e-49
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 emb|AI779013|AI779013 EST259892 tomato susceptible, Cornell Lyco... 92 6e-49
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 10 emb|AI780973|AI780973 EST261852 tomato susceptible, Cornell Lyco... 92 6e-49
 emb|AI895236|AI895236 EST264679 tomato callus, TAMU Lycopersicon... 92 6e-49

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 15 emb|caa50677.1|(x71794) peroxidase [arabidopsis thaliana]
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 (1236 letters)

- Database: plantfungal
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Searching.....done

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| | Sequences producing significant alignments: | | | (bits) Value |
| | gb M60729 HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge... | 744 | 0.0 | |
| | emb A00741 A00741 A.rusticana synthetic gene (reverse complement... | 692 | 0.0 | |
| | emb A00740 A00740 A.rusticana synthetic gene for peroxidase. | 692 | 0.0 | |
| 30 | dbj E01651 E01651 cDNA encoding horseradish peroxidase. | 692 | 0.0 | |
| | gb M37157 HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge... | 371 | e-133 | |
| | emb X97349 PTXP2PER P.trichocarpa mRNA for anionic peroxidase P... | 473 | e-132 | |
| | emb X97350 PTXP3PER P.trichocarpa mRNA for anionic peroxidase P... | 469 | e-131 | |
| | dbj D83224 POPP01 Populus nigra mRNA for peroxidase, complete cds. | 468 | e-131 | |
| 35 | gb M37156 HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge... | 363 | e-130 | |
| | emb X97348 PTXP1PER P.trichocarpa mRNA for anionic peroxidase P... | 463 | e-129 | |
| | dbj D30652 POPPA Populus kitakamiensis mRNA for peroxidase, part... | 441 | e-123 | |
| | emb X97351 PTXP4PER P.trichocarpa mRNA for anionic peroxidase P... | 383 | e-120 | |
| | dbj D30653 POPPB Populus kitakamiensis mRNA for peroxidase, part... | 356 | e-112 | |
| 40 | emb AF149277 AF149277 Phaseolus vulgaris peroxidase 1 precursor ... | 227 | e-107 | |
| | gb L36157 ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple... | 229 | e-107 | |
| | emb AF007211 AF007211 Glycine max peroxidase precursor (GMIPER1)... | 229 | e-106 | |
| | gb L07554 LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA... | 381 | e-105 | |
| | emb X90693 MSRNAPE1A M.sativa mRNA for peroxidase 1A. | 211 | e-105 | |
| 45 | dbj D90115 HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i... | 296 | e-103 | |
| | emb AJ242742 IBA242742 Ipomoea batatas mRNA for peroxidase (pod ... | 138 | 2e-97 | |
| | emb AF149280 AF149280 Phaseolus vulgaris peroxidase 5 precursor ... | 142 | 4e-97 | |
| | emb X90693 MSRNAPE1B M.sativa mRNA for peroxidase 1B. | 231 | 1e-95 | |
| | emb X90694 MSRNAPE1C M.sativa mRNA for peroxidase 1C. | 226 | 7e-94 | |
| 50 | gb L36111 SSNPEROXIB Stylosanthes humilis peroxidase mRNA. | 210 | 2e-89 | |
| | emb AI959837 AI959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone... | 228 | 6e-89 | |
| | emb AF244924 AF244924 Spinacia oleracea peroxidase prx15 precurs... | 208 | 9e-88 | |
| | emb AW559660 AW559660 EST314772 DSIR Medicago truncatula cDNA cl... | 236 | 1e-87 | |
| | emb AW774581 AW774581 EST333732 KV3 Medicago truncatula cDNA clo... | 236 | 7e-87 | |
| 55 | emb AF155124 AF155124 Gossypium hirsutum bacterial-induced perox... | 215 | 2e-86 | |
| | emb AW981426 AW981426 EST392579 DSIL Medicago truncatula cDNA cl... | 236 | 2e-85 | |
| | emb AB042103 AB042103 Asparagus officinalis AspPOX1 mRNA for per... | 209 | 2e-85 | |
| | emb AF244923 AF244923 Spinacia oleracea peroxidase prx14 precurs... | 205 | 9e-85 | |
| | emb AJ250121 PAB250121 Picea abies mRNA for SPI2 protein (spi2 g... | 253 | 1e-83 | |
| 60 | emb AW775762 AW775762 EST334827 DSIL Medicago truncatula cDNA cl... | 236 | 6e-83 | |
| | emb Y10466 SOPR XR5 S.oleracea mRNA for peroxidase, clone PC18. | 218 | 3e-82 | |

- emb|AW775425|AW775425 EST334490 *DSIL Medicago truncatula* cDNA cl... 208 1e-81
emb|AW685437|AW685437 NF029D09NR1F1000 *Nodulated root Medicago* t... 230 9e-80
emb|AB024439|AB024439 *Scutellaria baicalensis* mRNA for peroxidase... 209 2e-79
5 emb|AF244922|AF244922 *Spinacia oleracea* peroxidase prx13 precurs... 212 3e-79
emb|X57564|ARNEUPERO *A.rusticana* mRNA for neutral peroxidase. 115 6e-78
emb|AW776273|AW776273 EST335338 *DSIL Medicago truncatula* cDNA cl... 222 1e-77
emb|AW267813|AW267813 EST305941 *DSIR Medicago truncatula* cDNA cl... 200 1e-76
emb|X91232|MARNAPRX *M.annua* mRNA for peroxidase. 196 5e-76
10 emb|AF049881|AF049881 *Linum usitatissimum* peroxidase FLXPER4 (PE... 207 7e-76
emb|AW256487|AW256487 EST304624 *KV2 Medicago truncatula* cDNA clo... 200 9e-76
emb|AW775890|AW775890 EST334955 *DSIL Medicago truncatula* cDNA cl... 200 3e-74
emb|AW257195|AW257195 EST305332 *KV2 Medicago truncatula* cDNA clo... 214 5e-74
gb|M91373|CUSPREPER *Cucumis sativus* peroxidase mRNA, complete cds. 86 2e-73
gb|U41657|GMU41657 *Glycine max* seed coat peroxidase isozyme (SPO... 159 3e-73
15 emb|AB027752|AB027752 *Nicotiana tabacum* mRNA for peroxidase, com... 197 5e-73
gb|L36110|SSNPEROXIA *Stylosanthes humilis* peroxidase mRNA. 199 5e-73
gb|M37636|ARCPNC1 *Arachis hypogaea* cationic peroxidase (PNC1) mR... 204 7e-73
emb|AW685235|AW685235 NF027H10NR1F1000 *Nodulated root Medicago* t... 236 9e-73
emb|AW278775|AW278775 sf97d02.y1 *Gm-c1019 Glycine max* cDNA clone... 155 1e-72
20 emb|X71593|LECEV11A *L.esculentum* CEV1-1 mRNA. 99 2e-72
gb|J02979|TOBPXDLF *Nicotiana tabacum* lignin-forming peroxidase m... 100 2e-72
emb|AW559945|AW559945 EST314993 *DSIR Medicago truncatula* cDNA cl... 233 2e-72
emb|AW980744|AW980744 EST391897 *GVN Medicago truncatula* cDNA clo... 235 5e-70
emb|Y10467|SOPRXR6 *S.oleracea* mRNA for peroxidase, clone PC23. 105 1e-69
25 dbj|D83225|POPP02 *Populus nigra* peroxidase gene, complete cds. 196 2e-69
gb|M74103|TOBANPER *Nicotiana sylvestris* anionic peroxidase mRNA,... 205 6e-69
emb|AF043234|AF043234 *Striga asiatica* ferriprotein porphyrin-con... 211 1e-68
gb|BE034991|BE034991 MM01A12 *MM Mesembryanthemum crystallinum* cD... 202 6e-68
emb|AW574244|AW574244 EST316835 *GVN Medicago truncatula* cDNA clo... 202 1e-67
30 emb|Y10465|SOPRXR4 *S.oleracea* mRNA for peroxidase, clone PC44. 98 3e-67
emb|AW686084|AW686084 NF038B07NR1F1000 *Nodulated root Medicago* t... 236 5e-67
emb|AW561032|AW561032 EST316080 *DSIR Medicago truncatula* cDNA cl... 203 7e-67
emb|X56011|TAPERO *Wheat* mRNA for peroxidase. 111 2e-66
emb|AW185769|AW185769 se59d08.y1 *Gm-c1019 Glycine max* cDNA clone... 219 4e-65
35 emb|Y17192|CPY17192 *Cucurbita pepo* mRNA for peroxidase. 96 2e-64
gb|BE033422|BE033422 ME01E09 *ME Mesembryanthemum crystallinum* cD... 184 4e-64
emb|AB024438|AB024438 *Scutellaria baicalensis* mRNA for peroxidase... 205 7e-64
gb|M91374|CUSPREPERA *Cucumis sativus* peroxidase mRNA, complete cds. 76 2e-63
gb|L24120|LINFLXP *Linum usitatissimum* peroxidase precursor (FLXP... 167 2e-63
40 gb|M91372|CUSPREPERB *Cucumis sativus* peroxidase mRNA, complete cds. 134 2e-63
emb|AF043235|AF043235 *Striga asiatica* ferriprotein porphyrin-con... 199 3e-63
emb|AW288002|AW288002 N100846e rootphos(-) *Medicago truncatula* c... 182 7e-63
emb|AW126121|AW126121 N100318e rootphos(-) *Medicago truncatula* c... 216 1e-62
gb|L36093|BLYPRX *Barley* peroxidase mRNA, complete cds. 133 5e-62
45 emb|AW687443|AW687443 NF009F07RT1F1062 *Developing root Medicago* ... 235 1e-61
emb|AW687957|AW687957 NF001D11ST1F1000 *Developing stem Medicago* ... 236 3e-61
emb|AB024437|AB024437 *Scutellaria baicalensis* mRNA for peroxidase... 163 3e-61
emb|X58396|HVPEROXI *Barley* mRNA for peroxidase (EC=1.11.1.7). 133 5e-61
emb|AI496388|AI496388 sb04a11.y1 *Gm-c1004 Glycine max* cDNA clone... 224 6e-61
50 emb|AW686765|AW686765 NF042E07NR1F1000 *Nodulated root Medicago* t... 222 8e-61
dbj|D38050|POPP1 *Aspen* prxA3a gene for peroxidase, complete cds. 121 9e-61
emb|AW704659|AW704659 sk54h10.y1 *Gm-c1019 Glycine max* cDNA clone... 149 9e-61
emb|Y10464|SOPRXR3 *S.oleracea* mRNA for peroxidase, clone PC42. 80 3e-60
emb|AW705730|AW705730 sk51b02.y1 *Gm-c1019 Glycine max* cDNA clone... 149 8e-60
55 gb|U51191|GMU51191 *Glycine max* peroxidase precursor (sEPa1) mRNA... 100 9e-60
gb|U12314|CCU12314 *Cenchrus ciliaris* clone PX7 peroxidase mRNA, ... 105 9e-60
emb|AI938533|AI938533 sb46h09.y1 *Gm-c1015 Glycine max* cDNA clone... 145 1e-59
emb|AW705617|AW705617 sk50d03.y1 *Gm-c1019 Glycine max* cDNA clone... 149 2e-59
emb|AI781859|AI781859 EST262738 *tomato susceptible, Cornell Lyco*... 102 2e-59
60 emb|AF149278|AF149278 *Phaseolus vulgaris* peroxidase 3 precursor ... 90 3e-59
gb|U51192|GMU51192 *Glycine max* peroxidase precursor (sEPa2) mRNA... 102 4e-59

emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59
 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 156 8e-59
 gb|M32742|CUSCUPER C.sativus peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58
 emb|AW705946|AW705946 sk52h07.y1 Gm-c1019 Glycine max cDNA clone... 224 6e-58

5

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 gb|aac49117.1| (u18993) tryptophan synthase alpha chain [arabidopsis
 thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova
 /gb_link /ncgi
 (939 letters)

10

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E
 Sequences producing significant alignments: (bits) Value

20

emb|AW730233|AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa ... 352 5e-98
 emb|AW649960|AW649960 EST328414 tomato germinating seedlings, TA... 308 4e-83
 emb|AW621664|AW621664 EST312462 tomato root during/after fruit s... 290 1e-77
 emb|AW031327|AW031327 EST274781 tomato callus, TAMU Lycopersicon... 282 3e-75
 25 gb|U38804|PPU38804 Porphyra purpurea chloroplast, complete genome. 271 4e-72
 emb|AW775853|AW775853 EST334918 DSIL Medicago truncatula cDNA cl... 264 9e-70
 emb|Z21642|CHASTRNA Antithamnion sp. Chloroplast trnK, trnE, trpA... 255 4e-67
 gb|BE124387|BE124387 EST393422 GVN Medicago truncatula cDNA clon... 227 9e-59
 gb|BE121873|BE121873 894015F07.y1 C. reinhardtii CC-1690, normal... 227 1e-58
 30 emb|AF022186|AF022186 Cyanidium caldarium strain RK1 chloroplast... 220 1e-56
 emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
 emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
 dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
 emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
 35 emb|AA660642|AA660642 00530 MRHE Medicago truncatula cDNA 5' si... 190 1e-47
 dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
 emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
 dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
 gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
 40 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42
 emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
 emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
 emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
 emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
 45 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycop... 138 5e-32
 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30
 emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
 emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
 emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
 50 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
 emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
 emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptoph... 53 4e-10
 emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10
 emb|AF084885|AF084885 Neurospora crassa NG61-6A mutant tryptoph... 64 1e-09
 55 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
 emb|AF084883|AF084883 Neurospora crassa 314-709A mutant tryptoph... 64 1e-09
 emb|AF084882|AF084882 Neurospora crassa 314-682A mutant tryptoph... 64 1e-09
 emb|AF084881|AF084881 Neurospora crassa 314-693A mutant tryptoph... 64 2e-09
 emb|AF084889|AF084889 Neurospora crassa 314-492-2A mutant trypto... 53 3e-09
 60 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
 emb|AU011013|AU011013 AU011013 Schizosaccharomyces pombe late lo... 54 2e-06

	emb AW693052 AW693052 NF059C08ST1F1065 Developing stem Medicago ...	51	1e-05
	emb AV390244 AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla...	49	4e-05
	emb AW616467 AW616467 EST322878 L. hirsutum trichome, Cornell Un...	48	7e-05
	emb AL354022 P761R Leishmania major Friedlin PAC P761 right end...	44	0.002
5	gb M91656 CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1...	43	0.005
	emb AQ903789 AQ903789 GSSTc04230 Trypanosome cruzi random genom...	35	0.24
	emb AW727215 AW727215 GA_Ea0023N23 Gossypium arboreum 7-10 dpa ...	36	0.52
	gb M91654 CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1...	36	0.52
	emb AW728975 AW728975 GA_Ea0018P19 Gossypium arboreum 7-10 dpa ...	35	0.64
10	emb AL139794 LMFP1105 Leishmania major Friedlin chromosome 4 PAC...	35	0.87
	emb AW926438 AW926438 HVSMEg0007D14 Hordeum vulgare pre-anthesis...	34	1.2
	emb AA965348 AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	gb U12630 ENU12630 Emericella nidulans R153 core histone H3 (H3)...	34	1.3
	emb AI007494 AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
15	emb AA787433 AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu...	34	1.3
	emb X55548 ANH3GENE A.nidulans gene for core histone for H3.	34	1.3
	emb AQ396426 AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P...	34	1.6
	emb AF262997 AF262997 Ricinus communis NADP-dependent malic prot...	34	1.6
	gb M19025 CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c...	34	1.6
20	emb AF084888 AF084888 Neurospora crassa 656-2A mutant tryptophan...	31	1.7
	emb AF084887 AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta...	31	1.7
	emb AW694774 AW694774 NF080A05ST1F1036 Developing stem Medicago ...	34	1.8
	emb Y18012 TVE18012 Trametes versicolor mRNA for laccase.	33	2.3
	emb AQ500614 AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc...	33	2.5
25	emb AW187498 AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187530 AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW694072 AW694072 NF072B12ST1F1096 Developing stem Medicago ...	33	3.1
	emb AW186883 AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AW187537 AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ...	33	3.1
30	emb AW187474 AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ...	33	3.1
	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor...	33	3.5
	emb AV421993 AV421993 AV421993 Lotus japonicus young plants (two...	33	4.3
	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp...	33	4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un...	33	4.7
35	gb BE028433 BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li...	32	5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom...	32	5.9
	emb AW728623 AW728623 GA_Ea0017G06 Gossypium arboreum 7-10 dpa ...	32	5.9
	gb BE027723 BE027723 EtESTea86c08.y1 Eimeria M5-6 Merozoite stag...	32	5.9
40	emb AI757375 AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st...	32	5.9
	gb BE027843 BE027843 EtESTea88c05.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI973878 AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone...	32	5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit...	32	5.9
	dbj D85251 D85251 Plasmodium vivax clone TD207B DNA for merozoit...	32	5.9
45	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	32	6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O...	32	6.5
	emb AW707662 AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien...	28	7.3
	emb AF083075 AF083075 Fusarium oxysporum f. sp. lycopersici exop...	32	8.1
	emb AV411934 AV411934 AV411934 Lotus japonicus young plants (two...	32	8.1
50	emb AW703740 AW703740 sk23g09.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AW703739 AW703739 sk23g08.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
	emb AV419698 AV419698 AV419698 Lotus japonicus young plants (two...	32	8.1
	emb AV419299 AV419299 AV419299 Lotus japonicus young plants (two...	32	8.1
	emb AV420652 AV420652 AV420652 Lotus japonicus young plants (two...	32	8.1
55	emb AV408860 AV408860 AV408860 Lotus japonicus young plants (two...	32	8.1
	emb AV420989 AV420989 AV420989 Lotus japonicus young plants (two...	32	8.1
	emb AV419314 AV419314 AV419314 Lotus japonicus young plants (two...	32	8.1
	emb AW720540 AW720540 LjNEST18h4r Lotus japonicus nodule library...	32	8.1
60	emb X77895 CPGPRNL28 G.pyrenaica chloroplast trnL gene intron.	32	8.1

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gb|aa32879.1| (m81620) tryptophan synthase beta-subunit [arabidopsis
thaliana] thaliana /blast_score 0 /ec_number /family /chip nova
/gb_link /ncgi

5 (1526 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

10 Searching.....done

		Score	E	
	Sequences producing significant alignments:		(bits)	Value
15	emb AF042320 AF042320 <i>Camptotheca acuminata</i> tryptophan synthase ...	858	0.0	
	emb AF047024 AF047024 <i>Chlamydomonas reinhardtii</i> tryptophan synth...	712	0.0	
	gb J04594 NEUTRP3A <i>N.crassa</i> tryptophan synthetase (trp3) alpha-2...	473	e-140	
	emb Z98974 SPAC19A8 <i>S.pombe</i> chromosome I cosmid c19A8.	462	e-135	
	emb AW031813 AW031813 EST275267 tomato callus, TAMU <i>Lycopersicon</i> ...	429	e-119	
20	emb AF121272 AF121272 <i>Gracilaria gracilis</i> putative NAD-myo-inosi...	426	e-118	
	dbj D89113 D89113 <i>Schizosaccharomyces pombe</i> mRNA, partial cds, c...	310	e-114	
	emb AI055312 AI055312 coau0003K07 Cotton Boll Abscission Zone cD...	404	e-112	
	emb AF042321 AF042321 <i>Camptotheca acuminata</i> tryptophan synthase ...	346	e-109	
	gb BE126222 BE126222 DG1_68_D09.b1_A002 Dark Grown 1 (DG1) <i>Sorgh...</i>	379	e-104	
25	emb AW650635 AW650635 EST329089 tomato germinating seedlings, TA...	372	e-102	
	emb AI487343 AI487343 EST245665 tomato ovary, TAMU <i>Lycopersicon</i> ...	354	8e-97	
	emb AI488733 AI488733 EST247072 tomato ovary, TAMU <i>Lycopersicon</i> ...	353	2e-96	
	emb AA495663 AA495663 c313 Zhou and Ragan 1993 <i>Gracilaria gracil...</i>	350	1e-95	
	emb AW160221 AW160221 EST290079 <i>L. pennellii</i> trichome, Cornell U...	327	1e-88	
30	emb V01342 SCTRP5A Yeast gene (trp5) for tryptophan synthetase.	270	6e-88	
	emb Z72548 SCYGL026C <i>S.cerevisiae</i> chromosome VII reading frame O...	270	6e-88	
	emb AI485149 AI485149 EST243453 tomato ovary, TAMU <i>Lycopersicon</i> ...	319	3e-86	
	emb AI966766 AI966766 sc57f10.y1 Gm-c1016 Glycine max cDNA clone...	306	3e-82	
	gb M91659 CCITRP08 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	302	4e-81	
35	gb BE058277 BE058277 sn13h12.y1 Gm-c1016 Glycine max cDNA clone ...	259	6e-68	
	emb AI488512 AI488512 EST246851 tomato ovary, TAMU <i>Lycopersicon</i> ...	237	2e-63	
	emb AI487792 AI487792 EST246114 tomato ovary, TAMU <i>Lycopersicon</i> ...	232	8e-62	
	emb AW696637 AW696637 NF109C11ST1F1085 Developing stem <i>Medicago</i> ...	213	2e-59	
	emb AI898827 AI898827 EST268270 tomato ovary, TAMU <i>Lycopersicon</i> ...	228	7e-59	
40	emb AQ450225 AQ450225 500009D01.x1 CpIOWAM13mp18gDNA1 <i>Cryptospor...</i>	175	3e-58	
	emb AW160220 AW160220 EST290078 <i>L. pennellii</i> trichome, Cornell U...	223	3e-57	
	emb AF084902 AF084902 <i>Neurospora crassa</i> TD2(4A-4A)2A mutant trypt...	214	2e-54	
	emb AF084903 AF084903 <i>Neurospora crassa</i> TD71-19A mutant tryptoph...	213	3e-54	
45	emb AF084904 AF084904 <i>Neurospora crassa</i> TD54-6A mutant tryptoph...	210	3e-53	
	emb AI779245 AI779245 EST260124 tomato susceptible, Cornell Lyco...	208	8e-53	
	emb AI487088 AI487088 EST245410 tomato ovary, TAMU <i>Lycopersicon</i> ...	149	3e-51	
	emb AQ876415 AQ876415 V99F5 mTn-3xHA/lacZ Insertion Library, str...	183	4e-50	
	emb AL116518 CNS01D8U <i>Botrytis cinerea</i> strain T4 cDNA library un...	160	2e-47	
50	emb AW745773 AW745773 WS1_37_G06.b1_A002 Water-stressed 1 (WS1) ...	167	2e-40	
	emb AF084893 AF084893 <i>Neurospora crassa</i> TD24-2A-28A mutant trypt...	130	8e-38	
	emb AF084892 AF084892 <i>Neurospora crassa</i> 314-567-9A mutant trypt...	132	1e-37	
	emb AF084891 AF084891 <i>Neurospora crassa</i> 314-616-2A mutant trypt...	132	1e-37	
	emb AF084895 AF084895 <i>Neurospora crassa</i> TD10-8A mutant tryptoph...	130	1e-37	
55	emb AF084894 AF084894 <i>Neurospora crassa</i> TD7(13A-11A)13A mutant t...	130	1e-37	
	emb AF084901 AF084901 <i>Neurospora crassa</i> TD72-1-25A mutant trypt...	129	1e-37	
	emb AF084900 AF084900 <i>Neurospora crassa</i> TD85-1-24A mutant trypt...	129	1e-37	
	emb AF084899 AF084899 <i>Neurospora crassa</i> TD86-1-22A mutant trypt...	129	1e-37	
	emb AF084898 AF084898 <i>Neurospora crassa</i> TD6(1-8A)22A mutant trypt...	129	1e-37	
60	emb AF084896 AF084896 <i>Neurospora crassa</i> NG29-3A mutant tryptoph...	129	1e-37	
	emb AW745836 AW745836 WS1_37_G06.g1_A002 Water-stressed 1 (WS1) ...	157	2e-37	

	emb AF084897 AF084897 <i>Neurospora crassa</i> TD3-32-16A mutant trypto...	128	3e-37
	emb AI399300 AI399300 NCW07F11T3 Westergaards <i>Neurospora crassa</i> ...	145	3e-37
	emb AF084906 AF084906 <i>Neurospora crassa</i> NG40-5A mutant tryptopha...	152	8e-36
	emb AF084905 AF084905 <i>Neurospora crassa</i> NG25-4A mutant tryptopha...	152	8e-36
5	gb BE024522 BE024522 894003E01.y1 <i>C. reinhardtii</i> CC-1690, normal...	142	6e-33
	emb AJ229567 KLAJ9567 <i>Kluyveromyces lactis</i> DNA fragment for sequ...	137	3e-31
	emb AQ449630 AQ449630 500002F12.x2 CpIOWAM13mp18gDNA1 <i>Cryptospor...</i>	116	1e-27
	emb AW695848 AW695848 NF099D01ST1F1012 Developing stem <i>Medicago</i> ...	116	9e-27
10	emb AW098758 AW098758 ga01a03.y1 Moss EST library CPU <i>Ceratodon</i> ...	118	1e-25
	gb M91658 CCITRP07 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	115	8e-25
	emb AW086510 AW086510 ga01a03.x1 Moss EST library CPU <i>Ceratodon</i> ...	103	4e-21
	emb AW221168 AW221168 EST297637 tomato fruit mature green, TAMU ...	96	5e-19
	emb AW650217 AW650217 EST328671 tomato germinating seedlings, TA...	95	1e-18
15	emb AV408265 AV408265 AV408265 <i>Lotus japonicus</i> young plants (two...	77	4e-13
	emb AW688230 AW688230 NF005A01ST1F1000 Developing stem <i>Medicago</i> ...	72	1e-11
	emb AI488384 AI488384 EST246706 tomato ovary, TAMU <i>Lycopersicon</i> ...	70	4e-11
	emb AW032971 AW032971 EST276530 tomato callus, TAMU <i>Lycopersicon</i> ...	60	6e-08
	emb AW755317 AW755317 sl01e06.y1 Gm-c1036 <i>Glycine max</i> cDNA clone...	57	4e-07
20	emb AW153250 AW153250 se37h08.y1 Gm-c1015 <i>Glycine max</i> cDNA clone...	56	1e-06
	emb AQ450041 AQ450041 500007C05.x1 CpIOWAM13mp18gDNA1 <i>Cryptospor...</i>	37	2e-04
	emb AW625162 AW625162 EST319069 tomato radicle, 5 d post-imbibit...	45	0.001
	gb M91656 CCITRP05 <i>Coprinus cinereus</i> tryptophan synthetase (TRP1...	45	0.002
	emb AW926725 AW926725 HVSMEg0007P16 <i>Hordeum vulgare</i> pre-anthesis...	42	0.013
25	emb X99652 ANG3PDEHY <i>A.niger</i> gpd gene.	35	0.084
	emb AV418759 AV418759 AV418759 <i>Lotus japonicus</i> young plants (two...	38	0.17
	emb AV417838 AV417838 AV417838 <i>Lotus japonicus</i> young plants (two...	38	0.17
	emb AV414417 AV414417 AV414417 <i>Lotus japonicus</i> young plants (two...	38	0.17
	emb AV419253 AV419253 AV419253 <i>Lotus japonicus</i> young plants (two...	38	0.17
30	emb AV424994 AV424994 AV424994 <i>Lotus japonicus</i> young plants (two...	38	0.17
	emb AA901537 AA901537 NCC2B7T7 Conidial <i>Neurospora crassa</i> cDNA c...	38	0.23
	gb BE060085 BE060085 HVSMEg0011G11f <i>Hordeum vulgare</i> pre-anthesis...	38	0.23
	gb U30626 SCU30626 <i>Saccharomyces cerevisiae</i> var. diastaticus glu...	37	0.32
	emb AJ010201 GMA010201 <i>Glycine max</i> mRNA for inosine monophosphat...	37	0.32
35	emb AW185330 AW185330 se90b04.y1 Gm-c1027 <i>Glycine max</i> cDNA clone...	37	0.32
	emb Z38061 SC9168 <i>S.cerevisiae</i> chromosome IX cosmid 9168.	37	0.32
	emb AF160799 AF160799 <i>Sporidiobolus salmonicolor</i> aldehyde reduct...	37	0.44
	emb AC016161 AC016161 <i>Leishmania major</i> chromosome 35 clone L8149...	37	0.44
	emb AW185636 AW185636 se80e06.y1 Gm-c1023 <i>Glycine max</i> cDNA clone...	37	0.44
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	emb AW278827 AW278827 sf99b01.y1 Gm-c1019 <i>Glycine max</i> cDNA clone...	36	0.60
	emb Z93048 SLZ93048 <i>S.latifolia</i> mRNA, clone CCLS 37.1.	30	0.72
	emb AV393412 AV393412 AV393412 <i>Chlamydomonas reinhardtii</i> C9 Chla...	36	0.83
	emb AL035581 SPBC1677 <i>S.pombe</i> chromosome II cosmid c1677.	36	0.83
45	emb AV425767 AV425767 AV425767 <i>Lotus japonicus</i> young plants (two...	36	0.83
	emb AI727538 AI727538 BNLGHi8343 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	gb BE053957 BE053957 GA__Ea0033K12f <i>Gossypium arboreum</i> 7-10 dpa ...	35	1.1
	emb AI731384 AI731384 BNLGHi8894 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	emb AW596016 AW596016 si96g09.y1 Gm-c1032 <i>Glycine max</i> cDNA clone...	35	1.1
50	emb AI730998 AI730998 BNLGHi8370 Six-day Cotton fiber <i>Gossypium</i> ...	35	1.1
	emb AJ276509 TAE276509 <i>Triticum aestivum</i> grp1 gene for glycine-r...	28	1.3
	gb B13527 B13527 jd421 Trypanosome Shotgun M13 genomic Trypanoso...	29	1.4
	gb U56698 CPU56698 <i>Ceratodon purpureus</i> phytochrome photoreceptor...	35	2.2
	emb AF079252 AF079252 <i>Dichanthium aristatum</i> granule-bound starch...	35	2.2
55	emb AJ133604 TAE133604 <i>Triticum aestivum</i> mRNA for alpha-gliadin ...	34	4.1

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 60. [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|wt1012a|/ncgi)
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Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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Database: plantfungal

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	emb AW171733 AW171733 N100627e rootphos(-) Medicago truncatula c...	36	0.099	
	emb AW185514 AW185514 se80g03.y1 Gm-c1023 Glycine max cDNA clone...	36	0.099	
35	emb AI777176 AI777176 EST258141 tomato resistant, Cornell Lycopen...	35	0.26	
	gb C22084 C22084 C22084 Miyagawa-wase satsuma mandarin orange (M...	35	0.26	
	emb AW755041 AW755041 PC10A02 Pine TriplEx pollen cone library P...	35	0.26	
	emb AW218263 AW218263 EST303444 tomato radicle, 5 d post-imbibit...	35	0.26	
	emb AI488300 AI488300 EST246622 tomato ovary, TAMU Lycopersicon ...	35	0.26	
40	emb AA557085 AA557085 927 Loblolly pine N Pinus taeda cDNA clone...	35	0.26	
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	emb AF101786 AF101786 Pinus taeda clone PtaADH1 adhesive/proline...	35	0.35	
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45	emb AI812646 AI812646 17D5 Pine Lambda Zap Xylem library Pinus t...	35	0.35	
	emb AI776730 AI776730 EST257830 tomato resistant, Cornell Lycopen...	34	0.49	
	emb AW040418 AW040418 EST283282 tomato mixed elicitor, BTI Lycop...	34	0.49	
	emb AI490164 AI490164 EST246756 tomato resistant, Cornell Lycopen...	34	0.49	
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	emb AW329045 AW329045 N200244e rootphos(-) Medicago truncatula c...	34	0.67	
	emb AA556671 AA556671 526 Loblolly pine CA Pinus taeda cDNA clon...	34	0.67	
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	emb AI416664 AI416664 sa10c07.x1 Gm-c1003 Glycine max cDNA clone...	33	0.92	
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	emb AW064558 AW064558 ST33A05 Pine TriplEx shoot tip library Pin...	33	1.3	
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60	emb AW011244 AW011244 ST18E01 Pine TriplEx shoot tip library Pin...	33	1.3	
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 emb|AW043248|AW043248 ST31B02 Pine TriplEx shoot tip library Pin... 32 1.7
 emb|AW255053|AW255053 ML1348 peppermint glandular trichome Menth... 32 2.4
 10 emb|AW255347|AW255347 ML358 peppermint glandular trichome Menth... 32 2.4
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 15 emb|AW568662|AW568662 si60e08.y1 Gm-r1030 Glycine max cDNA clone... 31 3.3
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 20 emb|AW102024|AW102024 sd82b01.y1 Gm-cl1009 Glycine max cDNA clone... 31 3.3
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 30 emb|AF039708|AF039708 Maackia amurensis early nodulin (ENOD2) mR... 30 8.5
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45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 60 emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 105 1e-22
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- emb|AW399412|AW399412 EST309912 *L. pennellii* trichome, Cornell U... 104 2e-22
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5 emb|AI736542|AI736542 sb30b04.y1 Gm-c1009 Glycine max cDNA clone... 64 5e-17
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10 emb|AI899328|AI899328 EST268771 tomato ovary, TAMU Lycopersicon ... 82 2e-15
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40 emb|AW623982|AW623982 EST321927 tomato flower buds 3-8 mm, Corne... 29 2.5
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10 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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20 emb AW729009 AW729009 GA_Ea0019F23 Gossypium arboreum 7-10 dpa ...	35	0.59	
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emb AW278522 AW278522 sf45e07.y1 Gm-c1009 Glycine max cDNA clone...	33	1.5	
emb AW424313 AW424313 sh63h04.y1 Gm-c1015 Glycine max cDNA clone...	33	1.5	
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45 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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emb AI778230 AI778230 EST259109 tomato susceptible, Cornell Lyco...	287	6e-77	
emb AW218621 AW218621 EST303804 tomato radicle, 5 d post-imbibit...	287	6e-77	
emb AW668548 AW668548 GA_Ea0014I16 Gossypium arboreum 7-10 dpa ...	287	6e-77	
emb AW668413 AW668413 GA_Ea0013N18 Gossypium arboreum 7-10 dpa ...	287	6e-77	
60 emb AI782495 AI782495 EST263374 tomato susceptible, Cornell Lyco...	285	3e-76	
emb AI779421 AI779421 EST260300 tomato susceptible, Cornell Lyco...	285	3e-76	

- emb|AI775630|AI775630 EST256730 tomato resistant, Cornell Lycopersicon... 285 3e-76
gb|BE055389|BE055389 GA_Ea0026N20f Gossypium arboreum 7-10 dpa ... 284 5e-76
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emb|AW349482|AW349482 GM210007A20G5R Gm-r1021 Glycine max cDNA 3... 282 2e-75
- 5 emb|AW041006|AW041006 EST283870 tomato mixed elicitor, BTI Lycopersicon... 279 2e-74
emb|AW597183|AW597183 sj74f03.y1 Gm-c1034 Glycine max cDNA clone... 278 3e-74
gb|BE055703|BE055703 GA_Ea0033C16f Gossypium arboreum 7-10 dpa ... 275 2e-73
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- 10 emb|AW569109|AW569109 si63e02.y1 Gm-r1030 Glycine max cDNA clone... 275 2e-73
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emb|AW733947|AW733947 sk85e02.y1 Gm-c1035 Glycine max cDNA clone... 271 4e-72
- 15 emb|AW508057|AW508057 si49e04.y1 Gm-r1030 Glycine max cDNA clone... 271 4e-72
emb|AW573705|AW573705 EST316296 GVN Medicago truncatula cDNA clone... 271 4e-72
emb|AW508326|AW508326 si52e11.y1 Gm-r1030 Glycine max cDNA clone... 270 7e-72
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emb|AI930835|AI930835 sc47h06.y1 Gm-c1015 Glycine max cDNA clone... 269 1e-71
- 20 emb|AI930828|AI930828 sc47g06.y1 Gm-c1015 Glycine max cDNA clone... 269 1e-71
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emb|AW101773|AW101773 sd70b02.y1 Gm-c1008 Glycine max cDNA clone... 261 4e-69
- 25 emb|AW559683|AW559683 EST314795 DSIR Medicago truncatula cDNA clone... 260 6e-69
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- 30 emb|AW094638|AW094638 EST287806 tomato mixed elicitor, BTI Lycopersicon... 255 3e-67
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- 35 emb|AW756544|AW756544 sl23d11.y1 Gm-c1036 Glycine max cDNA clone... 247 6e-65
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- 40 emb|AW720300|AW720300 LjNEST20d9r Lotus japonicus nodule library... 236 2e-61
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- 45 emb|AI774108|AI774108 EST255208 tomato resistant, Cornell Lycopersicon... 227 7e-59
emb|AI163857|AI163857 A050p05u Hybrid aspen plasmid library Populus... 226 9e-59
emb|AW065077|AW065077 ST39D01 Pine TriplEx shoot tip library Pinus... 225 2e-58
emb|AW704118|AW704118 sk16b03.y1 Gm-c1028 Glycine max cDNA clone... 221 4e-57
emb|AI507795|AI507795 sb12g09.y1 Gm-c1004 Glycine max cDNA clone... 216 1e-55
- 50 emb|AW289649|AW289649 NXNV003G05F Nsf Xylem Normal wood Vertical... 215 2e-55
emb|AV422946|AV422946 AV422946 Lotus japonicus young plants (two... 122 3e-55
gb|T14824|T14824 crs266 lambdaZAPST Ricinus communis cDNA clone ... 212 2e-54
emb|AW443507|AW443507 EST308437 tomato mixed elicitor, BTI Lycopersicon... 207 6e-53
emb|AW226029|AW226029 ST76E07 Pine TriplEx shoot tip library Pinus... 207 8e-53
- 55 emb|AW747461|AW747461 WS1_68_B01.g1_A002 Water-stressed 1 (WS1) ... 181 1e-51
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gb|BE054071|BE054071 GA_Ea0035D19f Gossypium arboreum 7-10 dpa ... 93 4e-50
gb|C96251|C96251 C96251 Marchantia polymorpha immature sex organ... 98 5e-50
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- 60 emb|AI164569|AI164569 A065P13U Hybrid aspen plasmid library Populus... 180 2e-48
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emb|AI777234|AI777234 EST258199 tomato resistant, Cornell Lycopersicon... 148 1e-44
emb|AI165310|AI165310 A081P03U Hybrid aspen plasmid library Populus... 152 7e-44
emb|AW870064|AW870064 NXNV_123_F09_F Nsf Xylem Normal wood Verticillium... 176 1e-43
5 emb|AI484178|AI484178 EST249331 tomato resistant, Cornell Lycopersicon... 144 2e-43
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emb|AW255890|AW255890 ML976 peppermint glandular trichome Mentha... 143 7e-42
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10 emb|AI161700|AI161700 A005P46U Hybrid aspen plasmid library Populus... 150 3e-38
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emb|AW651357|AW651357 EST329811 tomato germinating seedlings, TA... 157 6e-38
emb|AW623884|AW623884 EST321829 tomato flower buds 3-8 mm, Cornell... 157 6e-38
15 emb|AI484189|AI484189 EST249342 tomato resistant, Cornell Lycopersicon... 157 9e-38
gb|L37653|L37653 BNAESTGU Mustard flower buds Brassica rapa cDNA... 156 1e-37
emb|AW944894|AW944894 EST336944 tomato flower buds 3-8 mm, Cornell... 154 8e-37
emb|AW726742|AW726742 GA_Ea0022J15 Gossypium arboreum 7-10 dpa ... 152 2e-36
emb|AW694116|AW694116 NF072H11ST1F1095 Developing stem Medicago ... 150 2e-36
20 emb|AW649234|AW649234 EST327688 tomato germinating seedlings, TA... 151 5e-36
emb|AW725828|AW725828 GA_Ea0019N04 Gossypium arboreum 7-10 dpa ... 95 8e-36
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emb|AW317704|AW317704 sg56c06.y1 Gm-c1007 Glycine max cDNA clone... 148 4e-35
emb|AW432260|AW432260 sh71d04.y1 Gm-c1015 Glycine max cDNA clone... 143 2e-33
25 emb|AI165031|AI165031 A073p61u Hybrid aspen plasmid library Populus... 131 6e-32
emb|AI507718|AI507718 sb10g09.y1 Gm-c1004 Glycine max cDNA clone... 131 2e-31
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30 emb|AI899479|AI899479 EST268922 tomato susceptible, Cornell Lycopersicon... 124 7e-28
emb|AI460396|AI460396 sa81a06.y1 Gm-c1004 Glycine max cDNA clone... 119 2e-26
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emb|AI166161|AI166161 B00964U Hybrid aspen plasmid library Populus... 113 1e-24
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50 emb|AI486200|AI486200 EST244521 tomato ovary, TAMU Lycopersicon ... 377 e-103
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emb|AI488742|AI488742 EST247081 tomato ovary, TAMU Lycopersicon ... 347 2e-94
emb|AF042184|AF042184 Brassica napus lysine-ketoglutarate reduct... 334 1e-93
emb|AI054604|AI054604 coau0001I01 Cotton Boll Abscission Zone cD... 319 3e-92
55 emb|AW034280|AW034280 EST277851 tomato callus, TAMU Lycopersicon... 316 7e-85
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emb|AW933092|AW933092 EST358935 tomato fruit mature green, TAMU ... 287 4e-76
emb|AW442160|AW442160 EST311556 tomato fruit red ripe, TAMU Lyco... 220 8e-74
emb|AW681014|AW681014 WS1_8_B05.b1_A002 Water-stressed I (WS1) S... 275 1e-72
60 emb|AW933411|AW933411 EST359350 tomato fruit mature green, TAMU ... 272 1e-71
emb|AW931846|AW931846 EST357689 tomato fruit mature green, TAMU ... 264 3e-69

	emb AI485129 AI485129 EST243433 tomato ovary, TAMU Lycopersicon ...	253	8e-66
	emb AW035300 AW035300 EST280663 tomato callus, TAMU Lycopersicon...	241	3e-62
	emb AW934545 AW934545 EST353353 tomato flower buds 0-3 mm, Corne...	230	4e-59
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5	emb AL022244 SPBC3B8 S.pombe chromosome II cosmid c3B8.	181	2e-56
	emb AW037965 AW037965 EST279609 tomato mixed elicitor, BTI Lycop...	211	2e-53
	emb AW931630 AW931630 EST357473 tomato fruit mature green, TAMU ...	208	3e-52
	emb AW035261 AW035261 EST280523 tomato callus, TAMU Lycopersicon...	142	4e-52
10	emb AI896768 AI896768 EST266211 tomato callus, TAMU Lycopersicon...	192	2e-47
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	emb X77363 SCLYS9 S.cerevisiae LYS9 gene.	155	5e-47
	emb AW224200 AW224200 EST301107 tomato fruit red ripe, TAMU Lyco...	188	2e-46
	emb AW930672 AW930672 EST356515 tomato fruit mature green, TAMU ...	110	4e-45
	emb AI771935 AI771935 EST253035 tomato ovary, TAMU Lycopersicon ...	173	6e-42
15	emb AI899372 AI899372 EST268815 tomato ovary, TAMU Lycopersicon ...	172	1e-41
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	emb AI483615 AI483615 EST249479 tomato ovary, TAMU Lycopersicon ...	110	2e-40
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	emb AI782310 AI782310 EST263189 tomato susceptible, Cornell Lyco...	139	1e-31
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	emb AU012735 AU012735 AU012735 Schizosaccharomyces pombe late lo...	125	5e-30
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	emb AU010645 AU010645 AU010645 Schizosaccharomyces pombe late lo...	118	2e-25
30	emb AW038858 AW038858 EST280814 tomato mixed elicitor, BTI Lycop...	114	5e-24
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	emb AI486763 AI486763 EST245085 tomato ovary, TAMU Lycopersicon ...	110	6e-23
	emb AI399018 AI399018 NCW10A5T3 Westergaards Neurospora crassa c...	63	1e-21
35	emb AW031018 AW031018 EST274325 tomato callus, TAMU Lycopersicon...	101	4e-20
	emb AW932183 AW932183 EST358026 tomato fruit mature green, TAMU ...	72	9e-13
	emb AW096237 AW096237 EST289417 tomato mixed elicitor, BTI Lycop...	67	8e-10
	emb AA577639 AA577639 EST213 Sugarcane leaf roll Saccharum sp. c...	65	3e-09
	emb AW224318 AW224318 EST301045 tomato fruit red ripe, TAMU Lyco...	51	5e-05
40	emb AI900022 AI900022 sb97g03.y1 Gm-c1012 Glycine max cDNA clone...	50	1e-04
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	emb Z38061 SC9168 S.cerevisiae chromosome IX cosmid 9168.	45	0.004
	emb X77362 SCLYS1 S.cerevisiae LYS1 gene.	45	0.004
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45	gb U13233 CAU13233 Candida albicans saccharopine dehydrogenase (...)	40	0.078
	emb AL110979 CNS018Z0 Botrytis cinerea strain T4 cDNA library un...	35	0.079
	emb AL133156 SPAC227 S.pombe chromosome I cosmid c227.	40	0.15
	emb AF178855 AF178855 Candida albicans Crm1p (CRM1) gene, comple...	37	0.99
	emb AI667978 AI667978 TENG0800 T. Cruzi epimastigote normalised ...	36	1.4
50	emb AW310192 AW310192 sf32e10.x1 Gm-c1028 Glycine max cDNA clone...	36	1.4
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	emb AL355930 NCB208 Neurospora crassa DNA linkage group II BAC c...	35	3.5
	gb N82089 N82089 TgESTzy41f01.r1 TgRH Tachyzoite cDNA Toxoplasma...	35	3.5
	emb AW713255 AW713255 g6f04ne.fl Neurospora crassa evening cDNA ...	33	4.1
55	emb AW710105 AW710105 e1c07ne.fl Neurospora crassa evening cDNA ...	33	4.1
	emb AW712320 AW712320 g1a02ne.fl Neurospora crassa evening cDNA ...	33	4.2
	emb AA451583 AA451583 AJK252 Onion seedling leaf cDNA library AI...	35	4.8
	emb AQ660868 AQ660868 Sheared DNA-27G4.TF Sheared DNA Trypanosom...	35	4.8
	emb AI773473 AI773473 EST254573 tomato resistant, Cornell Lycope...	30	5.4
60	emb X99000 CS39KBCIV S.cerevisiae 39kb DNA segment of chromosome...	34	6.7
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5	emb AV420631 AV420631 AV420631 Lotus japonicus young plants (two...	34 6.7
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10	emb AF202183 AF202183 Glycine max isoflavone reductase homolog 1...	34 9.2
	emb AW648458 AW648458 EST326912 tomato germinating seedlings, TA...	34 9.2
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	emb AW455238 AW455238 EST311898 tomato root during/after fruit s...	229 1e-63
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40	emb AI487264 AI487264 EST245586 tomato ovary, TAMU Lycopersicon ...	205 1e-55
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	emb AW667985 AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ...	128 4e-54
	emb AI485223 AI485223 EST243527 tomato ovary, TAMU Lycopersicon ...	203 5e-54
	emb AI897690 AI897690 EST267133 tomato ovary, TAMU Lycopersicon ...	205 7e-54
45	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	162 1e-53
	emb AI486547 AI486547 EST244868 tomato ovary, TAMU Lycopersicon ...	150 1e-53
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	165 1e-53
	emb AI489882 AI489882 EST248221 tomato ovary, TAMU Lycopersicon ...	205 3e-53
	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	168 5e-53
50	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	163 9e-53
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	170 8e-52
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	emb AI484547 AI484547 EST242777 tomato ovary, TAMU Lycopersicon ...	205 1e-51
	emb AI484020 AI484020 EST249891 tomato ovary, TAMU Lycopersicon ...	205 1e-51
55	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	160 2e-51
	emb AF142596 AF142596 Nicotiana tabacum LRR receptor-like protei...	144 2e-51
	emb AW616916 AW616916 EST323327 L. hirsutum trichome, Cornell Un...	145 3e-51
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	165 1e-50
	emb AI487456 AI487456 EST245778 tomato ovary, TAMU Lycopersicon ...	139 3e-50
60	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	154 7e-50
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	164 7e-50

- emb|AF220602|AF220602 *Lycopersicon pimpinellifolium* Rio Grande 7... 96 2e-49
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5 emb|AB008191|AB008191 *Brassica rapa* mRNA for SRK29, complete cds. 154 4e-48
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10 emb|X98520|BOSFR2 *B. oleracea* mRNA for receptor-like kinase, SFR2. 153 7e-47
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20 emb|Y14286|BOY14286 *Brassica oleracea* SFR3 gene, partial. 91 1e-45
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dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 134 2e-45
25 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 145 2e-45
emb|AI898918|AI898918 EST268361 tomato ovary, TAMU *Lycopersicon* ... 183 5e-45
emb|AF131222|AF131222 *Lophopyrum elongatum* protein serine/threon... 138 2e-44
emb|AW756743|AW756743 sl26f10.y1 Gm-c1027 *Glycine max* cDNA clone... 181 2e-44
emb|AF220603|AF220603 *Lycopersicon esculentum* VFNT Cherry Pto lo... 96 2e-44
30 emb|AI731504|AI731504 BNLGHi9991 Six-day Cotton fiber *Gossypium* ... 132 3e-44
emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 151 4e-44
emb|AI489009|AI489009 EST247348 tomato ovary, TAMU *Lycopersicon* ... 117 7e-44
emb|AI483732|AI483732 EST249603 tomato ovary, TAMU *Lycopersicon* ... 177 4e-43
emb|AA738545|AA738545 SbRLK3 *Sorghum bicolor* cv. TX430 leaf Sorg... 153 6e-43
35 gb|U59315|LPU59315 *Lycopersicon pimpinellifolium* serine/threonin... 88 1e-42
gb|U02271|LEU02271 *Lycopersicon pimpinellifolium* Rio Grande-PtoR... 88 1e-42
emb|AJ245479|BNA245479 *Brassica napus* SI13, slk, srk, CePP, Fmt,... 80 2e-42
emb|AI490032|AI490032 EST248371 tomato ovary, TAMU *Lycopersicon* ... 149 2e-42
emb|AW220490|AW220490 EST297043 tomato fruit mature green, TAMU ... 116 2e-42
40 gb|U28007|LEU28007 *Lycopersicon esculentum* Pto kinase interactor... 83 3e-42
emb|AW621706|AW621706 EST312504 tomato root during/after fruit s... 143 4e-42
emb|AW031255|AW031255 EST274630 tomato callus, TAMU *Lycopersicon*... 149 6e-42
emb|AW684940|AW684940 NF023C12NR1F1000 Nodulated root *Medicago* t... 113 6e-42
emb|AB000971|AB000971 *Brassica campestris* pseudogene for recepto... 78 8e-42
45 gb|U59316|LEU59316 *Lycopersicon esculentum* serine/threonine prot... 87 1e-41
emb|AW687233|AW687233 NF007D09RT1F1077 Developing root *Medicago* ... 93 1e-41
emb|AW220491|AW220491 EST297044 tomato fruit mature green, TAMU ... 116 2e-41
dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 81 2e-41
dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 81 2e-41
50 emb|AB041503|AB041503 *Populus nigra* PnPK1 mRNA for protein kinas... 77 3e-41
emb|AW220489|AW220489 EST297042 tomato fruit mature green, TAMU ... 112 3e-41
emb|AI937984|AI937984 sc06e07.y1 Gm-c1012 *Glycine max* cDNA clone... 170 5e-41
emb|AB041504|AB041504 *Populus nigra* PnPK2 mRNA for protein kinas... 75 1e-40
emb|AI484701|AI484701 EST242962 tomato ovary, TAMU *Lycopersicon* ... 127 1e-40
55 emb|AA738544|AA738544 SbRLK2 *Sorghum bicolor* cv. TX430 leaf Sorg... 122 1e-40
emb|AW672145|AW672145 LG1_357_A10.b1_A002 Light Grown 1 (LG1) So... 167 2e-40
gb|U59317|LPU59317 *Lycopersicon pimpinellifolium* serine/threonin... 93 3e-40
gb|U13923|LEU13923 *Lycopersicon pimpinellifolium* serine/threonin... 93 3e-40
emb|Z73295|CRPK1 *C. roseus* mRNA for receptor-like protein kinase. 74 5e-40
60 gb|U59318|LEU59318 *Lycopersicon esculentum* serine/threonine prot... 92 6e-40
emb|AW729859|AW729859 GA_Ea0026H04 *Gossypium arboreum* 7-10 dpa ... 81 1e-39

- emb|AW982539|AW982539 HVSMEg0003I16f Hordeum vulgare pre-anthesi... 129 1e-39
 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 125 1e-39
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 emb|Z18921|BOSRKL B.oleracea gene for S-receptor kinase-like pro... 72 2e-39
 5 emb|AW284352|AW284352 LG1_275_D12.g1_A002 Light Grown 1 (LG1) So... 165 2e-39
 emb|Y14600|SBRLK1 Sorghum bicolor mRNA for protein serine/threon... 123 2e-39
 emb|AW222552|AW222552 EST299363 tomato fruit red ripe, TAMU Lycop... 82 2e-39
 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 70 4e-39
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 10 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 71 5e-39
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 gb|BE053916|BE053916 GA_Ea0031D03f Gossypium arboreum 7-10 dpa ... 77 1e-38
 emb|AW760240|AW760240 sl59g07.y1 Gm-cl027 Glycine max cDNA clone... 130 2e-38
 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 73 3e-38

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 thaliana] /blast_score 0
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

25 Searching.....done

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| Sequences producing significant alignments: | (bits) | Value |
| 30 emb AW930291 AW930291 EST340748 tomato fruit mature green, TAMU ... | 403 | e-111 |
| emb AW625643 AW625643 EST319550 tomato radicle, 5 d post-imbibit... | 377 | e-103 |
| emb AW688234 AW688234 NF005A05ST1F1000 Developing stem Medicago ... | 367 | e-100 |
| emb AW666282 AW666282 sk34f11.y1 Gm-cl028 Glycine max cDNA clone... | 360 | 2e-98 |
| emb AW691093 AW691093 NF041B09ST1F1000 Developing stem Medicago ... | 332 | 5e-96 |
| 35 gb BE055044 BE055044 GA_Ea0031H08f Gossypium arboreum 7-10 dpa ... | 332 | 9e-95 |
| emb AW696933 AW696933 NF112E03ST1F1021 Developing stem Medicago ... | 347 | 3e-94 |
| emb AW926942 AW926942 HVSMEg0009B01 Hordeum vulgare pre-anthesis... | 295 | 6e-89 |
| emb AW737130 AW737130 EST338557 tomato flower buds, anthesis, Co... | 325 | 1e-87 |
| emb AW689358 AW689358 NF018C09ST1F1000 Developing stem Medicago ... | 281 | 3e-85 |
| 40 emb AW650696 AW650696 EST329150 tomato germinating seedlings, TA... | 179 | 2e-84 |
| emb AW625020 AW625020 EST313849 tomato radicle, 5 d post-imbibit... | 301 | 1e-80 |
| emb AI813214 AI813214 3C4 Pine Lambda Zap Xylem library Pinus ta... | 297 | 2e-80 |
| emb AW692700 AW692700 NF054C07ST1F1000 Developing stem Medicago ... | 279 | 6e-80 |
| gb BE036418 BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... | 258 | 2e-79 |
| 45 gb BE020170 BE020170 sm39e05.y1 Gm-cl028 Glycine max cDNA clone ... | 293 | 3e-78 |
| emb AW423801 AW423801 sh52b02.y1 Gm-cl017 Glycine max cDNA clone... | 293 | 4e-78 |
| emb AW731385 AW731385 GA_Ea0030K22 Gossypium arboreum 7-10 dpa ... | 289 | 6e-77 |
| gb BE052354 BE052354 GA_Ea0034P16f Gossypium arboreum 7-10 dpa ... | 282 | 5e-75 |
| emb AW687344 AW687344 NF008F03RT1F1029 Developing root Medicago ... | 269 | 5e-71 |
| 50 emb AW926887 AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis... | 264 | 1e-69 |
| emb AW944677 AW944677 00152 leafy spurge Lambda HybriZAP 2.1 two... | 248 | 1e-64 |
| emb AW727978 AW727978 GA_Ea0029C18 Gossypium arboreum 7-10 dpa ... | 231 | 2e-61 |
| emb AW755716 AW755716 sl08b12.y1 Gm-cl036 Glycine max cDNA clone... | 234 | 2e-60 |
| emb AW923236 AW923236 DG1_50_A11.g1_A002 Dark Grown 1 (DG1) Sorg... | 233 | 3e-60 |
| 55 gb BE060782 BE060782 HVSMEg0013F14f Hordeum vulgare pre-anthesis... | 226 | 7e-58 |
| emb AW203801 AW203801 sf38d05.y1 Gm-cl028 Glycine max cDNA clone... | 215 | 1e-54 |
| emb AW317181 AW317181 sf38d05.x1 Gm-cl028 Glycine max cDNA clone... | 200 | 4e-50 |
| emb AW398821 AW398821 EST309321 L. pennellii trichome, Cornell U... | 177 | 2e-43 |
| emb AW650818 AW650818 EST329272 tomato germinating seedlings, TA... | 148 | 2e-42 |
| 60 emb AW697347 AW697347 NF115F08ST1F1074 Developing stem Medicago ... | 168 | 2e-40 |
| emb AW428657 AW428657 Ljirmp22-731-a5 Ljirmp Lambda HybriZap ... | 168 | 2e-40 |

- emb|AW695961|AW695961 NF101A09ST1F1068 Developing stem Medicago ... 168 2e-40
emb|AV395160|AV395160 AV395160 Chlamydomonas reinhardtii C9 Chla... 164 2e-39
emb|AW907004|AW907004 EST343231 potato stolon, Cornell Universit... 163 5e-39
5 gb|BE123645|BE123645 NXNV_150_D07_F Nsf Xylem Normal wood Vertic... 158 1e-37
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gb|BE058285|BE058285 sn14b01.y1 Gm-cl016 Glycine max cDNA clone ... 152 8e-36
gb|BE055879|BE055879 GA_Ea0026P04f Gossypium arboreum 7-10 dpa ... 149 5e-35
emb|AA660997|AA660997 00894 MtrHE Medicago truncatula cDNA 5' si... 72 2e-34
10 emb|AW693956|AW693956 NF071B03ST1F1027 Developing stem Medicago ... 92 8e-33
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emb|AV428639|AV428639 AV428639 Lotus japonicus young plants (two... 133 7e-30
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15 gb|BE060772|BE060772 HVSMeg0013F04f Hordeum vulgare pre-anthesis... 99 2e-29
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emb|AJ273311|AJ273311 AJ273311 Metarhizium anisopliae ARSEF 2575... 77 4e-28
emb|AA840711|AA840711 CAN22 Anther cDNA library of Hot pepper Ca... 93 5e-28
emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 124 2e-27
20 emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 5e-27
emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186. 90 2e-26
gb|U18839|SCE9747 Saccharomyces cerevisiae chromosome V cosmids ... 80 2e-23
emb|AL033389|SPBC1773 S.pombe chromosome II cosmid c1773. 106 1e-22
emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 80 2e-22
25 emb|AW689996|AW689996 NF026G01ST1F1000 Developing stem Medicago ... 91 7e-20
emb|AL031180|SPUNK4 S.pombe chromosome I cosmid c2E11. 99 2e-19
dbj|D89185|D89185 Schizosaccharomyces pombe mRNA, partial cds, c... 99 2e-19
emb|AF079881|AF079881 Entodinium caudatum D-3-phosphoglycerate d... 53 2e-19
emb|AW736063|AW736063 EST332049 KV3 Medicago truncatula cDNA clo... 93 9e-18
30 gb|BE054038|BE054038 GA_Ea0008F24f Gossypium arboreum 7-10 dpa ... 88 2e-16
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gb|U43503|SCU43503 Saccharomyces cerevisiae chromosome XVI cosmi... 84 3e-15
emb|AW283359|AW283359 LG1_223_C04.g1_A002 Light Grown 1 (LG1) So... 84 5e-15
emb|AW625680|AW625680 EST319587 tomato radicle, 5 d post-imbibit... 83 1e-14
35 emb|AI486949|AI486949 EST245271 tomato ovary, TAMU Lycopersicon ... 83 1e-14
emb|Z71550|SCYNL274C S.cerevisiae chromosome XIV reading frame O... 83 1e-14
emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lyco... 83 1e-14
emb|AW030822|AW030822 EST274077 tomato callus, TAMU Lycopersicon... 83 1e-14
emb|AI484846|AI484846 EST243107 tomato ovary, TAMU Lycopersicon ... 83 1e-14
40 emb|AW442123|AW442123 EST311519 tomato fruit red ripe, TAMU Lyco... 83 1e-14
emb|AW651324|AW651324 EST329778 tomato germinating seedlings, TA... 83 1e-14
emb|AW647711|AW647711 EST307192 tomato germinating seedlings, TA... 83 1e-14
emb|Z21493|MISTFDHD S.tuberosum mRNA for formate dehydrogenase. 83 1e-14
emb|AI822999|AI822999 L30-850T3 Ice plant Lambda Uni-Zap XR expr... 82 1e-14
45 emb|AW693443|AW693443 NF065D03ST1F1000 Developing stem Medicago ... 71 2e-14
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emb|AT000538|AT000538 AT000538 Brassica rapa guard cell Brassica... 80 7e-14
emb|AI490350|AI490350 EST248676 tomato ovary, TAMU Lycopersicon ... 79 9e-14
emb|AQ874261|AQ874261 V105E9 mTn-3xHA/lacZ Insertion Library, st... 79 1e-13
50 emb|AI490396|AI490396 EST248734 tomato ovary, TAMU Lycopersicon ... 78 2e-13
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emb|AW037837|AW037837 EST279466 tomato mixed elicitor, BTI Lycop... 75 2e-12
emb|AW266848|AW266848 L48-192T3 Ice plant Lambda Uni-Zap XR expr... 74 3e-12
emb|AI897727|AI897727 EST267170 tomato ovary, TAMU Lycopersicon ... 74 4e-12
55 emb|AI898003|AI898003 EST267446 tomato ovary, TAMU Lycopersicon ... 74 4e-12
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60 emb|AW930862|AW930862 EST356705 tomato fruit mature green, TAMU ... 73 1e-11
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- gb|BE055276|BE055276 GA_Ea0034L16f *Gossypium arboreum* 7-10 dpa ... 57 2e-11
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 5 emb|AW100275|AW100275 sd22a06.y2 *Gm-c1012 Glycine max* cDNA clone... 71 4e-11
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- 10 Query= afl17063_s_at15641_s_at/id_source genbank /description
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- 15 Database: plantfungal
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- emb|AI898446|AI898446 EST267889 tomato ovary, TAMU Lycopersicon ... 209 e-108
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 25 emb|AI485780|AI485780 EST244101 tomato ovary, TAMU Lycopersicon ... 242 2e-86
 emb|AI485695|AI485695 EST244016 tomato ovary, TAMU Lycopersicon ... 261 5e-86
 emb|AI899197|AI899197 EST268640 tomato ovary, TAMU Lycopersicon ... 161 2e-78
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 30 emb|AI488812|AI488812 EST247151 tomato ovary, TAMU Lycopersicon ... 251 1e-65
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 emb|AI483614|AI483614 EST249464 tomato ovary, TAMU Lycopersicon ... 238 1e-61
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 35 emb|AW774994|AW774994 EST334145 KV3 *Medicago truncatula* cDNA clo... 182 3e-56
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 55 emb|AI488810|AI488810 EST247149 tomato ovary, TAMU Lycopersicon ... 121 3e-26
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 60 emb|AW034093|AW034093 EST277588 tomato callus, TAMU Lycopersicon... 111 3e-23
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- emb|AQ502761|AQ502761 V84A11 mTn-3xHA/lacZ Insertion Library Sac... 52 2e-22
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emb|AI771644|AI771644 EST252744 tomato ovary, TAMU Lycopersicon ... 104 4e-21
5 emb|AW731056|AW731056 GA_Ea0008D13 Gossypium arboreum 7-10 dpa ... 100 5e-20
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emb|AW616540|AW616540 EST322951 L. hirsutum trichome, Cornell Un... 98 2e-19
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emb|AW126841|AW126841 gal6f04.y1 Moss EST library PPU Physcomitr... 94 4e-18
10 emb|AI780067|AI780067 EST260946 tomato susceptible, Cornell Lyco... 94 6e-18
emb|AW687035|AW687035 NF005C05RT1F1037 Developing root Medicago ... 73 2e-17
emb|AW685930|AW685930 NF036F03NR1F1000 Nodulated root Medicago t... 73 2e-17
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emb|AW220291|AW220291 EST302774 tomato root during/after fruit s... 68 1e-14
15 emb|AQ644913|AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso... 53 2e-13
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25 emb|AZ048449|AZ048449 PSB67 Barley PstI genomic clones Hordeum v... 67 8e-10
emb|AW760518|AW760518 sl51d02.y1 Gm-cl027 Glycine max cDNA clone... 66 1e-09
emb|AW332143|AW332143 S4G7 AGS-1 Pneumocystis carinii f. sp. car... 36 1e-09
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emb|AI486692|AI486692 EST245014 tomato ovary, TAMU Lycopersicon ... 54 3e-09
30 emb|AW333870|AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c... 36 5e-09
emb|AQ850639|AQ850639 LMAJFV1_lm41a04.x1 Leishmania major FV1 ra... 44 6e-09
emb|AW127178|AW127178 M110117 GVN Medicago truncatula cDNA clone... 63 1e-08
emb|AW616547|AW616547 EST322958 L. hirsutum trichome, Cornell Un... 62 2e-08
emb|AW399291|AW399291 EST309791 L. pennellii trichome, Cornell U... 62 2e-08
35 emb|AW693686|AW693686 NF068A05ST1F1036 Developing stem Medicago ... 62 3e-08
emb|AW208046|AW208046 M111077e DSIR Medicago truncatula cDNA clo... 61 5e-08
emb|AQ642482|AQ642482 RPCI93-EcoRI-1A17.TV RPCI93-EcoRI Trypanos... 53 7e-08
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40 emb|AI781410|AI781410 EST262277 tomato susceptible, Cornell Lyco... 52 2e-05
emb|AW617564|AW617564 EST323975 L. hirsutum trichome, Cornell Un... 49 2e-04
emb|AQ946427|AQ946427 Sheared DNA-49M8.TF Sheared DNA Trypanosom... 47 5e-04
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emb|Z74807|SCYOL065C S.cerevisiae chromosome XV reading frame OR... 29 0.003
45 emb|AQ655271|AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso... 38 0.004
emb|AW685854|AW685854 NF031A06NR1F1000 Nodulated root Medicago t... 43 0.009
emb|AW437996|AW437996 ST83C09 Pine TriplEx shoot tip library Pin... 42 0.016
emb|AI440709|AI440709 sa62e11.y1 Gm-cl004 Glycine max cDNA clone... 31 0.045
emb|AW979881|AW979881 EST341528 tomato root deficiency, Cornell ... 37 0.54
50 emb|AF263282|AF263282 Filobasidiella neoformans var. neoformans ... 34 0.64
emb|AW702543|AW702543 TgESTzz85a12.y1 TgRH*-Tachyzoite cDNA Toxo... 32 0.69
emb|AZ214873|AZ214873 Sheared DNA-109E2.TR Sheared DNA Trypanoso... 37 0.74
emb|AQ939979|AQ939979 Sheared DNA-42A15.TF Sheared DNA Trypanoso... 37 0.74
emb|AQ651205|AQ651205 Sheared DNA-30N15.TF Sheared DNA Trypanoso... 37 0.74
55 emb|AQ945454|AQ945454 Sheared DNA-54H22.TF Sheared DNA Trypanoso... 37 0.74
emb|AW774740|AW774740 EST333891 KV3 Medicago truncatula cDNA clo... 36 1.4
emb|Z38060|SC5610 S.cerevisiae chromosome IX sequence derived fr... 36 1.4
emb|AL049183|PFMAL13P6 Plasmodium falciparum chromosome 13 strai... 35 2.6
gb|M28064|PFAHRKP Plasmodium brasilianum DNA homologous to the h... 35 2.6
60 emb|AI482770|AI482770 EST242093 tomato shoot, Cornell Lycopersic... 35 2.6
emb|AQ653909|AQ653909 Sheared DNA-1G20.TR Sheared DNA Trypanosom... 35 2.6

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 5 factor [arabidopsis thaliana] /blast_score 3.00e-94
 (938 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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15 gb U68763 GMU68763 Glycine max putative transcription factor SCO...	71	1e-35
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emb AF053077 AF053077 Nicotiana tabacum osmotic stress-induced z...	70	3e-33
emb AW729218 AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ...	71	5e-33
20 emb AW781249 AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone...	70	7e-31
dbj D26086 PETZFP4 Petunia zinc-finger protein gene.	68	3e-30
emb AW560934 AW560934 EST315982 DSIR Medicago truncatula cDNA cl...	68	8e-30
emb AW775559 AW775559 EST334624 DSIL Medicago truncatula cDNA cl...	70	1e-29
gb BE123920 BE123920 EST394045 DSIL Medicago truncatula cDNA clo...	70	1e-29
25 emb AI988657 AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone...	70	9e-29
emb AW102472 AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone...	64	1e-28
dbj D26084 PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro...	69	1e-28
dbj D26083 PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin...	68	4e-28
emb AI988290 AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone...	64	3e-27
30 emb AW706944 AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone...	69	2e-26
emb AW153229 AW153229 se37f05.y1 Gm-c1015 Glycine max cDNA clone...	69	3e-26
emb AW616587 AW616587 EST322998 L. hirsutum trichome, Cornell Un...	68	5e-26
gb BE095284 BE095284 00345 leafy spurge Lambda HybriZAP 2.1 two-...	69	5e-26
emb AW278572 AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone...	65	8e-26
35 emb AI487287 AI487287 EST245609 tomato ovary, TAMU Lycopersicon ...	68	9e-26
dbj D26085 PETZFDB3 Petunia zinc-finger DNA binding protein gene.	60	1e-25
emb AI778714 AI778714 EST259593 tomato susceptible, Cornell Lyco...	68	1e-25
emb AW279005 AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone...	67	2e-25
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40 emb AF119050 AF119050 Datisca glomerata zinc-finger protein 1 (z...	71	2e-25
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gb U76554 BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR...	63	9e-25
gb U76555 BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA...	62	3e-24
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45 emb AW034622 AW034622 EST278306 tomato callus, TAMU Lycopersicon...	62	6e-24
emb AI488218 AI488218 EST246540 tomato ovary, TAMU Lycopersicon ...	62	9e-24
emb AW037956 AW037956 EST279600 tomato mixed elicitor, BTI Lycop...	59	4e-23
emb Y16131 Y16131 Y16131 young root nodules Medicago sativa subs...	67	8e-23
emb AW030858 AW030858 EST274148 tomato callus, TAMU Lycopersicon...	66	9e-23
50 emb AW032112 AW032112 EST275566 tomato callus, TAMU Lycopersicon...	68	5e-22
emb AW625323 AW625323 EST319146 tomato radicle, 5 d post-imbibit...	59	8e-21
emb AW033257 AW033257 EST276828 tomato callus, TAMU Lycopersicon...	66	2e-20
emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon ...	62	2e-20
emb AW033574 AW033574 EST277145 tomato callus, TAMU Lycopersicon...	66	2e-20
55 emb AI896031 AI896031 EST265474 tomato callus, TAMU Lycopersicon...	66	3e-20
emb AI771191 AI771191 EST252387 tomato ovary, TAMU Lycopersicon ...	66	3e-20
emb AW032357 AW032357 EST275811 tomato callus, TAMU Lycopersicon...	66	3e-20
emb AW219736 AW219736 EST302218 tomato root during/after fruit s...	59	1e-19
emb AW219517 AW219517 EST301915 tomato root during/after fruit s...	59	2e-19
60 emb AW706014 AW706014 sk64g01.y1 Gm-c1016 Glycine max cDNA clone...	69	1e-18
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5	emb AW648971 AW648971 EST327425 tomato germinating seedlings, TA...	59 9e-17
	emb AB000455 AB000455 Petunia hybrida mRNA for PETHy;ZPT4-1, com...	60 1e-16
	gb BE058334 BE058334 sn14g01.yl Gm-c1016 Glycine max cDNA clone ...	62 1e-16
	emb AW035987 AW035987 EST282846 tomato callus, TAMU Lycopersicon...	55 2e-16
	emb AV422432 AV422432 AV422432 Lotus japonicus young plants (two...	66 3e-16
10	emb AW277333 AW277333 sf80a11.yl Gm-c1019 Glycine max cDNA clone...	64 4e-16
	emb AI900061 AI900061 sb98d02.yl Gm-c1012 Glycine max cDNA clone...	64 5e-16
	emb AW684558 AW684558 NF018C10NR1F1000 Nodulated root Medicago t...	63 6e-16
	emb AI960244 AI960244 sc80g07.yl Gm-c1018 Glycine max cDNA clone...	64 7e-16
	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	62 1e-15
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	emb AI894999 AI894999 EST264442 tomato callus, TAMU Lycopersicon...	68 9e-15
	emb AW622660 AW622660 EST313460 tomato root during/after fruit s...	68 9e-15
	emb AW755973 AW755973 sl11h06.yl Gm-c1036 Glycine max cDNA clone...	64 4e-14
	emb AI938565 AI938565 sb55e03.yl Gm-c1018 Glycine max cDNA clone...	64 4e-14
20	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge...	52 1e-13
	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet...	52 1e-13
	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge...	50 4e-13
	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple...	50 4e-13
	emb AB006606 AB006606 Petunia x hybrida mRNA for ZPT4-4, complet...	51 8e-13
25	emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root Medicago t...	54 8e-13
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	emb AB006601 AB006601 Petunia x hybrida mRNA for ZPT2-14, comple...	50 7e-12
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45	dbj D16415 WHTWZF1A Wheat gene for WZF1, complete cds.	56 1e-11
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50	emb AI775063 AI775063 EST256163 tomato resistant, Cornell Lycopen...	59 2e-11
	emb AI484099 AI484099 EST249970 tomato ovary, TAMU Lycopersicon ...	59 2e-11
	emb AW738399 AW738399 EST339826 tomato flower buds, anthesis, Co...	59 2e-11
	emb AB006602 AB006602 Petunia x hybrida mRNA for ZPT2-7, complet...	49 2e-11
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60 (1352 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

	emb AJ000728 LEAJ728 Lycopersicon esculentum mRNA for MAP kinase...	555	e-157
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	emb AW756736 AW756736 sl26f02.y1 Gm-cl027 Glycine max cDNA clone...	174	9e-75
	dbj D31964 TOBNPK2 Tobacco mRNA for protein kinase (NPK2), compl...	183	8e-65
	gb BE054500 BE054500 GA_Ea0031F11f Gossypium arboreum 7-10 dpa ...	165	1e-59
15	emb AW220008 AW220008 EST302491 tomato root during/after fruit s...	228	6e-59
	emb AW624623 AW624623 EST322568 tomato flower buds 3-8 mm, Corne...	215	9e-55
	emb AI438023 AI438023 sa34h10.y1 Gm-cl004 Glycine max cDNA clone...	208	7e-53
	emb AW617901 AW617901 EST296829 L. hirsutum trichome, Cornell Un...	203	2e-51
	emb AJ007393 YLI7393 Yarrowia lipolytica ste7 gene.	92	4e-49
20	emb AW931392 AW931392 EST357235 tomato fruit mature green, TAMU ...	189	3e-47
	emb AW039087 AW039087 EST281060 tomato mixed elicitor, BTI Lycop...	183	2e-45
	emb Z99259 SPAC2C4 S.pombe chromosome I cosmid c2C4.	85	6e-43
	emb AW032808 AW032808 EST276367 tomato callus, TAMU Lycopersicon...	175	9e-43
	gb U07801 UMU07801 Ustilago maydis serine/threonine/tyrosine kin...	121	2e-42
25	emb AJ009609 BNA9609 Brassica napus mRNA for MAP4K alpha2 protein.	87	1e-41
	dbj D13001 YSCSSP32 Yeast Mkk1/SSP32 gene for Mkk1 protein kinas...	72	3e-41
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35	gb L19195 YASTKIN Candida albicans (clone pKB66) serine/threoni...	128	2e-37
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45	gb U12237 SCU12237 Saccharomyces cerevisiae suppressor of fluori...	78	5e-35
	gb J02946 YSCPBS2 Saccharomyces cerevisiae putative protein kina...	78	5e-35
	emb AJ243184 LIN243184 Leishmania infantum mkk gene for putative...	78	2e-34
	emb AW032663 AW032663 EST276222 tomato callus, TAMU Lycopersicon...	82	2e-34
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- emb|AF069777|AF069777 *Cryptonectria parasitica* mitogen-activated... 66 2e-30
 emb|AW099876|AW099876 sd17g06.y2 *Gm-c1012* Glycine max cDNA clone... 80 3e-30
 emb|AF249887|AF249887 *Pneumocystis carinii* map kinase kinase (mk... 72 6e-30
 emb|AW622016|AW622016 EST312814 tomato root during/after fruit s... 97 7e-29
 5 emb|Z69239|SPAC1D4 *S.pombe* chromosome I cosmid c1D4. 116 2e-28
 emb|X07445|SPBYR1 *Fission yeast* byr1 gene. 116 2e-28
 emb|Z67750|SC41KCIV *S.cerevisiae* DNA (cosmid 31A2; chromosome IV... 77 7e-28
 emb|X97751|SCIV23 *S.cerevisiae* chrIV genes STE7, CLB3, MSH5, RPC... 77 7e-28
 emb|Z74207|SCYDL159W *S.cerevisiae* chromosome IV reading frame OR... 77 8e-28
 10 gb|M14097|YSCSTE7 *Yeast (S.cerevisiae)* regulatory gene STE7, com... 77 8e-28
 dbj|D26601|TOBPK Tobacco mRNA for protein kinase, complete cds. 54 1e-27
 dbj|E05289|E05289 DNA encoding a protein kinase that is homologo... 54 1e-27
 emb|AL358652|LMFP1408 *Leishmania major* Friedlin chromosome 14 PA... 100 3e-27
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 15 emb|AF169643|AF169643 *Glomerella cingulata* MAP kinase (EM... 74 5e-27
 emb|AQ849880|AQ849880 LMAJFV1_lm51a11.x1 *Leishmania major* FV1 ra... 104 1e-26
 emb|AW564378|AW564378 LG1_292_H08.b1_A002 Light Grown 1 (LG1) So... 121 1e-26
 emb|AC005140|AC005140 *Plasmodium falciparum* chromosome 12 clone ... 88 2e-26
 emb|AW030150|AW030150 EST273405 tomato callus, TAMU Lycopersicon... 120 3e-26
 20 emb|Z28126|SCYKL126W *S.cerevisiae* chromosome XI reading frame OR... 84 5e-26
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 gb|M24929|YSCYKR2A *Saccharomyces cerevisiae* protein kinase (YKR2... 85 9e-26
 25 emb|AI779511|AI779511 EST260390 tomato susceptible, Cornell Lyco... 118 1e-25
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 gb|L04655|YSCSERKIN *Saccharomyces cerevisiae* serine/threonine ki... 86 2e-25
 30 emb|AW922296|AW922296 DG1_17_G11.g1_A002 Dark Grown 1 (DG1) Sorg... 116 4e-25
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 40 gb|U73457|CAU73457 *Candida albicans* Cst20p (CST20) gene, complet... 86 8e-24
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 gb|U22371|SPU22371 *Schizosaccharomyces pombe* Pak1p (PAK1) mRNA, ... 87 5e-23
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 (930 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

	Sequences producing significant alignments:	(bits)	Value
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	emb AW622008 AW622008 EST312806 tomato root during/after fruit s...	287	2e-76
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15	emb AW775898 AW775898 EST334963 DSIL <i>Medicago truncatula</i> cDNA cl...	243	2e-71
	emb AW774377 AW774377 EST333528 KV3 <i>Medicago truncatula</i> cDNA clo...	242	4e-71
	emb AW620616 AW620616 sj07e05.y1 Gm-c1032 <i>Glycine max</i> cDNA clone...	230	3e-69
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	emb AI938231 AI938231 sc41d07.y1 Gm-c1014 <i>Glycine max</i> cDNA clone...	184	2e-45
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Database: plantfungal
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 60 emb|X98582|TAX98582 T.aestivum mRNA for HSP80-2 protein. 572 0.0
 emb|X63195|NTHSP82 N.tabacum mRNA for heat shock protein 82. 601 0.0

- emb|AF123259|AF123259 *Lycopersicon esculentum* heat shock protein... 483 0.0
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5 gb|M57386|THEHSP90 *T. parva* heat shock protein 90 (hsp90) mRNA, c... 500 0.0
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15 emb|AF212996|AF212996 *Neurospora crassa* heat shock protein 80 ge... 473 e-165
emb|AL110469|SPAC926 *S. pombe* chromosome I cosmid c926. 460 e-165
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30 emb|AW982575|AW982575 HVSMeg0003K07f *Hordeum vulgare* pre-anthesi... 471 e-131
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50 emb|AW011081|AW011081 ST16E03 Pine TriplEx shoot tip library Pin... 421 e-116
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Database: plantfungal
30 661,018 sequences; 426,114,510 total letters

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| | emb X07280 NPGLUCB Nicotiana plumbaginifolia mRNA for beta-glucan... | 265 | e-106 | | |
| | gb U49454 PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene... | 292 | e-106 | | |
| | gb M23120 TOBGLUCB2 Tobacco (N.plumbaginifolia) beta-glucanase m... | 265 | e-105 | | |
| 35 | emb AJ277900 VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas... | 284 | e-104 | | |
| | dbj E03985 E03985 DNA encoding beta-1,3-endoglucanase. | 226 | e-100 | | |
| | dbj E02108 E02108 cDNA sequence coding for beta-1,3-endoglucanase. | 226 | e-100 | | |
| | gb M37753 SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple... | 226 | e-100 | | |
| | gb U41323 GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c... | 171 | e-100 | | |
| 40 | emb X77990 BCBGL B.campestris (Just Right) bgl mRNA. | 133 | 1e-99 | | |
| | gb U01901 U01901 Solanum tuberosum Datura endo-1,3-beta-D-glucan... | 209 | 8e-99 | | |
| | gb M80608 TOMB13GLUB Lycopersicon esculentum beta-1,3-glucanase ... | 210 | 1e-98 | | |
| | emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl... | 289 | 1e-98 | | |
| | emb AJ000081 CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. | 99 | 2e-98 | | |
| 45 | gb U22147 HBU22147 Hevea brasiliensis beta-1,3-glucanase (HGN1) ... | 265 | 1e-95 | | |
| | emb X54456 NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana... | 106 | 3e-95 | | |
| | emb AF067863 AF067863 Solanum tuberosum 1,3-beta-glucan glucanoh... | 210 | 6e-95 | | |
| | gb U01900 U01900 Solanum tuberosum Datura endo-1,3-beta-D-glucan... | 210 | 8e-95 | | |
| | emb AJ133470 HBR133470 Hevea brasiliensis mRNA for beta-1,3-gluc... | 262 | 1e-94 | | |
| 50 | gb M60402 TOBGLA13B Nicotiana tabacum glucan beta-1,3-glucanase ... | 208 | 9e-94 | | |
| | emb X53600 NTGLN2G Tobacco gln2 gene for beta -1,3-glucanase. | 208 | 9e-94 | | |
| | emb A26453 A26453 Recombinant soya beta-1,3-glucanase plasmid. | 244 | 3e-93 | | |
| | emb A26449 A26449 Soya mutant beta-1,3-glucanase cDNA. | 244 | 3e-93 | | |
| | emb A26447 A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f... | 244 | 3e-93 | | |
| 55 | emb Z68154 GHBGLUCS G.hirsutum mRNA for 1,3-beta-glucanase. | 174 | 3e-93 | | |
| | gb M60403 TOBGLB13B Nicotiana tabacum glucan beta-1,3-glucosidas... | 207 | 3e-93 | | |
| | emb X54742 NPB13GG Nicotiana plumbaginifolia beta-(1,3)-glucanas... | 205 | 4e-93 | | |
| | gb M59442 TOBGLUCA N.tabacum basic-1,3-glucanase gene, complete cds. | 204 | 1e-92 | | |
| | emb A16121 A16121 Intracellular Beta-1, 3 glucanase gene (SEQ ID... | 204 | 1e-92 | | |
| 60 | emb A26451 A26451 Soya beta-1,3-glucanase plasmid pBR59 NdeI-Hin... | 244 | 3e-92 | | |
| | emb X53129 PV13BDGL P. vulgaris mRNA for 1,3-beta-D-glucanase. | 240 | 6e-91 | | |

- emb|X74905|LEQA *L. esculentum* TomQ'a mRNA for beta(1,3)glucanase. 105 2e-90
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 5 emb|X74906|LEQB *L. esculentum* TomQ'b mRNA for beta(1,3)glucanase. 110 1e-86
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 emb|AF004838|AF004838 *Musa acuminata* beta-1,3-glucanase mRNA, pa... 148 7e-86
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 10 gb|S51479|S51479 beta-1,3-glucanase [*Pisum sativum*=peas, cultiva... 180 2e-85
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 25 gb|M20618|TOBGLUBA *N. tabacum* beta-1,3-glucanase mRNA, clones pGL... 207 9e-73
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 30 emb|X52572|HVBDG Barley DNA for (1-3,1-4)-beta-D-glucanase (EC 3... 158 1e-69
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 35 emb|AF034107|AF034107 *Glycine max* beta-1,3-glucanase 2 (SGlu2) g... 122 2e-67
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 50 gb|M62907|BLYCBGL32 *H. vulgare* L. (1-3)-beta-glucanase mRNA, comp... 92 2e-60
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	dbj D38123 TOBBY4A Nicotiana tabacum mRNA for ERF1, complete cds.	134	6e-41	
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Database: plantfungal
15 661,018 sequences; 426,114,510 total letters

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20 Sequences producing significant alignments: (bits) Value

emb|AB000408|AB000408 Populus kitakamiensis mRNA for caffeoyl-Co... 215 3e-73
gb|U20736|MSU20736 Medicago sativa S-adenosyl-L-methionine:trans... 142 2e-68
emb|AW624860|AW624860 EST313689 tomato radicle, 5 d post-imbibit... 139 2e-67
25 emb|AF022775|AF022775 Nicotiana tabacum caffeoyl-CoA 3-O-methyl... 138 2e-67
emb|Z54233|VVCCOAMT V.vinifera mRNA for caffeoyl-CoA O-methyltr... 136 9e-67
gb|M69184|PUMCCOAMT Petroselinum crispum caffeoyl-CoA 3-O-methyl... 133 2e-66
gb|U27116|PTU27116 Populus tremuloides caffeoyl-CoA 3-O-methyltr... 135 3e-66
emb|AJ224894|PBT AJ4894 Populus balsamifera subsp. trichocarpa mR... 135 3e-66
30 gb|U13151|ZEU13151 Zinnia elegans S-adenosyl-L-methionine:trans-... 136 4e-66
emb|AI489305|AI489305 EST247644 tomato ovary, TAMU Lycopersicon ... 139 4e-66
emb|AJ224895|PBT AJ4895 Populus balsamifera subsp. trichocarpa mR... 136 6e-66
emb|AJ224896|PBT AJ4896 Populus balsamifera subsp. trichocarpa mR... 136 6e-66
emb|AF168780|AF168780 Eucalyptus globulus caffeoyl-CoA O-methyl... 133 8e-66
35 emb|AF053553|AF053553 Mesembryanthemum crystallinum caffeoyl-CoA... 132 1e-65
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emb|A22706|A22706 Caffeoyl-CoA-3-O-Methyltransferase gene. 129 3e-65
gb|U62734|NTU62734 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 134 5e-65
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45 gb|U62735|NTU62735 Nicotiana tabacum caffeoyl-CoA O-methyltransf... 134 3e-64
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5 emb|AW030736|AW030736 EST273991 tomato callus, TAMU Lycopersicon... 133 8e-53
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15 emb|AI898952|AI898952 EST268395 tomato ovary, TAMU Lycopersicon ... 139 2e-51
emb|AW424002|AW424002 sh59c10.y1 Gm-c1015 Glycine max cDNA clone... 115 2e-51
emb|AW707192|AW707192 sk22a02.y1 Gm-c1028 Glycine max cDNA clone... 132 3e-50
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emb|AW980337|AW980337 EST391490 GVN Medicago truncatula cDNA clo... 127 3e-50
20 emb|AW648499|AW648499 EST326953 tomato germinating seedlings, TA... 99 7e-50
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25 emb|AW684885|AW684885 NF022F07NR1F1000 Nodulated root Medicago t... 142 2e-47
emb|AA660318|AA660318 00189 MtRHE Medicago truncatula cDNA 5' si... 144 2e-47
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30 emb|AW620537|AW620537 sj06d09.y1 Gm-c1032 Glycine max cDNA clone... 133 1e-46
emb|AI775483|AI775483 EST256583 tomato resistant, Cornell Lycop... 139 2e-46
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45 gb|BE059325|BE059325 sn31c09.y1 Gm-c1016 Glycine max cDNA clone ... 140 3e-43
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50 emb|AW774697|AW774697 EST333848 KV3 Medicago truncatula cDNA clo... 84 8e-42
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55 emb|AI488060|AI488060 EST246382 tomato ovary, TAMU Lycopersicon ... 100 7e-41
emb|AW622558|AW622558 EST313358 tomato root during/after fruit s... 139 1e-40
emb|AW625461|AW625461 EST319368 tomato radicle, 5 d post-imbibit... 99 1e-40
emb|AW625476|AW625476 EST319383 tomato radicle, 5 d post-imbibit... 139 3e-40
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60 emb|Z82982|NTZ82982 N.tabacum mRNA for caffeoyl-CoA O-methyltran... 136 1e-39
emb|AW218486|AW218486 EST303669 tomato radicle, 5 d post-imbibit... 136 1e-39

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Database: plantfungal
 10 661,018 sequences; 426,114,510 total letters

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	emb AJ012689 CAR012689 Cicer arietinum mRNA for ribonuclease T2.	384	e-106	
	gb U13256 NAU13256 Nicotiana glauca RNase NE mRNA, complete cds.	361	4e-99	
	gb U19924 ZEU19924 Zinnia elegans wounding-induced ribonuclease ...	358	4e-98	
20	emb AB034638 AB034638 Nicotiana glauca mRNA for RNase, complete...	353	1e-96	
	emb X79337 LERNAL L. esculentum mRNA for ribonuclease le.	212	2e-93	
	dbj D49529 D49529 Pyrus pyrifolia mRNA for ribonuclease, complet...	335	4e-91	
	emb AI486253 AI486253 EST244574 tomato ovary, TAMU Lycopersicon ...	212	2e-89	
	emb AI485206 AI485206 EST243510 tomato ovary, TAMU Lycopersicon ...	212	1e-81	
25	gb U19923 ZEU19923 Zinnia elegans ribonuclease mRNA, complete cds.	232	3e-80	
	emb X79338 LERNALX L. esculentum mRNA for ribonuclease lx.	177	1e-73	
	emb AB032257 AB032257 Nicotiana glauca NGR3 mRNA for RNase NG...	176	7e-70	
	emb AI484830 AI484830 EST243091 tomato ovary, TAMU Lycopersicon ...	212	7e-70	
	emb AW684365 AW684365 NF016B03NR1F1000 Nodulated root Medicago t...	251	7e-66	
30	emb AI489460 AI489460 EST247799 tomato ovary, TAMU Lycopersicon ...	212	3e-63	
	emb Y17444 LES17444 Lycopersicon esculentum RNALX gene, exons 1 ...	152	2e-57	
	emb AI772676 AI772676 EST253776 tomato resistant, Cornell Lycopersicon ...	152	2e-57	
	emb AI775352 AI775352 EST256452 tomato resistant, Cornell Lycopersicon ...	212	3e-56	
	gb BE037115 BE037115 MP15C03 MP Mesembryanthemum crystallinum cD....	153	4e-55	
35	emb AF000939 AF000939 Hordeum vulgare aleurone ribonuclease mRNA...	89	7e-55	
	gb M83668 NELSTORAGE Nelumbo nucifera storage protein mRNA, comp...	127	2e-54	
	emb AI812905 AI812905 22D1 Pine Lambda Zap Xylem library Pinus t...	165	3e-54	
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	emb AF000940 AF000940 Hordeum vulgare ribonuclease gene, complet...	116	2e-44	
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	emb AI777654 AI777654 EST258449 tomato susceptible, Cornell Lycopersicon ...	152	2e-41	
45	emb AW596890 AW596890 sj84b03.y1 Gm-cl034 Glycine max cDNA clone...	162	3e-39	
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	gb BE060590 BE060590 HVSMEg0012L10f Hordeum vulgare pre-anthesis...	89	2e-36	
	emb AW704136 AW704136 sk16e03.y1 Gm-cl028 Glycine max cDNA clone...	145	4e-34	
	emb AW289659 AW289659 NXNV003D07F Nsf Xylem Normal wood Vertical...	109	8e-32	
50	gb U19794 MDU19794 Malus domestica S-like RNase gene, partial cds.	76	2e-25	
	emb AI967855 AI967855 Ljimp14-054-a9 Ljimp Lambda HybriZap ...	109	4e-23	
	emb Y17446 LES17446 Lycopersicon esculentum RNALX gene, exons 1 ...	104	1e-21	
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	emb AW053670 AW053670 L30-1447T3 Ice plant Lambda Uni-Zap XR exp...	45	2e-20	
55	gb BE020073 BE020073 sm38f09.y1 Gm-cl028 Glycine max cDNA clone ...	45	7e-20	
	emb AW039494 AW039494 EST281775 tomato mixed elicitor, BTI Lycopersicon ...	43	6e-19	
	emb AW216541 AW216541 EST295255 tomato callus, TAMU Lycopersicon ...	43	6e-19	
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	emb AB026836 AB026836 Prunus dulcis mRNA for Sa-RNase, complete ...	76	1e-18	
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	gb BE124916 BE124916 EST393951 GVN Medicago truncatula cDNA clon...	44	4e-18	

- emb|AB032256|AB032256 *Nicotiana glutinosa* NGR2 mRNA for RNase NG... 41 9e-18
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5 emb|AW926310|AW926310 HVSMEg0006001 *Hordeum vulgare* pre-anthesis... 52 4e-17
emb|AB034248|AB034248 *Volvox carteri* vrn1 mRNA for S-like RNase,... 58 8e-17
emb|AF176533|AF176533 *Solanum chacoense* self-incompatibility rib... 82 2e-16
emb|AI416638|AI416638 sa17c06.y1 Gm-c1004 *Glycine max* cDNA clone... 45 6e-16
emb|X96465|AHS2RNASE *A.hispanicum* mRNA for S2-Rnase. 60 2e-15
10 emb|AB028153|AB028153 *Prunus avium* mRNA for S1-RNase, complete cds. 56 3e-15
emb|AW223027|AW223027 EST299838 tomato fruit red ripe, TAMU Lyco... 43 4e-15
emb|AW224120|AW224120 EST300931 tomato fruit red ripe, TAMU Lyco... 43 5e-15
emb|AW223831|AW223831 EST300642 tomato fruit red ripe, TAMU Lyco... 43 5e-15
emb|AF191732|AF191732 *Solanum chacoense* self-incompatibility rib... 82 6e-15
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15 emb|X76065|LPSRNASE *L.peruvianum* mRNA for S-RNase S3. 60 2e-14
emb|AB010304|AB010304 *Prunus avium* mRNA for S2-RNase, partial cds. 60 4e-14
emb|AI729649|AI729649 BNLGH13860 Six-day Cotton fiber *Gossypium*... 45 9e-14
emb|AI729386|AI729386 BNLGH13239 Six-day Cotton fiber *Gossypium*... 45 1e-13
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25 emb|AW623083|AW623083 EST321028 tomato flower buds 3-8 mm, *Corne*... 43 8e-13
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emb|Z26583|LPSLGS6 *L.peruvianum* (Mill) self-incompatibility glyc... 56 1e-12
emb|AB011471|AB011471 *Prunus dulcis* mRNA for Sd-RNase, partial cds. 57 1e-12
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dbj|E01266|E01266 cDNA encoding S2-protein linked to part of its... 56 1e-11
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45 emb|X96466|AHS4RNASE *A.hispanicum* mRNA for S4-Rnase. 46 7e-11
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50 emb|AI460477|AI460477 sa79g07.y1 Gm-c1004 *Glycine max* cDNA clone... 42 3e-10
emb|Z26582|LPSLGS7 *L.peruvianum* (Mill) self-incompatibility glyc... 61 3e-10
dbj|D63887|D63887 *Nicotiana alata* mRNA for ribonuclease, complet... 61 3e-10
emb|AF105363|AF105363 *Lycium andersonii* self-incompatibility rib... 66 4e-10
gb|U07362|PHU07362 *Petunia hybrida* S1 self-incompatibility ribon... 62 4e-10
55 gb|L40542|POTDSCS *Solanum carolinense* self-incompatibility ribon... 65 7e-10

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(1480 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	emb AI776928 AI776928 EST258028 tomato resistant, Cornell Lycope... 174 1e-42	
	emb AW441294 AW441294 EST310690 tomato fruit red ripe, TAMU Lyco... 88 9e-42	
	emb AW035369 AW035369 EST280931 tomato callus, TAMU Lycopersicon... 88 3e-35	
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	gb BE058288 BE058288 sn14b07.y1 Gm-cl016 Glycine max cDNA clone ... 88 2e-34	
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20	emb AW761120 AW761120 sl63e05.y1 Gm-cl027 Glycine max cDNA clone... 127 9e-32	
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40	emb AW034079 AW034079 EST277574 tomato callus, TAMU Lycopersicon... 77 3e-13	
	emb AW991119 AW991119 SsS0174 Suaeda salsa ZAP cDNA library Suac... 58 7e-10	
	emb X95732 NPZEAXANT N.plumbaginifolia mRNA for zeaxanthin epoxi... 63 6e-09	
	emb AV418279 AV418279 AV418279 Lotus japonicus young plants (two... 48 8e-09	
	emb X91491 CAXANEPOX C.annuum mRNA for xanthophyll epoxidase. 61 2e-08	
45	emb J83835 LEZEAXAN L.esculentum mRNA for zeaxanthin epoxidase. 59 1e-07	
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	emb AF071888 AF071888 Prunus armeniaca zeaxanthin epoxidase (ZEA... 54 3e-06	
	dbj D38415 AED4ABH Agaricus bisporus DNA for 4-aminobenzoate hyd... 47 3e-04	
50	emb AQ274524 AQ274524 mgxb0022E01r CUGI Rice Blast BAC Library P... 47 3e-04	
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	emb Z35859 SCYBL098W S.cerevisiae chromosome II reading frame OR... 39 0.12	
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	gb U35892 NHU35892 Nectria haematococca maackiain detoxification... 36 0.80	

- emb|AI496271|AI496271 sb01f06.y1 Gm-c1004 Glycine max cDNA clone... 36 0.80
 emb|AJ223325|CRAJ3325 Chlamydomonas reinhardtii mRNA for ascorba... 35 1.1
 emb|AW185727|AW185727 se58h04.y1 Gm-c1019 Glycine max cDNA clone... 35 1.5
 emb|AW279175|AW279175 sf67d04.y1 Gm-c1013 Glycine max cDNA clone... 35 1.5
 5 emb|AF211986|AF211986 Acleisanthes anisophylla 18S ribosomal RNA... 35 1.5
 emb|AW348744|AW348744 GM210003A22C7R Gm-r1021 Glycine max cDNA 3... 35 2.1
 emb|AZ217020|AZ217020 Sheared DNA-75G4.TF Sheared DNA Trypanosom... 35 2.1
 emb|X80690|SCDNASEQ S.cerevisiae DNA sequence. 35 2.1
 emb|Z73040|SCYGR255C S.cerevisiae chromosome VII reading frame O... 35 2.1
 10 emb|AW680385|AW680385 WS1_52_D05.g1_A002 Water-stressed 1 (WS1) ... 35 2.1
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 emb|AW311010|AW311010 sg31e02.x1 Gm-c1024 Glycine max cDNA clone... 35 2.1
 emb|AL114377|CNS01BLD Botrytis cinerea strain T4 cDNA library un... 35 2.1
 15 gb|BE122310|BE122310 894019A08.y1 C. reinhardtii CC-1690, normal... 35 2.1
 emb|AF003698|AF003698 Saccharomyces cerevisiae COQ6 monooxygenas... 35 2.1
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 emb|AJ011587|KLA011587 Kluyveromyces lactis mufl gene. 34 2.9
 20 emb|AI068756|AI068756 mgae0004aD11f Magnaporthe grisea Appressor... 34 2.9
 emb|AW286092|AW286092 LG1_261_C09.b1_A002 Light Grown 1 (LG1) So... 34 2.9
 emb|AW925351|AW925351 HVSMEg0001B14 Hordeum vulgare pre-anthesis... 34 2.9
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 30 emb|AW477291|AW477291 ga44f01.y1 Moss EST library PPU Physcomitr... 34 3.9
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 35 emb|AF008953|AF008953 Octomeles sumatrana 18S ribosomal RNA gene... 34 3.9
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 gb|M62862|TRBRTE Trypanosoma cruzi retrotransposon encoding gag ... 33 5.4
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- emb|AI896318|AI896318 EST265761 tomato callus, TAMU Lycopersicon... 182 5e-65
emb|A67797|A67797 Sequence 2 from Patent WO9743427. 128 5e-51
gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor-... 128 5e-51
5 emb|AW432288|AW432288 sh71g05.y1 Gm-c1015 Glycine max cDNA clone... 200 5e-50
emb|AI730535|AI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ... 152 1e-49
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emb|AF085166|AF085166 Hordeum vulgare receptor-like kinase gene,... 86 2e-45
emb|AF085167|AF085167 Hordeum vulgare receptor-like kinase ARK1A... 85 3e-45
10 gb|U51330|TAU51330 Triticum aestivum leaf rust resistance kinase... 82 8e-45
emb|AF100771|AF100771 Hordeum vulgare receptor-like kinase (Hv3A... 100 2e-44
gb|U78762|TAU78762 Triticum aestivum receptor-like kinase ARK1AS... 86 2e-44
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15 emb|AF085164|AF085164 Hordeum vulgare receptor-like kinase LRK10... 82 2e-43
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20 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 123 8e-42
emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 87 2e-41
dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 84 2e-41
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30 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 78 5e-39
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emb|AW621706|AW621706 EST312504 tomato root during/after fruit s... 122 1e-38
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35 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 84 2e-38
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40 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 82 3e-38
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45 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 81 6e-38
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55 emb|AW030223|AW030223 EST273478 tomato callus, TAMU Lycopersicon... 92 2e-36
emb|AW929662|AW929662 EST338450 tomato flower buds 8 mm to pre-a... 118 2e-36
emb|AW704997|AW704997 sk41c03.y1 Gm-c1019 Glycine max cDNA clone... 89 2e-36
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60 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 82 4e-36
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- emb|AW687349|AW687349 NF008F08RT1F1074 Developing root Medicago ... 80 9e-36
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 10 emb|AW597214|AW597214 si71g06.y1 Gm-cl031 Glycine max cDNA clone... 126 2e-34
 emb|AW092144|AW092144 EST285240 tomato mixed elicitor, BTI Lycop... 122 2e-34
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 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 74 3e-34
 15 emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Corne... 93 3e-34
 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 67 3e-34
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 30 emb|AF197947|AF197947 Glycine max receptor protein kinase-like p... 72 4e-32
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Database: plantfungal

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- emb|AI483399|AI483399 EST241520 tomato shoot, Cornell Lycopersic... 289 2e-89
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 60 emb|AI490817|AI490817 EST241526 tomato shoot, Cornell Lycopersic... 189 3e-71
 emb|AW757393|AW757393 sl32g05.y1 Gm-cl027 Glycine max cDNA clone... 185 8e-63

- emb|AI731648|AI731648 BNLGHi10360 Six-day Cotton fiber *Gossypium*... 182 2e-61
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emb|AW033644|AW033644 EST277215 tomato callus, TAMU *Lycopersicon*... 144 1e-51
emb|AW704608|AW704608 sk54c06.y1 *Gm-c1019 Glycine max* cDNA clone... 153 5e-51
5 emb|AW458875|AW458875 sh16b06.y1 *Gm-c1016 Glycine max* cDNA clone... 113 3e-49
emb|AW648549|AW648549 EST327003 tomato germinating seedlings, TA... 116 3e-48
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10 emb|AI773256|AI773256 EST254356 tomato resistant, Cornell *Lycopersicon*... 99 5e-38
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emb|AW758260|AW758260 874006H11.y1 *C. reinhardtii* CC-1690, Lambd... 132 6e-30
emb|AW564868|AW564868 LG1_310_H09.b1_A002 Light Grown 1 (LG1) *So*... 104 3e-29
15 emb|AL096874|SPBC1539 *S.pombe* chromosome II cosmid c1539. 57 5e-29
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emb|Y09137|SPTRP1 *S.pombe* trp-1 mRNA. 57 1e-28
emb|AW618611|AW618611 EST320597 *L. pennellii* trichome, Cornell U... 82 4e-24
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20 emb|AI490823|AI490823 EST241532 tomato shoot, Cornell *Lycopersicon*... 104 2e-21
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25 emb|X07071|ANTRPC *Aspergillus niger* trpC gene. 64 3e-09
emb|X05033|PCTRPC *Penicillium chrysogenum* trpC gene for put. tri... 62 7e-09
emb|X02390|ANTRPC1 *Aspergillus nidulans* trpC gene. 62 7e-09
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30 emb|A11156|A11156 MOX structural gene and it's 5'and 3'-flanking... 58 1e-07
emb|X02425|HPMOXG *Hansenula polymorpha* MOX gene for methanol oxi... 58 1e-07
emb|X70035|CHTRP1 *C.heterostrophus* gene for trifunctional trypto... 58 2e-07
gb|M64473|PHTTRP1 *Phytophthora parasitica* N-(5'-phosphoribosyl)a... 57 3e-07
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5 (1424 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments:				
15	emb AJ002057 BVMRNAC Beta vulgaris mRNA for calreticulin.	577	e-163	
	emb Z71395 NPCAL1MNR N.plumbaginifolia mRNA for calreticulin.	575	e-163	
	gb U74630 RCU74630 Ricinus communis calreticulin mRNA, complete ...	575	e-163	
	emb AF052040 AF052040 Berberis stolonifera calreticulin mRNA, co...	571	e-162	
	emb X85382 NTRNATCAL N.tabacum mRNA for calreticulin.	570	e-161	
20	emb AF134733 AF134733 Prunus armeniaca calcium-binding protein c...	565	e-160	
	gb L27349 BLYCRH2A Hordeum vulgare calreticulin (CRH2) mRNA, par...	560	e-159	
	gb L27348 BLYCRH1A Hordeum vulgare calreticulin (CRH1) mRNA, par...	560	e-159	
	emb AF019376 AF019376 Brassica napus calreticulin mRNA, complete...	465	e-156	
	emb X80756 CAPCRTC C.annuum PCRTC mRNA.	344	e-154	
25	gb U74631 RCU74631 Ricinus communis calreticulin gene, complete ...	149	e-123	
	emb AJ000765 CRAJ765 Chlamydomonas reinhardtii mRNA for calretic...	369	e-122	
	emb AI728389 AI728389 BNLGHi10665 Six-day Cotton fiber Gossypium...	438	e-122	
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	emb AB018243 AB018243 Solanum melongena EEF22 mRNA for calreticu...	402	e-111	
30	emb AW667951 AW667951 GA__Ea0012A11 Gossypium arboreum 7-10 dpa ...	402	e-111	
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35	emb AW626316 AW626316 EST320223 tomato radicle, 5 d post-imbibit...	375	e-103	
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	emb AW685878 AW685878 NF031C11NRIF1000 Nodulated root Medicago t...	341	6e-93	
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50	emb AW934135 AW934135 EST359978 tomato fruit mature green, TAMU ...	333	2e-90	
	emb AW621571 AW621571 EST312369 tomato root during/after fruit s...	333	2e-90	
	emb Y09816 EGCALRPR E.gracilis mRNA for calreticulin precursor.	257	3e-89	
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	emb AW033447 AW033447 EST277018 tomato callus, TAMU Lycopersicon...	323	2e-87	
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 5 emb|Y09078|DBCALLKPR D.bioculata mRNA for calreticulin-like prot... 225 7e-81
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 10 emb|AW727696|AW727696 GA_Ea0015K01 Gossypium arboreum 7-10 dpa ... 258 8e-79
 emb|AW705880|AW705880 sk52a09.y1 Gm-c1019 Glycine max cDNA clone... 293 2e-78
 emb|AW299150|AW299150 EST305824 KV2 Medicago truncatula cDNA clo... 293 2e-78
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 15 emb|AW933869|AW933869 EST359712 tomato fruit mature green, TAMU ... 287 1e-76
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 20 emb|AW184893|AW184893 se82a03.y1 Gm-c1023 Glycine max cDNA clone... 281 1e-74
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 30 emb|AW648010|AW648010 EST326464 tomato germinating seedlings, TA... 268 7e-71
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 35 emb|AW728940|AW728940 GA_Ea0018J21 Gossypium arboreum 7-10 dpa ... 262 6e-69
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 40 emb|AW649360|AW649360 EST327814 tomato germinating seedlings, TA... 254 1e-66
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 45 emb|AW587738|AW587738 ST66B09 Pine TriplEx shoot tip library Pin... 248 6e-65
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 50 emb|AW760501|AW760501 sl51b04.y1 Gm-c1027 Glycine max cDNA clone... 239 3e-62
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 emb|AF162779|AF162779 Trypanosoma cruzi Tc45-calreticulin precur... 143 2e-60
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60

(757 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

5

Score E

Sequences producing significant alignments: (bits) Value

	gb U70666 BNU70666 Brassica napus pathogenesis-related protein P...	323	3e-89
10	gb U21849 BNU21849 Brassica napus PR-1a (LSC94) mRNA, complete cds.	323	3e-89
	gb U64806 BNU64806 Brassica napus pathogenesis-related protein P...	209	4e-86
	emb AI352851 AI352851 MB69-8A PZ204.BNlib Brassica napus cDNA cl...	311	5e-84
	emb AI352893 AI352893 MB72-6D PZ204.BNlib Brassica napus cDNA cl...	165	3e-62
	emb AW217013 AW217013 EST295727 tomato callus, TAMU Lycopersicon...	152	4e-60
15	emb AW219671 AW219671 EST302153 tomato root during/after fruit s...	151	1e-59
	emb AW092403 AW092403 EST285583 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AI895090 AI895090 EST264533 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW625930 AW625930 EST319825 tomato radicle, 5 d post-imbibit...	151	1e-59
	emb AW032514 AW032514 EST276073 tomato callus, TAMU Lycopersicon...	151	1e-59
20	emb AW034260 AW034260 EST277831 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW040983 AW040983 EST283847 tomato mixed elicitor, BTI Lycop...	151	1e-59
	emb AW034206 AW034206 EST277777 tomato callus, TAMU Lycopersicon...	151	1e-59
	emb AW219480 AW219480 EST301878 tomato root during/after fruit s...	151	1e-59
	emb AW092623 AW092623 EST285803 tomato mixed elicitor, BTI Lycop...	151	1e-59
25	emb AW040954 AW040954 EST283818 tomato mixed elicitor, BTI Lycop...	151	1e-59
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	emb AW032723 AW032723 EST276282 tomato callus, TAMU Lycopersicon...	151	1e-59
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40	emb AW034330 AW034330 EST277901 tomato callus, TAMU Lycopersicon...	144	2e-57
	emb AW622143 AW622143 EST312941 tomato root during/after fruit s...	149	2e-57
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45	emb AI782621 AI782621 EST263500 tomato susceptible, Cornell Lyco...	144	8e-57
	emb AW126362 AW126362 N100469e rootphos(-) Medicago truncatula c...	160	3e-56
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50	emb X14065 NTPRP1 Nicotiana tabacum gene for basic form of patho...	140	5e-55
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	emb AW032727 AW032727 EST276286 tomato callus, TAMU Lycopersicon...	147	1e-53
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55	emb AW053720 AW053720 L30-1612T3 Ice plant Lambda Uni-Zap XR exp...	112	4e-52
	emb AW559969 AW559969 EST315017 DSIR Medicago truncatula cDNA cl...	81	4e-52
	emb AI352801 AI352801 MB61-9C PZ204.BNlib Brassica napus cDNA cl...	194	1e-51
	emb X17681 NTPR1CA Tobacco gene for pathogenesis-related protein...	111	2e-51
	emb X05454 NTPR1CR Nicotiana tabacum mRNA for PR-1c protein.	111	2e-51
60	emb X12487 NTPR1C Tobacco mRNA fragment for pathogenesis-related...	111	2e-51
	emb AJ011520 LES011520 Lycopersicon esculentum pr1a (P4) gene.	98	1e-50

- gb|M69247|TOMPRP4 Lycopersicon esculentum PR (pathogenesis relat... 98 1e-50
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 5 emb|AI896011|AI896011 EST265454 tomato callus, TAMU Lycopersicon... 116 3e-50
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 10 emb|X12737|NTPR1A1 Tobacco PR-1a gene for pathogenesis-related p... 104 4e-50
 emb|X06361|NTPR1AG1 Nicotiana tabacum gene for pathogenesis-rela... 104 4e-50
 emb|X12485|NTPR1A Tobacco mRNA fragment for pathogenesis-related... 104 4e-50
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 emb|X06930|NTPR1AG2 Tobacco PR-1a gene for pathogenesis-related ... 104 7e-50
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 20 emb|AF136636|AF136636 Glycine max PR1a precursor (PR1a) mRNA, co... 110 2e-49
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 25 emb|Y08804|LEPR1B1 L.esculentum mRNA for PR protein. 92 7e-49
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55 Database: plantfungal
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60 Score E
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- emb|AF079872|AF079872 *Nicotiana tabacum* cyclic nucleotide-gated ... 380 0.0
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emb|AJ002610|HVAJ2610 *Hordeum vulgare* mRNA for putative calmodul... 331 0.0
5 emb|AW625647|AW625647 EST319554 tomato radicle, 5 d post-imbibit... 255 6e-82
emb|AW038928|AW038928 EST280884 tomato mixed elicitor, BTI Lycop... 190 2e-80
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emb|AI486671|AI486671 EST244993 tomato ovary, TAMU Lycopersicon ... 241 4e-70
10 emb|AW725576|AW725576 GA_Ea0018M08 *Gossypium arboreum* 7-10 dpa ... 196 3e-69
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emb|AW626197|AW626197 EST320104 tomato radicle, 5 d post-imbibit... 132 1e-49
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40 emb|AW671345|AW671345 LG1_335_D05.b1_A002 Light Grown 1 (LG1) So... 100 2e-30
gb|C95565|C95565 C95565 Citrus unshiu Miyagawa-wase maturation s... 132 1e-29
emb|AW759050|AW759050 sl34a04.y1 Gm-c1027 Glycine max cDNA clone... 129 9e-29
emb|AW286638|AW286638 LG1_335_D05.g1_A002 Light Grown 1 (LG1) So... 127 2e-28
emb|AW831384|AW831384 sm24g05.y1 Gm-c1028 Glycine max cDNA clone... 87 9e-27
45 emb|AW037755|AW037755 EST279384 tomato mixed elicitor, BTI Lycop... 122 1e-26
emb|AW508715|AW508715 si35e10.y1 Gm-r1030 Glycine max cDNA clone... 117 3e-25
emb|AW350588|AW350588 GM210009A10H2R Gm-r1021 Glycine max cDNA 3... 106 1e-24
emb|AW350847|AW350847 GM210009B20G5R Gm-r1021 Glycine max cDNA 3... 106 2e-24
50 emb|AI776960|AI776960 EST251986 tomato callus, TAMU Lycopersicon... 111 2e-23
emb|AW781088|AW781088 sl88h09.y1 Gm-c1037 Glycine max cDNA clone... 111 3e-23
emb|AW039011|AW039011 EST280984 tomato mixed elicitor, BTI Lycop... 111 3e-23
emb|AW617273|AW617273 EST323684 *L. hirsutum* trichome, Cornell Un... 106 7e-22
55 gb|BE022211|BE022211 sm72b10.y1 Gm-c1028 Glycine max cDNA clone ... 106 7e-22
emb|AW668188|AW668188 GA_Ea0013B18 *Gossypium arboreum* 7-10 dpa ... 105 2e-21
emb|AA824914|AA824914 CT202.SK Tomato Leaf cDNA from cv. VFNT ch... 93 6e-21
emb|AT000374|AT000374 AT000374 Apple peel cDNA library *Malus x d*... 102 1e-20
emb|AW623583|AW623583 EST321528 tomato flower buds 3-8 mm, Corne... 69 7e-20
60 emb|AI495394|AI495394 sa97d10.y1 Gm-c1004 Glycine max cDNA clone... 98 2e-19
emb|AI725563|AI725563 BNLGHi12127 Six-day Cotton fiber *Gossypium*... 67 5e-18

emb|AW119379|AW119379 sd45d12.y1 Gm-c1016 Glycine max cDNA clone... 74 3e-17
 emb|AW617083|AW617083 EST323494 L. hirsutum trichome, Cornell Un... 65 7e-17
 emb|AW832684|AW832684 00046 leafy spurge Lambda HybriZAP 2.1 two... 60 4e-12
 5 emb|AI776961|AI776961 EST251987 tomato callus, TAMU Lycopersicon... 67 5e-12
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 emb|AW217336|AW217336 EST296159 tomato flower buds 0-3 mm, Corne... 67 7e-10
 emb|AW688833|AW688833 NF012B10ST1F1000 Developing stem Medicago ... 58 1e-09
 emb|AW164084|AW164084 Ljirnpst19-528-f6 Ljirnp Lambda HybriZap ... 56 1e-06
 10 emb|AJ249962|DCA249962 Daucus carota mRNA for potassium channel ... 55 3e-06
 emb|AW184978|AW184978 se85a09.y1 Gm-c1023 Glycine max cDNA clone... 54 4e-06
 emb|AW091651|AW091651 EST284747 tomato mixed elicitor, BTI Lycop... 51 3e-05
 emb|AW041519|AW041519 EST284383 tomato mixed elicitor, BTI Lycop... 51 3e-05
 emb|AF145272|AF145272 Samanea saman pulvinus inward-rectifying c... 49 1e-04
 gb|BE060413|BE060413 HVSMEg0012D21f Hordeum vulgare pre-anthesis... 38 2e-04
 15 emb|AW928912|AW928912 EST337700 tomato flower buds 8 mm to pre-a... 48 2e-04
 emb|AW756344|AW756344 sl19e03.y1 Gm-c1036 Glycine max cDNA clone... 47 6e-04
 emb|AI494962|AI494962 sa93c01.y1 Gm-c1004 Glycine max cDNA clone... 40 0.001
 emb|AW256509|AW256509 EST304646 KV2 Medicago truncatula cDNA clo... 45 0.003
 gb|U19908|PTU19908 Paramecium tetraurelia K+ channel (PaK2) gene... 42 0.015
 20 emb|AW256736|AW256736 EST304873 KV2 Medicago truncatula cDNA clo... 40 0.016
 emb|AI488021|AI488021 EST246343 tomato ovary, TAMU Lycopersicon ... 42 0.020
 emb|AI729515|AI729515 BNLGHi13574 Six-day Cotton fiber Gossypium... 41 0.027
 emb|AW687023|AW687023 NF005B04RT1F1032 Developing root Medicago ... 39 0.13
 emb|AL163552|LMFL5075 Leishmania major Friedlin chromosome 14 co... 38 0.25
 25 emb|AQ847838|AQ847838 LMAJFV1_lm42a03.y1 Leishmania major FV1 ra... 38 0.25
 emb|AI748348|AI748348 sb51d12.y1 Gm-c1016 Glycine max cDNA clone... 38 0.35
 emb|AL031530|SPCC970 S.pombe chromosome III cosmid c970. 38 0.35
 gb|U33057|SCD9717 Saccharomyces cerevisiae chromosome IV cosmids... 37 0.48
 gb|M84796|YSCEUG1 Saccharomyces cerevisiae endoplasmic reticulum... 37 0.48
 30 emb|AF099095|AF099095 Samanea saman pulvinus inward-rectifying c... 37 0.66
 emb|AI775282|AI775282 EST256382 tomato resistant, Cornell Lycope... 36 0.90
 emb|AF053314|AF053314 Exophiala dermatitidis chitin synthase 3 (... 36 1.2
 emb|AQ947260|AQ947260 Sheared DNA-45L23.TR Sheared DNA Trypanoso... 31 1.5
 emb|AC016528|AC016528 Leishmania major chromosome 35 clone L4123... 35 1.7
 35 emb|AI781524|AI781524 EST262403 tomato susceptible, Cornell Lyco... 31 2.0
 gb|U28374|YSCD9740 Saccharomyces cerevisiae chromosome IV cosmid... 35 2.3
 emb|AW399566|AW399566 EST310066 L. pennellii trichome, Cornell U... 35 2.3
 gb|BE034738|BE034738 ML03G05 ML Mesembryanthemum crystallinum cD... 35 2.3
 40 emb|AW929752|AW929752 EST354022 tomato flower buds 8 mm to pre-a... 35 2.3
 emb|AW648153|AW648153 EST326607 tomato germinating seedlings, TA... 35 2.3
 gb|M74798|HEVHMGR3A Hevea brasiliensis 3-hydroxy-3-methylglutary... 34 4.4
 emb|AW728887|AW728887 GA_Ea0018B11 Gossypium arboreum 7-10 dpa ... 34 4.4
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 45 protein [arabidopsis thaliana] /blast_score 6.00e-99
 (827 letters)
 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
 50 Searching.....done
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 Sequences producing significant alignments: (bits) Value
 55 emb|AI489346|AI489346 EST247685 tomato ovary, TAMU Lycopersicon ... 79 2e-28
 emb|AW350323|AW350323 GM210007B20E12R Gm-r1021 Glycine max cDNA ... 80 2e-27
 emb|AW509006|AW509006 si38h07.y1 Gm-r1030 Glycine max cDNA clone... 79 2e-26
 emb|AW685404|AW685404 NF028H10NR1F1000 Nodulated root Medicago t... 74 2e-24
 60 emb|AW781320|AW781320 sk68d07.y1 Gm-c1016 Glycine max cDNA clone... 86 2e-24
 emb|AI897832|AI897832 EST267275 tomato ovary, TAMU Lycopersicon ... 78 1e-23

- emb|AW102460|AW102460 sd88d10.y1 Gm-c1009 Glycine max cDNA clone... 70 2e-22
emb|AI490284|AI490284 EST248610 tomato ovary, TAMU Lycopersicon ... 103 2e-22
emb|AI487362|AI487362 EST245684 tomato ovary, TAMU Lycopersicon ... 72 3e-20
gb|BE125690|BE125690 DG1_54_A02.g1_A002 Dark Grown 1 (DG1) Sorgh... 96 3e-19
5 emb|X80231|LTCAMA L.tarentolae CAM A gene for calmodulin. 73 1e-18
emb|AL115248|CNS01C9K Botrytis cinerea strain T4 cDNA library un... 65 4e-18
dbj|D10521|TETCALW T.pyriformis mRNA for calmodulin. 73 7e-18
gb|M76407|SLECALMODU Stylonychia lemnae calmodulin gene, complet... 74 9e-18
emb|AF007889|AF007889 Symbiodinium microadriaticum calmodulin (S... 74 1e-17
10 emb|AF078679|AF078679 Olea europaea calcium-binding protein (PCA... 57 2e-17
emb|X56511|TBCALUBG T. brucei genes for calmodulin, EFH5 and ubi... 77 2e-17
emb|X52096|TCCALB2 Trypanosoma cruzi CalA2 calmodulin gene. 77 2e-17
emb|AF030033|AF030033 Phaseolus vulgaris calmodulin (CaM) mRNA, ... 75 2e-17
emb|X90560|PPCAMPROT Physcomitrella patens mRNA for calmodulin. 71 2e-17
15 gb|U91642|POU91642 Pleurotus ostreatus calmodulin mRNA, complete... 75 2e-17
emb|AF078680|AF078680 Olea europaea calcium-binding protein (PCA... 57 2e-17
emb|X85091|MPCAM M.pyrifera mRNA for calmodulin. 74 2e-17
gb|M83535|PHTCALPIA P.infestans calmodulin (calA) gene, complete... 75 2e-17
emb|Y08373|TGCM T.gondii mRNA for calmodulin. 74 2e-17
20 gb|C96396|C96396 C96396 Marchantia polymorpha immature sex organ... 73 3e-17
emb|AL113315|CNS01ARV Botrytis cinerea strain T4 cDNA library un... 72 3e-17
emb|AB044286|AB044286 Chara corallina ccam mRNA for calmodulin, ... 75 4e-17
emb|AB041712|AB041712 Chara corallina ccam2 mRNA for calmodulin... 75 4e-17
emb|AB041711|AB041711 Chara corallina ccam1 mRNA for calmodulin... 75 4e-17
25 gb|J05116|ACKCAL A.klebsiana calmodulin gene, complete cds. 75 4e-17
emb|X70923|NCCALMOE N.crassa mRNA for calmodulin. 74 6e-17
emb|AI328739|AI328739 a6d02ne.fl Neurospora crassa evening cDNA ... 74 6e-17
emb|AF034964|AF034964 Glomerella cingulata calmodulin (cam) mRNA... 74 6e-17
gb|U12505|HCCMD Histoplasma capsulatum 186AS calmodulin mRNA, co... 74 8e-17
30 gb|M34540|PARCAM P.tetraurelia calmodulin gene, complete cds. 74 8e-17
gb|S68025|S68025 CAM=calmodulin [Paramecium tetraurelia, Genomic... 74 8e-17
emb|AW164773|AW164773 se77e12.y1 Gm-c1023 Glycine max cDNA clone... 64 8e-17
emb|AW719875|AW719875 LjNEST11d4r Lotus japonicus nodule library... 57 8e-17
emb|AW830090|AW830090 sm22a12.y1 Gm-c1028 Glycine max cDNA clone... 64 8e-17
35 emb|AW126204|AW126204 N100049e rootphos(-) Medicago truncatula c... 57 8e-17
emb|X52242|TTCALM T.thermophila mRNA for calmodulin. 73 1e-16
gb|L02963|NEUCLMDLN Neurospora crassa calmodulin mRNA, complete ... 74 1e-16
emb|AW625406|AW625406 EST319229 tomato radicle, 5 d post-imbibit... 62 1e-16
gb|K02944|TRBCMRSG Trypanosoma brucei gambiense calmodulin genes... 73 2e-16
40 gb|M88307|BNACALM Brassica juncea calmodulin mRNA, complete cds. 73 2e-16
gb|U10150|BNU10150 Brassica napus Naehan calmodulin (bcm1) mRNA,... 73 2e-16
emb|X89890|BPCALMGEM B.pilosa mRNA for calmodulin. 73 2e-16
emb|AW099396|AW099396 sd39h01.y1 Gm-c1016 Glycine max cDNA clone... 76 2e-16
emb|AW101324|AW101324 sd77e09.y1 Gm-c1009 Glycine max cDNA clone... 59 2e-16
45 emb|AL112713|CNS01AB5 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
emb|AL114582|CNS01BR2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL112170|CNS019W2 Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL114124|CNS01BEC Botrytis cinerea strain T4 cDNA library un... 74 2e-16
emb|AL115056|CNS01C48 Botrytis cinerea strain T4 cDNA library un... 73 2e-16
50 emb|AL116760|CNS01DFK Botrytis cinerea strain T4 cDNA library un... 73 2e-16
emb|AW573768|AW573768 EST316359 GVN Medicago truncatula cDNA clo... 72 2e-16
emb|Y13784|MSCALMODU Mougeotia scalaris mRNA for calmodulin. 70 3e-16
emb|AI727960|AI727960 BNLGHi9833 Six-day Cotton fiber Gossypium ... 73 3e-16
emb|AA660367|AA660367 00239 MtRHE Medicago truncatula cDNA 5' si... 71 3e-16
55 emb|AW164628|AW164628 se74e01.y1 Gm-c1023 Glycine max cDNA clone... 60 3e-16
emb|AF150059|AF150059 Brassica napus calmodulin (CaM1) mRNA, com... 72 3e-16
emb|AW738989|AW738989 gb23c06.y1 Moss EST library PPN Physcomitr... 73 3e-16
gb|U48693|TAU48693 Triticum aestivum calmodulin TaCaM3-1 mRNA, c... 73 4e-16
gb|M27303|BLYCAMA Barley cam gene encoding calmodulin, complete ... 73 4e-16
60 gb|BE033450|BE033450 ME02B08 ME Mesembryanthemum crystallinum cD... 73 4e-16
emb|AF064552|AF064552 Apium graveolens calmodulin mRNA, complete... 73 4e-16

- gb|S81594|S81594 auxin-regulated calmodulin [*Vigna radiata*=mung ... 73 4e-16
 gb|L20691|VIRCALMOD *Vigna radiata* calmodulin mRNA, complete cds. 73 4e-16
 emb|AW730911|AW730911 GA__Ea0029I11 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|BE036340|BE036340 MO23E04 *Mesembryanthemum crystallinum* cD... 73 4e-16
 5 emb|AF030032|AF030032 *Phaseolus vulgaris* calmodulin (CaM) mRNA, ... 73 4e-16
 gb|L01431|SOYSCAM2X Soybean calmodulin (SCaM-2) mRNA, complete cds. 73 4e-16
 emb|Y09853|CACAM *Cicer arietinum* mRNA for CaM protein. 73 4e-16
 gb|L01432|SOYSCAM3X Soybean calmodulin (SCaM-3) mRNA, complete cds. 73 4e-16
 gb|U49104|TAU49104 *Triticum aestivum* calmodulin TaCaM3-3 mRNA, c... 73 4e-16
 10 gb|U49105|TAU49105 *Triticum aestivum* calmodulin TaCaM4-1 mRNA, c... 73 4e-16
 emb|AF030034|AF030034 *Phaseolus vulgaris* calmodulin (CaM) mRNA, ... 73 4e-16
 emb|AW728030|AW728030 GA__Ea0029H21 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|L20507|VIRCALMODU *Vigna radiata* (clone pMBCaM-1) calmodulin m... 73 4e-16
 gb|U48242|TAU48242 *Triticum aestivum* calmodulin TaCaM1-1 mRNA, c... 73 4e-16
 15 gb|M80836|PETCAM81 *Petunia hybrida* CAM81 mRNA,. 73 4e-16
 gb|U49103|TAU49103 *Triticum aestivum* calmodulin TaCaM3-2 mRNA, c... 73 4e-16
 emb|X52398|MSCAL1 *Alfalfa* call mRNA for calmodulin. 73 4e-16
 gb|U48688|TAU48688 *Triticum aestivum* calmodulin TaCaM1-2 mRNA, c... 73 4e-16
 gb|L01430|SOYSCAM1X Soybean calmodulin (SCaM-1) mRNA, complete cds. 73 4e-16
 20 emb|AW927068|AW927068 HVSMEg0009G21 *Hordeum vulgare* pre-anthesis... 73 4e-16
 gb|U48689|TAU48689 *Triticum aestivum* calmodulin TaCaM1-3 mRNA, c... 73 4e-16
 gb|M80831|PETCALPRO *Petunia hybrida* CAM53 mRNA, complete cds. 73 4e-16
 emb|AW348582|AW348582 GM210002B22C3R *Gm-r1021* Glycine max cDNA 3... 73 4e-16
 emb|X59751|DCCAM1G Carrot Ccam-1 gene for calmodulin. 73 4e-16
 25 emb|AW775754|AW775754 EST334819 *DSIL* *Medicago truncatula* cDNA cl... 73 4e-16
 gb|BE052400|BE052400 GA__Ea0001L24f *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 emb|AW666735|AW666735 GA__Ea0005N08 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 gb|U13882|PSU13882 *Pisum sativum* Alaska calmodulin mRNA, complet... 73 4e-16
 gb|BE051931|BE051931 GA__Ea0002G11f *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 30 emb|AW666619|AW666619 GA__Ea0005C16 *Gossypium arboreum* 7-10 dpa ... 73 4e-16
 emb|AW108833|AW108833 gate0001L24f *Gossypium arboreum* 7-10 dpa f... 73 4e-16
 emb|Z12839|LLCALMOD *L. longiflorum* mRNA encoding calmodulin. 73 4e-16
 gb|L18912|LILCALMODU *Lilium longiflorum* calmodulin mRNA, complet... 73 4e-16

35

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 gb|aab71482.1| (ac002294) similar to s-linalool synthase
 gp|u58314|1491939 [*arabidopsis thaliana*] /blast_score 0
 (2661 letters)

40

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

45 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- gb|U58314|CBU58314 *Clarkia breweri* S-linalool synthase (Lis) mRN... 146 e-171
 50 emb|AF067603|AF067603 *Clarkia breweri* linalool synthase 2 (LIS2)... 149 e-154
 emb|AF067602|AF067602 *Clarkia concinna* linalool synthase gene, c... 112 1e-53
 emb|AF097310|AF097310 *Stevia rebaudiana* kaurene synthase (KS1-1)... 88 5e-31
 emb|AF097311|AF097311 *Stevia rebaudiana* kaurene synthase (KS22-1... 88 5e-31
 emb|AF067604|AF067604 *Oenothera arizonica* linalool synthase-like... 75 5e-24
 55 emb|AF067601|AF067601 *Clarkia breweri* linalool synthase 1 (LIS1)... 86 1e-17
 gb|U43904|CMU43904 *Cucurbita maxima* ent-kaurene synthase B mRNA,... 63 5e-17
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 emb|AI485623|AI485623 EST243944 tomato ovary, TAMU *Lycopersicon* ... 55 9e-14
 gb|U92267|AGU92267 *Abies grandis* gamma-humulene synthase mRNA, c... 45 2e-10
 60 gb|U50768|AGU50768 *Abies grandis* abietadiene synthase (ac22) mRN... 58 6e-10
 emb|AW255432|AW255432 ML454 peppermint glandular trichome *Mentha*... 56 1e-08

- emb|AW255334|AW255334 ML343 peppermint glandular trichome Mentha... 56 1e-08
 emb|AF233894|AF233894 Perilla citriodora limonene synthase mRNA,... 62 2e-08
 gb|U87909|AGU87909 Abies grandis pinene synthase (AG3.18) mRNA, ... 61 5e-08
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 5 emb|AF006195|AF006195 Abies grandis E-alpha-bisabolene synthase ... 55 7e-08
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 10 gb|U92266|AGU92266 Abies grandis d-selinene synthase mRNA, compl... 60 1e-07
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 emb|AI491074|AI491074 EST241783 tomato shoot, Cornell Lycopersic... 38 1e-07
 emb|AW617193|AW617193 EST323604 L. hirsutum trichome, Cornell Un... 40 2e-07
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 15 emb|AF034545|AF034545 Stevia rebaudiana copalyl pyrophosphate sy... 59 2e-07
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 emb|AW616079|AW616079 EST296838 L. hirsutum trichome, Cornell Un... 39 3e-07
 20 emb|AW616201|AW616201 EST307240 L. hirsutum trichome, Cornell Un... 39 3e-07
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 emb|AW617347|AW617347 EST323758 L. hirsutum trichome, Cornell Un... 39 3e-07
 25 emb|AW617467|AW617467 EST323878 L. hirsutum trichome, Cornell Un... 39 3e-07
 emb|AW617665|AW617665 EST324076 L. hirsutum trichome, Cornell Un... 39 3e-07
 emb|AW617376|AW617376 EST323787 L. hirsutum trichome, Cornell Un... 39 3e-07
 emb|AF049905|AF049905 Cucurbita maxima copalyl diphosphate synth... 58 3e-07
 emb|AW616328|AW616328 EST322739 L. hirsutum trichome, Cornell Un... 38 5e-07
 30 emb|AW624730|AW624730 EST322675 tomato flower buds 3-8 mm, Corne... 37 6e-07
 emb|AB042424|AB042424 Croton sublyratus cps mRNA for copalyl dip... 57 7e-07
 emb|AW254843|AW254843 ML1265 peppermint glandular trichome Mentha... 57 7e-07
 emb|AW254789|AW254789 ML1071 peppermint glandular trichome Mentha... 57 7e-07
 emb|AW254821|AW254821 ML1244 peppermint glandular trichome Mentha... 57 7e-07
 35 emb|AW255149|AW255149 ML145 peppermint glandular trichome Mentha... 57 7e-07
 emb|AW255044|AW255044 ML1227 peppermint glandular trichome Mentha... 57 7e-07
 emb|AF139207|AF139207 Abies grandis (-)-limonene/(-)-alpha-pinen... 57 9e-07
 emb|AW616366|AW616366 EST322777 L. hirsutum trichome, Cornell Un... 36 2e-06
 emb|AW255042|AW255042 ML1225 peppermint glandular trichome Mentha... 55 2e-06
 40 emb|AW255052|AW255052 ML1347 peppermint glandular trichome Mentha... 55 2e-06
 emb|AW254888|AW254888 ML1312 peppermint glandular trichome Mentha... 55 2e-06
 emb|AW687409|AW687409 NF009C09RT1F1069 Developing root Medicago ... 54 5e-06
 emb|AB015675|AB015675 Lycopersicon esculentum CPS mRNA for copal... 54 5e-06
 emb|AF051901|AF051901 Salvia officinalis (+)-sabinene synthase m... 54 5e-06
 45 emb|AF175323|AF175323 Mentha longifolia limonene synthase mRNA, ... 54 6e-06
 gb|L13459|MHC4SLSP Mentha spicata 4S-limonene synthase mRNA, com... 54 6e-06
 emb|AW255678|AW255678 ML735 peppermint glandular trichome Mentha... 53 1e-05
 emb|AF139205|AF139205 Abies grandis beta-phellandrene synthase (... 52 2e-05
 emb|AW617714|AW617714 EST324125 L. hirsutum trichome, Cornell Un... 33 2e-05
 50 emb|AF154125|AF154125 Artemisia annua (3R)-linalool synthase (QH... 51 4e-05
 emb|AF049906|AF049906 Cucurbita maxima copalyl diphosphate synth... 51 4e-05
 emb|AW684730|AW684730 NF020C02NR1F1000 Nodulated root Medicago t... 51 4e-05
 gb|U87908|AGU87908 Abies grandis myrcene synthase (AG2.2) mRNA, ... 51 6e-05
 emb|AW255083|AW255083 ML1378 peppermint glandular trichome Mentha... 51 6e-05
 55 emb|AW254876|AW254876 ML1300 peppermint glandular trichome Mentha... 49 2e-04
 gb|U48796|TBU48796 Taxus brevifolia taxadiene synthase (TDC1) mR... 49 2e-04
 emb|AF051899|AF051899 Salvia officinalis 1,8-cineole synthase mR... 48 4e-04
 emb|AF006193|AF006193 Abies grandis (-)-4S-limonene synthase mRN... 47 5e-04
 emb|AF154124|AF154124 Artemisia annua (3R)-linalool synthase (QH... 46 0.001
 60 emb|AF139206|AF139206 Abies grandis terpinolene synthase (agc9) ... 45 0.004
 emb|AW687308|AW687308 NF008C02RT1F1008 Developing root Medicago ... 44 0.005

- emb|AF051900|AF051900 *Salvia officinalis* (+)-bornyl diphosphate ... 43 0.009
emb|AF212433|AF212433 *Capsicum annuum* UV-induced sesquiterpene c... 43 0.009
emb|AF061285|AF061285 *Capsicum annuum* sesquiterpene cyclase mRNA... 43 0.009
5 emb|AW685590|AW685590 NF029D03NR1F1000 Nodulated root *Medicago t...* 34 0.014
emb|AW125997|AW125997 N100193e rootphos(-) *Medicago truncatula* c... 34 0.015
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emb|AW254970|AW254970 ML1141 peppermint glandular trichome *Menth...* 41 0.034
emb|AB006530|AB006530 *Citrullus lanatus* Sat gene for serine acet... 41 0.046
10 emb|AW559431|AW559431 EST314479 DSIR *Medicago truncatula* cDNA cl... 32 0.065
emb|AB005744|AB005744 *Perilla frutescens* DNA for 1-limonene synt... 40 0.087
emb|AW616571|AW616571 EST322982 *L. hirsutum* trichome, Cornell Un... 30 0.17
emb|AW617415|AW617415 EST323826 *L. hirsutum* trichome, Cornell Un... 30 0.17
gb|U20189|HMU20189 *Hyoscyamus muticus* clone cVS2 vetispiradiene ... 39 0.23
15 emb|AF042382|AF042382 *Solanum tuberosum* vetispiradiene synthase ... 38 0.31
emb|AF043300|AF043300 *Solanum tuberosum* putative vetispiradiene ... 38 0.31
emb|AB022720|AB022720 *Solanum tuberosum* PVS3 mRNA for vetispirad... 38 0.31
gb|L32134|RCCASSYNT *Ricinus communis* casbene synthase mRNA. 38 0.43
emb|AW043070|AW043070 ST28H10 Pine TriplEx shoot tip library Pin... 38 0.43
20 emb|AI940878|AI940878 sb79b02.y1 Gm-c1010 Glycine max cDNA clone... 38 0.43
emb|AB022719|AB022719 *Solanum tuberosum* PVS2 mRNA for vetispirad... 37 0.58
emb|AF043298|AF043298 *Solanum tuberosum* putative vetispiradiene ... 37 0.58
emb|AF043299|AF043299 *Solanum tuberosum* putative vetispiradiene ... 37 0.58
emb|AJ001452|FVAJ1452 *Fragaria vesca* partial mRNA for putative s... 30 0.70
25 emb|AB022598|AB022598 *Solanum tuberosum* PVS1 mRNA for vetispirad... 36 1.1
emb|AB023816|AB023816 *Solanum tuberosum* PVS4 mRNA for vetispirad... 36 1.1

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(1580 letters)

35 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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| | emb AB001379 AB001379 <i>Glycyrrhiza echinata</i> CYP81E1 mRNA for cyto... | 376 | e-149 | | |
| | emb AB022732 AB022732 <i>Glycyrrhiza echinata</i> CYP Ge-31 mRNA for cy... | 376 | e-149 | | |
| | emb AJ238439 CAR238439 <i>Cicer arietinum</i> mRNA for a cytochrome P45... | 377 | e-147 | | |
| 45 | emb AJ012581 CAR012581 <i>Cicer arietinum</i> mRNA for cytochrome P450. | 376 | e-147 | | |
| | emb AJ239051 CAR239051 <i>Cicer arietinum</i> mRNA for cytochrome P450 ... | 255 | e-145 | | |
| | emb AB025016 AB025016 <i>Lotus japonicus</i> mRNA for cytochrome P450, ... | 340 | e-142 | | |
| | emb AJ249800 CAR249800 <i>Cicer arietinum</i> partial mRNA for cytochro... | 352 | 3e-96 | | |
| | emb AJ000478 HTCYP81L <i>Helianthus tuberosus</i> mRNA for cytochrome P... | 225 | 4e-84 | | |
| 50 | emb AJ000477 HTCYP81C <i>Helianthus tuberosus</i> mRNA for cytochrome P... | 225 | 4e-84 | | |
| | emb AW185361 AW185361 se90e02.y1 Gm-c1027 Glycine max cDNA clone... | 302 | 5e-81 | | |
| | emb AJ249801 CAR249801 <i>Cicer arietinum</i> partial mRNA for cytochro... | 298 | 6e-80 | | |
| | emb AF082028 AF082028 <i>Hemerocallis</i> hybrid cultivar senescence-as... | 209 | 4e-76 | | |
| | emb AW733691 AW733691 sk83g07.y1 Gm-c1016 Glycine max cDNA clone... | 277 | 2e-73 | | |
| 55 | emb AW307234 AW307234 sf54d12.y1 Gm-c1009 Glycine max cDNA clone... | 275 | 6e-73 | | |
| | emb AW234443 AW234443 sf25c03.y1 Gm-c1028 Glycine max cDNA clone... | 273 | 3e-72 | | |
| | emb AW775904 AW775904 EST334969 DSIL <i>Medicago truncatula</i> cDNA cl... | 242 | 3e-71 | | |
| | emb AW171738 AW171738 N100632e rootphos(-) <i>Medicago truncatula</i> c... | 265 | 7e-70 | | |
| | emb AJ725744 AJ725744 BNLGHi12803 Six-day Cotton fiber <i>Gossypium</i> ... | 193 | 3e-63 | | |
| 60 | emb AJ729126 AJ729126 BNLGHi12694 Six-day Cotton fiber <i>Gossypium</i> ... | 188 | 2e-62 | | |
| | emb AJ495626 AJ495626 sb11c08.y1 Gm-c1004 Glycine max cDNA clone... | 236 | 5e-61 | | |

- emb|AW329224|AW329224 N200436e rootphos(-) *Medicago truncatula* c... 228 1e-58
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emb|AW100311|AW100311 sd22g12.y2 Gm-c1012 *Glycine max* cDNA clone... 218 8e-56
5 emb|AF014802|AF014802 *Eschscholzia californica* (S)-N-methylcocla... 177 9e-56
emb|AI774414|AI774414 EST255514 tomato resistant, Cornell Lycop... 152 9e-56
emb|AW171672|AW171672 N100566e rootphos(-) *Medicago truncatula* c... 216 3e-55
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emb|AI776121|AI776121 EST257209 tomato resistant, Cornell Lycop... 116 1e-51
10 emb|AV412147|AV412147 AV412147 *Lotus japonicus* young plants (two... 204 2e-51
dbj|E13663|E13663 cDNA encoding cytochrome P450 which is induced... 116 5e-50
dbj|D83968|SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... 116 5e-50
emb|AW676742|AW676742 DG1_14_A08.g1_A002 Dark Grown 1 (DG1) Sorg... 116 1e-49
emb|AI731081|AI731081 BNLGH18648 Six-day Cotton fiber *Gossypium* ... 198 1e-49
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15 emb|AW309826|AW309826 sf25c03.x1 Gm-c1028 *Glycine max* cDNA clone... 196 5e-49
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emb|AF022461|AF022461 *Glycine max* cytochrome P450 monooxygenase ... 108 1e-47
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20 emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 160 4e-47
emb|AI973839|AI973839 sd11c06.y1 Gm-c1020 *Glycine max* cDNA clone... 116 7e-47
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emb|X71658|SMCYPEG8 S.melongena CYP76A1 mRNA. 161 7e-47
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25 emb|Y10982|GMP450CP6 *Glycine max* mRNA for cytochrome P450-like p... 159 9e-47
emb|Y09920|HT7ECODET *Helianthus tuberosus* mRNA for 7-ethoxycouma... 156 1e-46
emb|Y10098|HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... 156 1e-46
emb|AF124372|AF124372 *Nicotiana tabacum* NT7 mRNA, partial cds. 145 1e-46
emb|AW728802|AW728802 GA_Ea0028112 *Gossypium arboreum* 7-10 dpa ... 168 2e-46
30 emb|AF156976|AF156976 *Gerbera hybrida* flavone synthase II (CYP93... 103 2e-46
emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 162 6e-46
dbj|D14590|D14590 *Campanula medium* mRNA for flavonoid 3',5'-hydr... 157 1e-45
emb|AW616482|AW616482 EST322893 L. hirsutum trichome, Cornell Un... 124 2e-45
emb|AW617814|AW617814 EST324213 L. hirsutum trichome, Cornell Un... 124 2e-45
35 emb|AF155332|AF155332 *Petunia x hybrida* flavonoid 3'-hydroxylase... 183 2e-45
emb|AW616075|AW616075 EST296834 L. hirsutum trichome, Cornell Un... 124 5e-45
gb|U72654|EGU72654 *Eustoma grandiflorum* flavonoid 3',5'-hydroxyla... 160 6e-45
gb|M32885|AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... 160 8e-45
emb|AW679544|AW679544 WS1_29_D01.g1_A002 Water-stressed 1 (WS1) ... 101 8e-45
40 emb|AW102198|AW102198 sd84f03.y1 Gm-c1009 *Glycine max* cDNA clone... 181 1e-44
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45 emb|AW309498|AW309498 sf20c05.x1 Gm-c1028 *Glycine max* cDNA clone... 178 1e-43
emb|AF135485|AF135485 *Glycine max* cytochrome P450 monooxygenaseC... 100 1e-43
gb|U29333|PSU29333 *Pisum sativum* novel wound-inducible cytochrom... 157 1e-43
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emb|AW616066|AW616066 EST296823 L. hirsutum trichome, Cornell Un... 122 1e-43
50 emb|AW255096|AW255096 ML139 peppermint glandular trichome *Mentha*... 162 2e-43
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gb|L07634|PHVC4HYDRO *Phaseolus aureus* cinnamate 4-hydroxylase mR... 148 3e-42
55 emb|AB023636|AB023636 *Glycyrrhiza echinata* CYP Ge-8 mRNA for cyt... 107 4e-42
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60 emb|AI731481|AI731481 BNLGH19879 Six-day Cotton fiber *Gossypium* ... 171 9e-42
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 5 emb|AB022733|AB022733 Glycyrrhiza echinata CYP Ge-51 mRNA for cy... 104 4e-41
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 emb|AF135484|AF135484 Glycine max cytochrome P450 monooxygenase ... 100 6e-41
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 10 emb|AF195810|AF195810 Trifolium pratense isoflavone synthase 1 (... 100 6e-41
 emb|AF195808|AF195808 Vigna radiata isoflavone synthase 3 (ifs3)... 100 6e-41
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 emb|AF195802|AF195802 Medicago sativa isoflavone synthase 3 (ifs... 100 6e-41
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 15 emb|AF022458|AF022458 Glycine max cytochrome P450 monooxygenase ... 168 9e-41
 emb|AF195812|AF195812 Pisum sativum isoflavone synthase 1 (ifs1)... 100 2e-40
 emb|AF195817|AF195817 Beta vulgaris isoflavone synthase 2 (ifs2)... 100 2e-40
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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35 gb U64925 NTU64925 Nicotiana tabacum geranylgeranylated protein ...	260	1e-68	
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emb AW220184 AW220184 EST302667 tomato root during/after fruit s...	208	7e-53	
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40 emb AW685484 AW685484 NF030E02NR1F1000 Nodulated root Medicago t...	171	2e-41	
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emb AW397252 AW397252 sg76f06.y1 Gm-c1007 Glycine max cDNA clone...	168	1e-40	
emb AW033368 AW033368 EST276939 tomato callus, TAMU Lycopersicon...	162	5e-39	
emb AV417858 AV417858 AV417858 Lotus japonicus young plants (two...	153	4e-36	
45 emb AI780050 AI780050 EST260929 tomato susceptible, Cornell Lyco...	138	9e-32	
emb AW039095 AW039095 EST281068 tomato mixed elicitor, BTI Lycop...	111	2e-23	
emb AI780139 AI780139 EST261018 tomato susceptible, Cornell Lyco...	86	7e-16	
emb AW164180 AW164180 Ljirmp21-672-c8 Ljirmp Lambda HybriZap ...	84	2e-15	
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50 emb AW774764 AW774764 EST333915 KV3 Medicago truncatula cDNA clo...	62	7e-09	
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55 emb AW926585 AW926585 HVSMEg0007J19 Hordeum vulgare pre-anthesis...	29	0.025	
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5	emb Z99262 SPAC9E9 S.pombe chromosome I cosmid c9E9.	35	1.4
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10	emb AQ942780 AQ942780 Sheared DNA-42B15.TR Sheared DNA Trypanoso...	35	1.9
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30	emb Z71682 SCYNR067C S.cerevisiae chromosome XIV reading frame O...	34	3.6
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35	emb AF124792 AF124792 Sporothrix schenckii protein kinase C (PCK...	29	4.7
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5 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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15	emb AI485780 AI485780 EST244101 tomato ovary, TAMU Lycopersicon ...	242	1e-85
	emb AI485695 AI485695 EST244016 tomato ovary, TAMU Lycopersicon ...	261	3e-85
	emb AI485239 AI485239 EST243543 tomato ovary, TAMU Lycopersicon ...	291	1e-77
	emb AI899197 AI899197 EST268640 tomato ovary, TAMU Lycopersicon ...	161	1e-77
	emb AW034573 AW034573 EST278257 tomato callus, TAMU Lycopersicon...	272	8e-72
20	emb AI488812 AI488812 EST247151 tomato ovary, TAMU Lycopersicon ...	251	1e-65
	emb AW687082 AW687082 NF005G09RT1F1071 Developing root Medicago ...	182	6e-65
	emb AI898248 AI898248 EST267691 tomato ovary, TAMU Lycopersicon ...	204	1e-63
	emb AI483614 AI483614 EST249464 tomato ovary, TAMU Lycopersicon ...	238	1e-61
	emb AI897089 AI897089 EST266532 tomato ovary, TAMU Lycopersicon ...	226	7e-58
25	emb AW774994 AW774994 EST334145 KV3 Medicago truncatula cDNA clo...	182	2e-56
	emb AW559604 AW559604 EST314652 DSIR Medicago truncatula cDNA cl...	177	3e-53
	emb AI485284 AI485284 EST243588 tomato ovary, TAMU Lycopersicon ...	204	3e-51
	emb AI485664 AI485664 EST243985 tomato ovary, TAMU Lycopersicon ...	195	8e-49
	emb AW774741 AW774741 EST333892 KV3 Medicago truncatula cDNA clo...	90	2e-48
30	emb AI487608 AI487608 EST245930 tomato ovary, TAMU Lycopersicon ...	187	3e-46
	emb AI483438 AI483438 EST249259 tomato ovary, TAMU Lycopersicon ...	169	6e-41
	emb AW775688 AW775688 EST334753 DSIL Medicago truncatula cDNA cl...	157	2e-37
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35	emb AI967736 AI967736 Ljirmp11-837-a7 Ljirmp Lambda HybriZap ...	147	4e-34
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40	emb X94335 SC130KBXV S.cerevisiae 130kb DNA fragment from chromo...	51	1e-29
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	emb Z38062 SC9687 S.cerevisiae chromosome IX cosmid 9687.	72	2e-27
45	emb AI488810 AI488810 EST247149 tomato ovary, TAMU Lycopersicon ...	121	3e-26
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	emb AV406995 AV406995 AV406995 Lotus japonicus young plants (two...	67	2e-23
50	emb AW034093 AW034093 EST277588 tomato callus, TAMU Lycopersicon...	111	3e-23
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	emb AI771644 AI771644 EST252744 tomato ovary, TAMU Lycopersicon ...	104	3e-21
55	emb AW731056 AW731056 GA_Ea0008D13 Gossypium arboreum 7-10 dpa ...	102	1e-20
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60	emb AI780067 AI780067 EST260946 tomato susceptible, Cornell Lyco...	94	5e-18
	emb AW687035 AW687035 NF005C05RT1F1037 Developing root Medicago ...	73	2e-17

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 emb|AW220291|AW220291 EST302774 tomato root during/after fruit s... 68 1e-14
 5 emb|AQ644913|AQ644913 RPCI93-EcoRI-2C7.TV RPCI93-EcoRI Trypanoso... 53 1e-13
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 emb|AW830613|AW830613 sm04c07.y1 Gm-c1027 Glycine max cDNA clone... 77 4e-13
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 15 emb|AW695904|AW695904 NF099H04ST1F1043 Developing stem Medicago ... 49 2e-10
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 20 emb|AW333870|AW333870 S27C11 AGS-1 Pneumocystis carinii f. sp. c... 36 4e-09
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 25 emb|AW693686|AW693686 NF068A05ST1F1036 Developing stem Medicago ... 62 2e-08
 emb|AW208046|AW208046 M111077e DSIR Medicago truncatula cDNA clo... 61 4e-08
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 30 emb|AI781410|AI781410 EST262277 tomato susceptible, Cornell Lyco... 52 2e-05
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 35 emb|AQ655271|AQ655271 Sheared DNA-27A17.TR Sheared DNA Trypanoso... 38 0.004
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 40 gb|M28064|PFAHRKP Plasmodium brasilianum DNA homologous to the h... 37 0.45
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 emb|Z74892|BO15H11 B.oleracea mRNA for glycine-rich protein. 36 1.2
 emb|AW774740|AW774740 EST333891 KV3 Medicago truncatula cDNA clo... 36 1.2
 50 emb|Z38060|SC5610 S.cerevisiae chromosome IX sequence derived fr... 36 1.2
 emb|AL031745|PFMAL1P2 Plasmodium falciparum chromosome 1 strain ... 35 2.2

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 55 emb|cab52675.1| (aj010971) glucose-6-phosphate 1-dehydrogenase
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Database: plantfungal
 60 661,018 sequences; 426,114,510 total letters

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	(bits) Value		
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	emb X74421 STG6PDH	S.tuberosum mRNA for glucose-6-phosphate dehy...	911 0.0
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	emb AJ001770 NTTCG9	Nicotiana tabacum mRNA for cytosolic glucose...	893 0.0
	gb U18238 MSU18238	Medicago sativa glucose-6-phosphate dehydroge...	900 0.0
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	emb AF012863 AF012863	Petroselinum crispum cytosolic glucose-6-p...	887 0.0
	emb AJ001769 NTTCG6	Nicotiana tabacum mRNA cytosolic glucose-6-p...	895 0.0
	emb AF097663 AF097663	Mesembryanthemum crystallinum cytoplasmic ...	754 0.0
	emb AB011441 AB011441	Triticum aestivum WESR5 mRNA for glucose-6...	500 e-141
	emb X70373 KLETTZWF	K.lactis LET1 gene and ZWF gene for glucose-...	231 e-138
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	emb Z69381 SCCXIV39K	S.cerevisiae 38,855 bp segment of chromosom...	244 e-136
	gb M34709 YSCG6PD	S.cerevisiae glucose-6-phosphate dehydrogenase...	244 e-136
	emb X57336 SCMET19	S. cerevisiae MET19 gene for glucose-6-phosph...	244 e-136
	emb Z71517 SCYNL241C	S.cerevisiae chromosome XIV reading frame O...	244 e-136
	emb AJ010712 STU010712	Solanum tuberosum mRNA for glucose-6-phos...	240 e-136
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	emb X99405 NTG6PD	N.tabacum mRNA for chloroplast glucose-6-phosp...	242 e-135
	emb AF012861 AF012861	Petroselinum crispum plastidic glucose-6-p...	248 e-135
	emb AI730607 AI730607	BNLGH17371 Six-day Cotton fiber Gossypium ...	481 e-135
	emb X87942 ANG6PDHSE	A.niger mRNA for glucose-6-phosphate dehydr...	225 e-132
	emb AW686120 AW686120	NF038D09NR1F1000 Nodulated root Medicago t...	472 e-132
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	emb AJ132346 DBI132346	Dunaliella bioculata mRNA for plastidic g...	235 e-132
	emb AW925642 AW925642	HVSMEg0005C04 Hordeum vulgare pre-anthesis...	465 e-130
	emb AJ001772 NTTPG18	Nicotiana tabacum mRNA for plastidic glucos...	243 e-129
	emb AW930385 AW930385	EST340938 tomato fruit mature green, TAMU ...	444 e-124
	emb AW831416 AW831416	sm22g09.y1 Gm-c1028 Glycine max cDNA clone...	434 e-121
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	emb X83923 STG6PDHPI	S.tuberosum mRNA for glucose-6-phosphate de...	249 e-118
	emb AJ000182 SO000182	Spinacia oleracea mRNA for glucose-6-phosp...	242 e-117
	emb AJ001771 NTTPG16	Nicotiana tabacum mRNA for plastidic glucos...	247 e-116
	emb AI491202 AI491202	EST241911 tomato shoot, Cornell Lycopersic...	368 e-116
	emb AL121764 SPAC9	S.pombe chromosome I cosmid c9.	196 e-116
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	emb AW233801 AW233801	sf26h03.y1 Gm-c1028 Glycine max cDNA clone...	415 e-115
	emb Z95395 SPAC3A12	S.pombe chromosome I cosmid c3A12.	196 e-108
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	emb AW685333 AW685333	NF027C04NR1F1000 Nodulated root Medicago t...	356 e-105
	emb X77830 ANWGGSDA	A.nidulans (WG096) gsdA gene.	130 e-102
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	emb AJ006246 CCA6246	Cyanidium caldarium mRNA for glucose-6-phos...	239 e-102
	emb AJ000184 SO000184	Spinacia oleracea mRNA for glucose-6-phosp...	242 e-100
	emb AJ000183 SO000183	Spinacia oleracea mRNA for glucose-6-phosp...	190 3e-99
	emb X84001 ANDNAG6PD	A.nidulans g6pd gene.	130 2e-98
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	emb X74988 PFGLPH	P.falciparum gene for glucose-6-phosphate dehy...	192 5e-89
	emb AW560329 AW560329	EST315377 DSIR Medicago truncatula cDNA cl...	323 2e-87
	gb M80655 PFAG6PD	Plasmodium falciparum glucose-6-phosphate dehy...	192 1e-86
	emb AW497059 AW497059	ga53c08.y1 Moss EST library PPU Physcomitr...	319 5e-86
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	emb AW216550 AW216550	EST295264 tomato callus, TAMU Lycopersicon...	188 6e-84
	emb AW219903 AW219903	EST302386 tomato root during/after fruit s...	305 7e-82
	emb AW180861 AW180861	MgA1030f MgA Library Mycosphaerella gramin...	226 5e-80
	emb AW616585 AW616585	EST322996 L. hirsutum trichome, Cornell Un...	175 7e-80
	emb AW309937 AW309937	sf26h03.x1 Gm-c1028 Glycine max cDNA clone...	294 1e-78
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	emb AW031447 AW031447	EST274901 tomato callus, TAMU Lycopersicon...	166 6e-78
	emb AI894720 AI894720	EST264163 tomato callus, TAMU Lycopersicon...	291 1e-77
	emb AW690515 AW690515	NF030E09ST1F1000 Developing stem Medicago ...	174 3e-77
	emb AW736245 AW736245	EST332231 KV3 Medicago truncatula cDNA clo...	278 7e-76
	emb AW455246 AW455246	EST311906 tomato root during/after fruit s...	155 6e-75
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	emb AW980010 AW980010	EST310488 tomato root deficiency, Cornell ...	153 3e-74
	emb AL023595 SPCC794	S.pombe chromosome III cosmid c794.	177 1e-73

- emb|AW255521|AW255521 ML551 peppermint glandular trichome Mentha... 270 3e-71
 emb|AW567621|AW567621 si65f02.y1 Gm-r1030 Glycine max cDNA clone... 264 1e-69
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 emb|AW737104|AW737104 EST338531 tomato flower buds, anthesis, Co... 141 1e-64
 5 emb|AW255222|AW255222 ML216 peppermint glandular trichome Mentha... 142 2e-64
 emb|AW737079|AW737079 EST338506 tomato flower buds, anthesis, Co... 141 3e-64
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 emb|AQ952407|AQ952407 Sheared DNA-32N19.TF Sheared DNA Trypanoso... 84 2e-60
 10 emb|AA787466|AA787466 n3f1 la1.r1 Aspergillus nidulans 24hr asexu... 229 4e-59
 emb|AW254983|AW254983 ML1164 peppermint glandular trichome Menth... 134 2e-58
 emb|AW617385|AW617385 EST323796 L. hirsutum trichome, Cornell Un... 141 2e-57
 emb|AI773327|AI773327 EST254427 tomato resistant, Cornell Lycopers... 222 5e-57
 emb|AW704079|AW704079 sk27e10.y1 Gm-c1028 Glycine max cDNA clone... 219 6e-56
 15 emb|X77829|ANNGSDA A.niger (N400) gsdA gene. 131 4e-55
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 emb|AV424412|AV424412 AV424412 Lotus japonicus young plants (two... 205 9e-52
 20 emb|AQ875204|AQ875204 V123H11 mTn-3xHA/lacZ Insertion Library, s... 192 1e-49
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 25 emb|AJ279688|BPE279688 Betula pendula partial mRNA for Glucose-6... 93 7e-47
 emb|AW700124|AW700124 gb34g09.y1 Moss EST library PPN Physcomitr... 187 3e-46
 emb|AW223852|AW223852 EST300663 tomato fruit red ripe, TAMU Lyco... 141 6e-46
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 30 emb|AW980083|AW980083 EST341594 tomato root deficiency, Cornell ... 133 2e-42
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50 (887 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

55 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- 60 emb|AW725454|AW725454 GA_Ea0018A14 Gossypium arboreum 7-10 dpa ... 238 8e-81
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- gb|U34860|SCU34860 *Saccharomyces cerevisiae* origin recognition c... 122 2e-33
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 emb|Y12314|SPSPG1GEN *S.pombe spg1* gene. 67 9e-20
 5 emb|AJ001587|SPAJ1587 *Schizosaccharomyces pombe* sid3 gene. 67 9e-20
 emb|AW776339|AW776339 EST335404 *DSIL Medicago truncatula* cDNA cl... 67 5e-14
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 gb|L08691|YSCGSP2X Yeast GTP-binding protein (GSP2) gene, comple... 32 2e-06
 emb|X71946|SCCNR2A *S.cerevisiae* CNR2 gene. 32 2e-06
 emb|X71945|SCCNR1A *S.cerevisiae* CNR1 gene. 32 2e-06
 dbj|D17748|TETTRAN *Tetrahymena thermophila* mRNA for Ran/TC4, com... 33 3e-06
 15 dbj|D21825|TETPRAN *Tetrahymena pyriformis* mRNA for Ran/TC4, comp... 33 3e-06
 gb|U17086|TBU17086 *Trypanosoma brucei rhodesiense* RAN/TC4 GTPase... 30 6e-05
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 35 emb|AW930158|AW930158 EST340615 tomato fruit mature green, TAMU ... 36 0.33
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 emb|AW039993|AW039993 EST282484 tomato mixed elicitor, BTI Lycop... 35 0.56
 emb|AW705028|AW705028 sk41f03.y1 *Gm-c1019 Glycine max* cDNA clone... 35 0.57
 emb|AW929161|AW929161 EST337949 tomato flower buds 8 mm to pre-a... 35 0.57
 emb|AW705209|AW705209 sk43a11.y1 *Gm-c1019 Glycine max* cDNA clone... 35 0.57
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 emb|Z73962|LJRAC2 *L.japonicus* mRNA for small GTP-binding protein... 35 0.62
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 emb|AW573660|AW573660 EST316251 *GVN Medicago truncatula* cDNA clo... 35 0.62
 50 emb|AV413108|AV413108 AV413108 *Lotus japonicus* young plants (two... 35 0.62
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 55 emb|AW694335|AW694335 NF075C06ST1F1049 Developing stem *Medicago* ... 35 0.62
 emb|AW109094|AW109094 gate0002P07f *Gossypium arboreum* 7-10 dpa f... 35 0.62
 gb|L19093|PEARHOGTPP *Pisum sativum* rho (ras-related) GTP-binding... 35 0.62
 emb|AW565277|AW565277 LG1_332_G03.b1_A002 Light Grown 1 (LG1) So... 35 0.62
 emb|AV412205|AV412205 AV412205 *Lotus japonicus* young plants (two... 35 0.62
 60 gb|BE054534|BE054534 GA_Ea0033M19f *Gossypium arboreum* 7-10 dpa ... 35 0.62
 emb|AW108667|AW108667 gate0001G03f *Gossypium arboreum* 7-10 dpa f... 35 0.62

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	gb S79309 S79309 Rac9=21.5 kda GTP-binding protein [Gossypium hi...	35	0.62
	gb S79308 S79308 Rac13=21.8 kda GTP-binding protein [Gossypium h...	35	0.62
	emb AJ250174 NTA250174 Nicotiana tabacum mRNA for putative rac p...	35	0.62
5	gb BE055015 BE055015 GA__Ea0001G03f Gossypium arboreum 7-10 dpa ...	35	0.62
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	emb X73954 PFRAN1 P.falciparum gene for ras-related nuclear prot...	35	0.85
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	emb AW217581 AW217581 EST296295 tomato flower buds 3-8 mm, Corne...	34	1.6
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	emb Z36133 SCYBR264C S.cerevisiae chromosome II reading frame OR...	34	1.6
	emb X70529 SCCIORF S. cerevisiae chromosome II sequence for ORF...	34	1.6
30	emb AI778114 AI778114 EST258993 tomato susceptible, Cornell Lyco...	34	1.6
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	emb AW625569 AW625569 EST319476 tomato radicle, 5 d post-imbibit...	34	1.6
	emb AW931490 AW931490 EST357333 tomato fruit mature green, TAMU ...	34	1.6
	gb BE033825 BE033825 MG04D04 MG Mesembryanthemum crystallinum cD...	34	2.2
35	gb BE036577 BE036577 MP01F02 MP Mesembryanthemum crystallinum cD...	34	2.2
	emb AQ399302 AQ399302 mgxb0015O18f CUGI Rice Blast BAC Library P...	34	2.2
	emb AW697756 AW697756 Str1-D6 Sugar Beet germination cDNA librar...	34	2.2
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	gb U18557 RSU18557 Raphanus sativus antifungal protein 1 preprot...	166	7e-43
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	gb U18556 RSU18556 Raphanus sativus antifungal protein 2 preprot...	160	1e-38
	emb X97319 RSEFP3 R.sativus mRNA for antifungal protein 3.	133	8e-37
	gb U59459 BNU59459 Brassica napus antifungal protein mRNA, compl...	135	2e-36
	emb AT001728 AT001728 AT001728 Flower bud cDNA Brassica rapa sub...	82	2e-15
60	gb L47901 L47901 BNAF1712 Mustard flower buds Brassica rapa cDNA...	81	5e-15
	emb A26963 A26963 D.merkii AMP1 sequence.	74	5e-13

	emb A27062 A27062 <i>C.benedictus</i> AMP2 sequence.	73	1e-12
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10	dbj D29679 TOBPIT1A Tobacco pit1 mRNA (which expression is induc...	41	0.003
	emb AW621708 AW621708 EST312506 tomato root during/after fruit s...	36	0.007
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	emb AI483999 AI483999 EST249870 tomato ovary, TAMU <i>Lycopersicon</i> ...	40	0.010
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	emb AW929939 AW929939 EST354209 tomato flower buds 8 mm to pre-a...	40	0.010
	emb AW217552 AW217552 EST296266 tomato flower buds 3-8 mm, Corne...	40	0.012
	emb AI490062 AI490062 EST248401 tomato ovary, TAMU <i>Lycopersicon</i> ...	40	0.012
25	emb AW217379 AW217379 EST296063 tomato flower buds 0-3 mm, Corne...	40	0.012
	emb AI484887 AI484887 EST243150 tomato ovary, TAMU <i>Lycopersicon</i> ...	40	0.012
	emb AI485550 AI485550 EST243871 tomato ovary, TAMU <i>Lycopersicon</i> ...	40	0.012
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	emb AI486656 AI486656 EST244977 tomato ovary, TAMU <i>Lycopersicon</i> ...	38	0.031
	emb AW399651 AW399651 EST310151 <i>L. pennellii</i> trichome, Cornell U...	38	0.043
	emb AW621171 AW621171 EST311969 tomato root during/after fruit s...	34	0.048
	emb AW622051 AW622051 EST312849 tomato root during/after fruit s...	34	0.053
45	emb AI485044 AI485044 EST243324 tomato ovary, TAMU <i>Lycopersicon</i> ...	37	0.059
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	emb AW220086 AW220086 EST302569 tomato root during/after fruit s...	33	0.065
	emb AW621962 AW621962 EST312760 tomato root during/after fruit s...	33	0.070
50	emb AF153353 AF153353 <i>Dimocarpus longan</i> ribulose 1,5-bisphosphat...	36	0.15
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	emb Y15150 GMY15150 <i>Gonystylus macrophyllus</i> rbcL gene.	34	0.54
55	emb Y15139 BOY15139 <i>Bixa orellana</i> chloroplast rbcL gene.	34	0.54
	emb Y15149 ABY15149 <i>Aquilaria beccariana</i> rbcL gene.	34	0.54
	emb AF022128 AF022128 <i>Bixa orellana</i> ribulose 1,5-bisphosphate ca...	34	0.54
	emb AF022125 AF022125 <i>Theobroma cacao</i> ribulose 1,5-bisphosphate ...	34	0.54
	gb L12568 AKARBC <i>Akania bidwillii</i> ribulosebisphosphate carboxyla...	34	0.54
60	emb A27063 A27063 <i>L.cicera</i> AFP sequence.	34	0.54
	gb M95753 BCNCPRBCL <i>Bretschneidera sinensis</i> chloroplast ribulose...	34	0.54

	gb BE124525 BE124525 EST393560 GVN Medicago truncatula cDNA clon...	31	0.68
	emb AW725876 AW725876 GA_Ea0020A08 Gossypium arboreum 7-10 dpa ...	34	0.75
	gb L01579 PEADDR230B Pea (pi39) disease resistance response prot...	34	0.75
	emb AJ757757 AJ757757 EtESTea34d02.y1 Eimeria S5-2 Sporozoite st...	34	0.75
5	gb L14293 HDOCPRBCL Hydrolea ovata chloroplast ribulosebisphosph...	33	1.0
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	emb AJ233116 CSAJ3116 Chorisia speciosa chloroplast rbcL gene, p...	33	1.4
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 this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
 /chip nova /gb_link
[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006577|/ncgi)
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<http://www.ncgr.org/cgi-bin/ff?ac006577>
 (1194 letters)

Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

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	emb Y10156 BNMYAP12 B.napus for myrosinase-associated protein, c...	224	e-163
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	gb U39289 BNU39289 Brassica napus myrosinase-associated protein ...	227	e-156
55	gb U39319 BNU39319 Brassica napus myrosinase-associated protein ...	176	e-127
	emb AJ223307 BNAJ3307 Brassica napus gene encoding induced myros...	176	6e-99
	emb AW568594 AW568594 si78g03.y1 Gm-cl031 Glycine max cDNA clone...	47	1e-13
	emb AW288014 AW288014 N100858e rootphos(-) Medicago truncatula c...	67	3e-13
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	emb AW922141 AW922141 LG1_323_G11.b1_A002 Light Grown 1 (LG1) So...	65	5e-10

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	emb AW623994 AW623994 EST321939 tomato flower buds 3-8 mm, Corne...	48 6e-07
	emb AW621737 AW621737 EST312535 tomato root during/after fruit s...	47 6e-07
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	emb AW328890 AW328890 N200082e rootphos(-) Medicago truncatula c...	41 2e-06
	emb AW621604 AW621604 EST312402 tomato root during/after fruit s...	45 2e-06
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20	emb AI488194 AI488194 EST246516 tomato ovary, TAMU Lycopersicon ...	40 4e-06
	emb AW616223 AW616223 EST307262 L. hirsutum trichome, Cornell Un...	53 5e-06
	emb AW650481 AW650481 EST328935 tomato germinating seedlings, TA...	53 5e-06
	emb AI731912 AI731912 BNLGHi11257 Six-day Cotton fiber Gossypium...	51 6e-06
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30	emb AW509227 AW509227 sh92h02.y1 Gm-c1016 Glycine max cDNA clone...	42 2e-05
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	emb AW127684 AW127684 M110431 DSLC Medicago truncatula cDNA clon...	38 3e-05
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	emb AJ276421 CAR276421 Cicer arietinum partial mRNA for putative...	48 1e-04
35	emb AW277884 AW277884 sf88f10.y1 Gm-c1019 Glycine max cDNA clone...	42 2e-04
	emb AW459066 AW459066 sh18h02.y1 Gm-c1016 Glycine max cDNA clone...	40 2e-04
	emb AW926586 AW926586 HVSMEg0007J20 Hordeum vulgare pre-anthesis...	47 2e-04
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45	emb AW706408 AW706408 sj56h10.y1 Gm-c1033 Glycine max cDNA clone...	46 6e-04
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	emb AW109570 AW109570 gate0004H20f Gossypium arboreum 7-10 dpa f...	45 7e-04
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	emb AW720472 AW720472 LjNEST19f4r Lotus japonicus nodule library...	35 7e-04
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	emb AT000294 AT000294 AT000294 Apple young fruit cDNA library Ma...	42	0.010
	emb AW100112 AW100112 sd20e02.y2 Gm-c1012 Glycine max cDNA clone...	30	0.012
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 35 this gene. [arabidopsis thaliana]" /blast_score 0 /ec_number /family
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 40 (1194 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

45 Searching.....done

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50 emb Y10156 BNMYAP12 B.napus for myrosinase-associated protein, c...	224	e-163	
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gb U39289 BNU39289 Brassica napus myrosinase-associated protein ...	227	e-156	
gb U39319 BNU39319 Brassica napus myrosinase-associated protein ...	176	e-127	
emb AJ223307 BNAJ3307 Brassica napus gene encoding induced myros...	176	6e-99	
55 emb AW568594 AW568594 si78g03.y1 Gm-c1031 Glycine max cDNA clone...	47	1e-13	
emb AW288014 AW288014 N100858e rootphos(-) Medicago truncatula c...	67	3e-13	
emb AW774945 AW774945 EST334096 KV3 Medicago truncatula cDNA clo...	46	5e-13	
emb AW685185 AW685185 NF025E06NR1F1000 Nodulated root Medicago t...	62	1e-10	
emb AW922141 AW922141 LG1_323_G11.b1_A002 Light Grown 1 (LG1) So...	65	5e-10	
60 emb AW687872 AW687872 NF014D07RT1F1061 Developing root Medicago ...	46	2e-09	
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 (1194 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	Score	E
Sequences producing significant alignments:	(bits)	Value
45 emb Y10156 BNMYAP12 B.napus for myrosinase-associated protein, c...	224	e-163
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gb U39289 BNU39289 Brassica napus myrosinase-associated protein ...	227	e-156
gb U39319 BNU39319 Brassica napus myrosinase-associated protein ...	176	e-127
50 emb AJ223307 BNAJ3307 Brassica napus gene encoding induced myros...	176	6e-99
emb AW568594 AW568594 si78g03.y1 Gm-c1031 Glycine max cDNA clone...	47	1e-13
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emb AW774945 AW774945 EST334096 KV3 Medicago truncatula cDNA clo...	46	5e-13
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 (1335 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

35

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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 gb|U74631|RCU74631 Ricinus communis calreticulin gene, complete ... 201 e-172
 emb|AW039860|AW039860 EST282333 tomato mixed elicitor, BTI Lycop... 517 e-145
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 55 emb|AW441195|AW441195 EST310591 tomato fruit red ripe, TAMU Lyco... 487 e-136
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 60 emb|AW773947|AW773947 EST332933 KV3 Medicago truncatula cDNA clo... 469 e-131
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- emb|AW622049|AW622049 EST312847 tomato root during/after fruit s... 467 e-131
emb|AW216727|AW216727 EST295441 tomato callus, TAMU Lycopersicon... 460 e-128
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20 emb|AW738476|AW738476 EST339903 tomato flower buds, anthesis, Co... 412 e-114
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emb|AW649196|AW649196 EST327650 tomato germinating seedlings, TA... 391 e-108
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35 emb|AW033083|AW033083 EST276642 tomato callus, TAMU Lycopersicon... 385 e-106
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40 emb|AW727696|AW727696 GA_Ea0015K01 Gossypium arboreum 7-10 dpa ... 303 e-103
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50 emb|AW760501|AW760501 sl51b04.y1 Gm-c1027 Glycine max cDNA clone... 358 6e-98
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55 emb|AI437497|AI437497 sa34a12.y1 Gm-c1004 Glycine max cDNA clone... 329 4e-89
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60 emb|AW648456|AW648456 EST326910 tomato germinating seedlings, TA... 316 3e-85
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- emb|AW624478|AW624478 EST322423 tomato flower buds 3-8 mm, Corne... 312 3e-84
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 10 emb|AW728940|AW728940 GA_Ea0018J21 Gossypium arboreum 7-10 dpa ... 291 1e-77
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 15 emb|AW560421|AW560421 EST315469 DSIR Medicago truncatula cDNA cl... 270 1e-74
 emb|AW754529|AW754529 PC03C03 Pine TriplEx pollen cone library P... 280 2e-74
 emb|AW042889|AW042889 ST26F06 Pine TriplEx shoot tip library Pin... 279 3e-74
 emb|AW043146|AW043146 ST29H08 Pine TriplEx shoot tip library Pin... 273 2e-73

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 (1647 letters)

Database: plantfungal
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| 35 | Sequences producing significant alignments: | (bits) | Value |
| | emb AJ249799 CAR249799 Cicer arietinum partial mRNA for cytochro... | 308 | e-114 |
| | emb AB032833 AB032833 Cicer arietinum CYP76D1 mRNA for cytochrom... | 289 | 5e-87 |
| | emb AJ011862 CRO011862 Catharanthus roseus mRNA for flavonoid 3'... | 191 | 5e-86 |
| 40 | gb U72654 EGU72654 Eustoma grandiflorum flavonoid 3',5'-hydroxyla... | 179 | 8e-85 |
| | emb AI897763 AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... | 305 | 7e-82 |
| | emb X71658 SMCYPEG8 S.melongena CYP76A1 mRNA. | 278 | 3e-81 |
| | emb X71657 SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. | 269 | 6e-81 |
| | emb Y09920 HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... | 300 | 2e-80 |
| 45 | emb Y10098 HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... | 300 | 2e-80 |
| | dbj D85184 D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... | 121 | 9e-79 |
| | emb X70824 SMPEG1 S.melongena pEG1 mRNA for hydroxylase P450. | 171 | 1e-77 |
| | dbj E05111 E05111 cDNA encoding solanum flavonoid 3',5'-hydroxyg... | 171 | 1e-77 |
| | gb M32885 AVOCYP Avocado cytochrome P-450LXXIA1 (cyp71A1) mRNA, ... | 283 | 3e-75 |
| 50 | emb AF134590 AF134590 Papaver somniferum (S)-N-methylcoclaurine ... | 223 | 6e-75 |
| | emb AF191772 AF191772 Papaver somniferum (S)-N-methylcoclaurine ... | 221 | 1e-74 |
| | emb AF022459 AF022459 Glycine max cytochrome P450 monooxygenase ... | 280 | 3e-74 |
| | emb AI484957 AI484957 EST243220 tomato ovary, TAMU Lycopersicon ... | 280 | 3e-74 |
| | emb AF155332 AF155332 Petunia x hybrida flavonoid 3'-hydroxylase... | 186 | 2e-70 |
| 55 | emb AF014800 AF014800 Eschscholzia californica (S)-N-methylcocla... | 212 | 9e-70 |
| | gb U09610 U09610 Berberis stolonifera cytochrome P-450 CYP80 mRN... | 264 | 1e-69 |
| | emb AF014801 AF014801 Eschscholzia californica (S)-N-methylcocla... | 211 | 3e-69 |
| | emb AI488646 AI488646 EST246985 tomato ovary, TAMU Lycopersicon ... | 260 | 2e-68 |
| | emb Y09424 NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... | 260 | 2e-68 |
| 60 | emb AF022458 AF022458 Glycine max cytochrome P450 monooxygenase ... | 259 | 3e-68 |
| | emb AI938505 AI938505 sb46e03.y1 Gm-cl015 Glycine max cDNA clone... | 259 | 4e-68 |

- emb|Y10490|GMC450CP3 *G.max* mRNA for putative cytochrome P450, cl... 259 4e-68
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emb|Y09423|NRCYP71A5 *Nepeta racemosa* mRNA for cytochrome P450, C... 256 3e-67
5 emb|AW726065|AW726065 GA_Ea0020I21 *Gossypium arboreum* 7-10 dpa ... 186 4e-67
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10 emb|AW730128|AW730128 GA_Ea0027P19 *Gossypium arboreum* 7-10 dpa ... 184 6e-63
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15 emb|Y10493|GMC450CP7 *G.max* mRNA for putative cytochrome P450, cl... 160 2e-61
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20 dbj|D14589|D14589 *Eustoma russellianum* mRNA for flavonoid 3',5'-... 179 5e-61
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25 gb|BE054146|BE054146 GA_Ea0034H12f *Gossypium arboreum* 7-10 dpa ... 234 2e-60
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emb|AI730111|AI730111 BNLGHi6162 Six-day Cotton fiber *Gossypium* ... 226 5e-60
30 emb|AF122821|AF122821 *Capsicum annuum* cytochrome P450 (PepCYP) m... 231 8e-60
emb|AJ238612|CRO238612 *Catharanthus roseus* mRNA for cytochrome P... 230 2e-59
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emb|Z33875|CYMPCP450 *M.piperita* gene for cytochrome P-450 oxidase. 228 8e-59
35 emb|AI726383|AI726383 BNLGHi5702 Six-day Cotton fiber *Gossypium* ... 227 2e-58
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60 emb|AB022733|AB022733 *Glycyrrhiza echinata* CYP Ge-51 mRNA for cy... 109 3e-53
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- emb|AF022157|AF022157 Glycine max cytochrome P450 monooxygenase ... 158 7e-53
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 10 emb|AI729430|AI729430 BNLGHI13332 Six-day Cotton fiber Gossypium... 171 2e-51
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 15 emb|AI727414|AI727414 BNLGHI7936 Six-day Cotton fiber Gossypium ... 181 1e-50

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Database: plantfungal
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Score E

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- gb|BE020282|BE020282 sm42g12.y1 Gm-c1028 Glycine max cDNA clone ... 91 2e-39
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	emb AB028022 AB028022 Nicotiana tabacum wizz mRNA, complete cds.	45	0.001
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	emb AW693799 AW693799 NF069C11ST1F1085 Developing stem Medicago ...	44	0.003
	emb AW696711 AW696711 NF110A11ST1F1084 Developing stem Medicago ...	44	0.003
15	emb AW222373 AW222373 EST299184 tomato fruit red ripe, TAMU Lyco...	44	0.004
	emb AW164824 AW164824 se78d01.y1 Gm-c1023 Glycine max cDNA clone...	43	0.005
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	emb AW568563 AW568563 si78d04.y1 Gm-c1031 Glycine max cDNA clone...	43	0.007
	emb AW219364 AW219364 EST301846 tomato root during/after fruit s...	43	0.007
25	gb BE059498 BE059498 sn32h03.y1 Gm-c1016 Glycine max cDNA clone ...	42	0.013
	emb AW432526 AW432526 sh75d09.y1 Gm-c1015 Glycine max cDNA clone...	42	0.013
	emb AW930573 AW930573 EST341030 tomato fruit mature green, TAMU ...	42	0.013
	emb AW310205 AW310205 sf32g08.x1 Gm-c1028 Glycine max cDNA clone...	42	0.013
	gb L35779 L35779 BNAESTG Mustard flower buds Brassica rapa cDNA ...	42	0.013
30	emb AW233985 AW233985 sf32g08.y1 Gm-c1028 Glycine max cDNA clone...	42	0.013
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50	emb AW035780 AW035780 EST281934 tomato callus, TAMU Lycopersicon...	41	0.017
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	emb AI486874 AI486874 EST245196 tomato ovary, TAMU Lycopersicon ...	41	0.017
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	emb AW031802 AW031802 EST275256 tomato callus, TAMU Lycopersicon...	41	0.017
	emb AI489016 AI489016 EST247355 tomato ovary, TAMU Lycopersicon ...	41	0.017
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	emb AW568786 AW568786 si61a10.y1 Gm-r1030 Glycine max cDNA clone...	41	0.024
60	emb AI938647 AI938647 sb56f08.y1 Gm-c1018 Glycine max cDNA clone...	41	0.024
	emb AI938638 AI938638 sb56e08.y1 Gm-c1018 Glycine max cDNA clone...	41	0.024

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 5 emb|AW733406|AW733406 sk73b02.y1 Gm-cl016 Glycine max cDNA clone... 40 0.060
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 10 emb|AW559645|AW559645 EST314757 DSIR Medicago truncatula cDNA cl... 39 0.083
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 (1062 letters)

20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

25 Score E
 Sequences producing significant alignments: (bits) Value

emb|X61488|BNCHITIN B.napus mRNA for chitinase. 453 e-166
 gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 212 1e-95
 30 gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 211 4e-95
 emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 135 8e-86
 dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 136 5e-82
 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 185 5e-81
 emb|Z46948|SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... 182 8e-80
 35 emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 156 4e-79
 emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 156 4e-79
 dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 119 4e-78
 dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 119 7e-78
 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 119 1e-77
 40 emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase class 4 (p... 103 6e-77
 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 105 1e-75
 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 84 7e-73
 gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 140 1e-72
 gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 139 3e-72
 45 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 133 2e-70
 gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 131 1e-69
 emb|AF112963|AF112963 Triticum aestivum chitinase II precursor (... 239 1e-66
 gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 130 2e-66
 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 177 5e-66
 50 gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 167 9e-65
 emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 172 2e-64
 gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 165 4e-64
 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 111 7e-64
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 55 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 93 4e-63
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 60 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 147 3e-57
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emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 141 2e-55
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5 emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 140 6e-55
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gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 116 1e-51
15 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 117 9e-51
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 124 2e-50
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 141 6e-50
emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 149 1e-49
emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 165 4e-49
20 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 120 4e-49
emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 115 9e-49
emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 112 1e-48
gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 112 1e-48
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 115 1e-48
25 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 140 2e-48
gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 83 3e-48
gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 112 5e-48
emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 112 5e-48
emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 139 9e-48
30 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 139 9e-48
emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 118 3e-47
emb|AF061806|AF061806 Elaeagnus umbellata basic chitinase mRNA, ... 118 4e-47
gb|M94105|ALCCHITIN Allium sativum chitinase mRNA, 3' end. 116 7e-47
emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 120 2e-46
35 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 116 3e-46
emb|AW922596|AW922596 DG1_46_C01.b1_A002 Dark Grown 1 (DG1) Sorg... 79 3e-46
emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 116 3e-46
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gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 122 4e-46
40 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 116 4e-46
emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 112 7e-46
emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 121 9e-46
emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 109 1e-45
emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 112 2e-45
45 emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 135 2e-45
gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 116 2e-45
gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 109 2e-45
gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 116 3e-45
gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 109 6e-45
50 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 108 8e-45
emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 147 2e-44
gb|BE033398|BE033398 ME01A01 ME Mesembryanthemum crystallinum cD... 141 4e-44
emb|AA739579|AA739579 344 PfFG2 Pinus taeda cDNA clone 8562M 3'... 107 1e-43
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55 emb|A23396|A23396 B.vulgaris gene for chitinase 76. 105 3e-43
emb|AW267781|AW267781 EST305909 DSIR Medicago truncatula cDNA cl... 115 4e-43
emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 108 8e-43
emb|AF098302|AF098302 Brassica juncea chitinase mRNA, complete cds. 125 1e-42
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60 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 80 5e-42
emb|AI729668|AI729668 BNLGHI13889 Six-day Cotton fiber Gossypium... 111 2e-41

- emb|AF061805|AF061805 Elaeagnus umbellata acidic chitinase mRNA,... 116 3e-41
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 emb|Z15138|LECHI14 L.esculentum mRNA for chitinase (partial). 114 1e-40
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 5 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 100 1e-39

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 10 emb|caa20567.1| (al031394) putative protein [arabidopsis thaliana]
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 http://www.ncgr.org/cgi-bin/ff?al031394
 (1116 letters)

15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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25	emb AW671006 AW671006 LG1_278_H12.b1_A002 Light Grown 1 (LG1) So...	81	6e-28
	emb AA520813 AA520813 TgESTzz64d07.r1 TgME49 invivo Bradyzoite c...	38	0.16
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	emb Z74916 SCYOR008C S.cerevisiae chromosome XV reading frame OR...	37	0.31
	gb U39481 SCU39481 Saccharomyces cerevisiae Slglp (SLG1) gene, c...	37	0.31
	emb AA680906 AA680906 LmFrAm0494 Leishmania major Amastigote ful...	33	1.0
30	emb AF193903 AF193903 Cafeteria roenbergensis mitochondrial DNA,...	35	1.1
	emb AF229795 AF229795 Vigna radiata beta galactosidase mRNA, com...	35	1.5
	emb AW683786 AW683786 NF001A06NR1F1038 Nodulated root Medicago t...	35	1.5
	emb AC005802 AC005802 Leishmania major chromosome 3 clone L6202 ...	34	2.1
	emb AC005893 AC005893 Leishmania major chromosome 3 clone L822 s...	34	2.1
35	emb AA520166 AA520166 TgESTzz39b08.s1 TgME49 invivo Bradyzoite c...	34	2.9
	emb AW618793 AW618793 EST320779 L. pennellii trichome, Cornell U...	34	2.9
	emb AW306460 AW306460 se51a02.y1 Gm-c1017 Glycine max cDNA clone...	34	2.9
	emb AQ502036 AQ502036 V10E12 mTn-3xHA/lacZ Insertion Library Sac...	33	3.9
	gb U87148 HVU87148 Hordeum vulgare nucellin mRNA, complete cds.	33	3.9
40	emb AF017430 AF017430 Hordeum vulgare EEA1 mRNA, complete cds.	33	3.9
	emb AQ500344 AQ500344 V41B12 mTn-3xHA/lacZ Insertion Library Sac...	33	3.9
	emb Z71686 SCYNR071C S.cerevisiae chromosome XIV reading frame O...	33	3.9
	emb AQ501720 AQ501720 V15F6 mTn-3xHA/lacZ Insertion Library Sacc...	33	3.9
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45	emb AW126050 AW126050 N100246e rootphos(-) Medicago truncatula c...	33	5.4
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50	emb AQ503147 AQ503147 V44D10 mTn-3xHA/lacZ Insertion Library Sac...	33	5.4
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55	emb AA783066 AA783066 alh02c9.r1 Aspergillus nidulans 24hr asexu...	26	5.7
	emb AC013353 AC013353 Trypanosoma brucei chromosome VI clone RPC...	32	7.4
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	emb AW780906 AW780906 sl86c03.y1 Gm-c1037 Glycine max cDNA clone...	32	7.4
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60	emb AW156670 AW156670 se29c01.y1 Gm-c1015 Glycine max cDNA clone...	32	7.4
	emb AW277786 AW277786 sf86e12.y1 Gm-c1019 Glycine max cDNA clone...	32	7.4

- emb|AE001432|AE001432 Plasmodium falciparum chromosome 2, sectio... 32 7.4
 emb|AW734710|AW734710 sk98e12.y1 Gm-c1035 Glycine max cDNA clone... 32 7.4
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 emb|AW704821|AW704821 sk40a01.y1 Gm-c1019 Glycine max cDNA clone... 32 7.4
 5 emb|AW277436|AW277436 sf82a10.y1 Gm-c1019 Glycine max cDNA clone... 32 7.4
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 emb|AW757240|AW757240 sl30h11.y1 Gm-c1027 Glycine max cDNA clone... 32 7.4
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 dehydrogenase /chip nova /gb_link
 15 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al021961|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al021961>
 (1812 letters)
- 20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
- Searching.....done
- 25 Score E
 Sequences producing significant alignments: (bits) Value
- emb|AW930291|AW930291 EST340748 tomato fruit mature green, TAMU ... 415 e-115
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 30 emb|AW666282|AW666282 sk34f11.y1 Gm-c1028 Glycine max cDNA clone... 393 e-108
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 emb|AW691093|AW691093 NF041B09ST1F1000 Developing stem Medicago ... 355 e-102
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 35 emb|AW696933|AW696933 NF112E03ST1F1021 Developing stem Medicago ... 357 4e-98
 emb|AW731385|AW731385 GA_Ea0030K22 Gossypium arboreum 7-10 dpa ... 344 2e-95
 emb|AW688234|AW688234 NF005A05ST1F1000 Developing stem Medicago ... 348 6e-95
 gb|BE036418|BE036418 MO24D12 MO Mesembryanthemum crystallinum cD... 279 1e-94
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 40 emb|AW423801|AW423801 sh52b02.y1 Gm-c1017 Glycine max cDNA clone... 339 4e-92
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 45 gb|BE020170|BE020170 sm39e05.y1 Gm-c1028 Glycine max cDNA clone ... 291 1e-77
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 emb|AW926887|AW926887 HVSMEg0008N09 Hordeum vulgare pre-anthesis... 280 3e-74
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 50 emb|AW625020|AW625020 EST313849 tomato radicle, 5 d post-imbibit... 253 4e-66
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 55 emb|AW398821|AW398821 EST309321 L. pennellii trichome, Cornell U... 201 2e-50
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 60 emb|AW736943|AW736943 NXNV_081_H10_F Nsf Xylem Normal wood Verti... 180 3e-44
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- emb|AW695961|AW695961 NF101A09ST1F1068 Developing stem Medicago ... 172 6e-42
 gb|BE055879|BE055879 GA_Ea0026P04f Gossypium arboreum 7-10 dpa ... 172 8e-42
 gb|L47851|L47851 BNAF1389 Mustard flower buds Brassica rapa cDNA... 166 8e-41
 5 emb|AW688606|AW688606 NF009E07ST1F1000 Developing stem Medicago ... 112 2e-39
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 10 dbj|D89185|D89185 Schizosaccharomyces pombe mRNA, partial cds, c... 103 1e-36
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 15 emb|AL157811|SPAC186 S.pombe chromosome I cosmid c186. 98 1e-32
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 20 emb|AC005761|AC005761 Leishmania major chromosome 3 clone L952 s... 78 7e-31
 emb|AW693956|AW693956 NF071B03ST1F1027 Developing stem Medicago ... 89 5e-30
 emb|AI165568|AI165568 A086P59U Hybrid aspen plasmid library Popu... 132 5e-30
 emb|Z37997|SC9877 S.cerevisiae chromosome IX cosmid 9877. 84 5e-30
 emb|AW599036|AW599036 gb01c10.y1 Moss EST library PPN Physcomitr... 116 5e-25
 25 emb|AF079881|AF079881 Entodinium caudatum D-3-phosphoglycerate d... 56 1e-24
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 35 emb|AQ874261|AQ874261 V105E9 mTn-3xHA/lacZ Insertion Library, st... 84 2e-15
 gb|H74366|H74366 270 Deletion-treated Brassica napus cDNA clone ... 82 2e-14
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 40 emb|AW442114|AW442114 EST311510 tomato fruit red ripe, TAMU Lycop... 77 4e-13
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 55 dbj|D49433|D49433 Pumpkin clone HPR2 hydroxypyruvate reductases ... 72 1e-11
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 60 emb|X14609|CSNDHR Cucumis sativus mRNA for NAPH-dependent hydrox... 70 5e-11
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15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E
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 25 emb|AW622441|AW622441 EST313229 tomato root during/after fruit s... 204 2e-51
 emb|AL157994|SPAC105 S.pombe chromosome I cosmid c105. 192 1e-47
 emb|AQ841817|AQ841817 T134068 Soybean RFLP probe Glycine max gen... 186 8e-46
 emb|X77087|SJ100567 S.cerevisiae (S288C) J0909, J0911, J0914 and... 150 5e-35
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 30 emb|AW774205|AW774205 EST333356 KV3 Medicago truncatula cDNA clo... 120 8e-28
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 emb|AW980088|AW980088 EST341613 tomato root deficiency, Cornell ... 45 8e-07
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 40 emb|AV410314|AV410314 AV410314 Lotus japonicus young plants (two... 40 0.010
 emb|AW163886|AW163886 Ljirnp17-312-a12 Ljirnp Lambda HybriZap... 34 0.019
 emb|AQ849208|AQ849208 LMAJFV1_lm43f12.y1 Leishmania major FV1 ra... 41 0.042
 emb|AW690188|AW690188 NF029E07ST1F1000 Developing stem Medicago ... 35 0.044
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 45 emb|AL112906|CNS01AGI Botrytis cinerea strain T4 cDNA library un... 38 0.28
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 55 gb|BE036059|BE036059 MO19C02 MO Mesembryanthemum crystallinum cD... 35 3.6
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 60 emb|AI612607|AI612607 TENG0370 T. Cruzi epimastigote normalised ... 34 5.0
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- emb|AW010989|AW010989 ST15D02 Pine TriplEx shoot tip library Pin... 34 5.0
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 15 emb|AI050199|AI050199 TENU1447 *T. cruzi* epimastigote normalized ... 34 6.8
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 20 emb|AW126974|AW126974 ga16h04.y1 Moss EST library PPU Physcomitr... 33 9.4
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 25 gb|BE035627|BE035627 MO12F02 *Mesembryanthemum crystallinum* cD... 33 9.4
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 http://www.ncgr.org/cgi-bin/ff?ac002387
 35 (2371 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| Sequences producing significant alignments: | (bits) | Value |
| 45 emb Z50099 STTKETMR <i>S.tuberosum</i> mRNA for transketolase. | 1372 | 0.0 |
| gb L76554 SPITRAN <i>Spinacia oleracea</i> transketolase mRNA, chloropl... | 1350 | 0.0 |
| emb Y15781 CAY15781 <i>Capsicum annuum</i> mRNA for plastid transketola... | 1344 | 0.0 |
| emb A52295 A52295 Sequence 1 from Patent EP0723017. | 1283 | 0.0 |
| emb Z46648 CPTKT7 <i>C.plantagineum</i> tkt7 gene for transketolase. | 1063 | 0.0 |
| 50 emb Z46647 CPTKT10 <i>C.plantagineum</i> tkt10 gene for transketolase. | 1038 | 0.0 |
| emb Z46646 CPTKT3 <i>C.plantagineum</i> tkt3 gene for transketolase. | 1014 | 0.0 |
| emb AJ249787 CPA249787 <i>Cyanophora paradoxa</i> mRNA for putative tra... | 557 | 0.0 |
| emb AL033501 CAC41C10 <i>C.albicans</i> cosmid Ca41C10. | 253 | e-175 |
| emb AC007872 AC007872 The sequence of an <i>Aspergillus parasiticus</i> ... | 167 | e-158 |
| 55 gb H55032 H55032 HHU58a <i>Sorghum bicolor</i> cv. TX430 <i>Sorghum bicol</i> ... | 233 | e-151 |
| emb AC005299 AC005299 <i>emericella nidulans</i> chromosome viii cosmid... | 166 | e-147 |
| emb AC004395 AC004395 <i>Emericella nidulans</i> Chromosome VIII Cosmid... | 166 | e-147 |
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| 60 emb AI778813 AI778813 EST259692 tomato susceptible, Cornell Lyco... | 453 | e-126 |
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5 gb|BE052708|BE052708 GA_Ea0031N21f Gossypium arboreum 7-10 dpa ... 431 e-119
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15 emb|AW720123|AW720123 LjNEST14e4r Lotus japonicus nodule library... 369 e-101
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20 emb|AW979915|AW979915 EST341564 tomato root deficiency, Cornell ... 349 6e-95
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60 emb|AV395290|AV395290 AV395290 Chlamydomonas reinhardtii C9 Chla... 288 1e-76
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- emb|AW907301|AW907301 EST343424 potato stolon, Cornell Universit... 281 1e-74
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 emb|AV394221|AV394221 AV394221 Chlamydomonas reinhardtii C9 Chla... 275 4e-73
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 5 emb|AI162975|AI162975 A028P14U Hybrid aspen plasmid library Popu... 273 1e-72
 emb|AJ234429|HVU234429 Hordeum vulgare partial mRNA; clone cMWG0... 271 1e-71
 emb|AW398784|AW398784 EST309284 L. pennellii trichome, Cornell U... 271 2e-71
 gb|BE056580|BE056580 894010C09.y1 C. reinhardtii CC-1690, normal... 267 2e-70
 emb|AW694944|AW694944 NF081G03ST1F1023 Developing stem Medicago ... 258 4e-70
 10 emb|AW041543|AW041543 EST284407 tomato mixed elicitor, BTI Lycop... 265 8e-70
 emb|AW980590|AW980590 EST391743 GVN Medicago truncatula cDNA clo... 265 1e-69
 emb|AF173677|AF173677 Beta vulgaris clone TK109UNI transketolase... 132 2e-69
 emb|AQ842082|AQ842082 T134371 Soybean RFLP probe Glycine max gen... 263 4e-69
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 15 emb|AI726103|AI726103 BNLGHi5028 Six-day Cotton fiber Gossypium ... 260 3e-68
 emb|AW695133|AW695133 NF091E12ST1F1098 Developing stem Medicago ... 258 6e-68
 emb|AA819992|AA819992 L0-171M13R Ice plant Lambda Uni-Zap XR exp... 258 1e-67
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 emb|AI563214|AI563214 EST00338 watermelon lambda zap library Cit... 249 1e-65
 20 emb|AF086822|AF086822 Candida boidinii dihydroxyacetone synthase... 163 7e-65
 emb|AW696579|AW696579 NF106E10ST1F1082 Developing stem Medicago ... 249 7e-65
 gb|M63302|YSCTRANSK S.cerevisiae transketolase gene, complete cds. 168 5e-64
- 25 Query= AL022347.46_at 13659_at /id_source genbank /description
 emb|caa18462.1| (al022347) serine/threonine kinase-like protein
 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
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 30 http://www.ncgr.org/cgi-bin/ff?al022347
 (2037 letters)
- Database: plantfungal
 661,018 sequences; 426,114,510 total letters
- 35 Searching.....done
- Score E
 Sequences producing significant alignments: (bits) Value
- 40 emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 385 e-125
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 343 e-111
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 348 e-109
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 346 e-109
 45 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 347 e-109
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 333 e-108
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 342 e-107
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 328 e-106
 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 334 e-105
 50 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase ... 329 e-104
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 205 e-104
 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 326 e-103
 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 330 e-103
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 336 e-102
 55 emb|AB013720|AB013720 Brassica oleracea mRNA for SRK23Bol, parti... 325 e-101
 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 290 e-100
 emb|Y12530|BOARLKGGEN B.oleraceae gene encoding serine/threonine ... 131 1e-95
 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 282 3e-94
 dbj|D38564|BOLRPKB Brassica campestris mRNA for receptor protein... 281 3e-93
 60 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 276 4e-93
 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 129 1e-91

- emb|AW620957|AW620957 sj98a07.y1 Gm-cl023 Glycine max cDNA clone... 275 9e-91
 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 254 1e-90
 emb|AB000971|AB000971 Brassica campestris pseudogene for recepto... 115 8e-90
 emb|AF088885|AF088885 Nicotiana tabacum receptor-like kinase CHR... 292 1e-89
 5 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 127 2e-88
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 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 284 8e-86
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 10 emb|X79432|BOSRK3 B.oleracea SRK3 gene. 118 6e-84
 emb|AB024420|AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,... 112 8e-84
 emb|AB013718|AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,... 113 7e-83
 emb|AB024422|AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ... 113 1e-82
 emb|Z30211|BOSRK29G B.oleracea (alboglabra) srk29 gene. 122 9e-82
 15 gb|BE057261|BE057261 sm99f12.y1 Gm-cl015 Glycine max cDNA clone ... 296 4e-79
 emb|AW831390|AW831390 sm22a06.y1 Gm-cl028 Glycine max cDNA clone... 216 1e-75
 emb|Y12531|BOBRLKGEN B.oleraceae gene encoding serine/threonine ... 126 2e-75
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 emb|AJ245479|BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,... 122 5e-75
 20 emb|AW442344|AW442344 EST311740 tomato fruit red ripe, TAMU Lyco... 221 3e-72
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 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 268 1e-70
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 25 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 242 2e-66
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 30 emb|AI897876|AI897876 EST267319 tomato ovary, TAMU Lycopersicon ... 166 1e-61
 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 236 6e-61
 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 166 1e-60
 emb|Y16999|TCA16999 Theobroma cacao microsatellite DNA, clone mT... 132 2e-58
 emb|AW309544|AW309544 sf20h08.x1 Gm-cl028 Glycine max cDNA clone... 177 4e-58
 35 emb|AI822907|AI822907 L30-754T3 Ice plant Lambda Uni-Zap XR expr... 126 3e-57
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 emb|AW736407|AW736407 EST332421 KV3 Medicago truncatula cDNA clo... 223 4e-57
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 emb|AI901283|AI901283 sc31d08.y1 Gm-cl014 Glycine max cDNA clone... 171 3e-54
 emb|AI771857|AI771857 EST252957 tomato ovary, TAMU Lycopersicon ... 169 7e-54
 emb|AI488101|AI488101 EST246423 tomato ovary, TAMU Lycopersicon ... 169 7e-54
 45 emb|AW687233|AW687233 NF007D09RTIF1077 Developing root Medicago ... 109 1e-53
 emb|AI898581|AI898581 EST268024 tomato ovary, TAMU Lycopersicon ... 172 3e-53
 emb|AW054349|AW054349 L30-1774T3 Ice plant Lambda Uni-Zap XR exp... 126 5e-53
 emb|AI899156|AI899156 EST268599 tomato ovary, TAMU Lycopersicon ... 172 1e-52
 emb|AB041503|AB041503 Populus nigra PnPK1 mRNA for protein kinas... 137 2e-52
 50 emb|AB041504|AB041504 Populus nigra PnPK2 mRNA for protein kinas... 136 1e-51
 emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 118 5e-51
 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 172 7e-51
 emb|AW667985|AW667985 GA_Ea0012C15 Gossypium arboreum 7-10 dpa ... 106 1e-50
 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 72 2e-50
 55 emb|AW684339|AW684339 NF015G04NR1F1000 Nodulated root Medicago t... 135 2e-50
 emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 108 3e-49
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 emb|Z18884|BOSRKRPC B.oleracea encoding S-receptor kinase relate... 121 1e-48
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 60 emb|AW034624|AW034624 EST278308 tomato callus, TAMU Lycopersicon... 192 1e-47
 emb|AI484701|AI484701 EST242962 tomato ovary, TAMU Lycopersicon ... 96 1e-47

- emb|AW394449|AW394449 sh05d09.y1 Gm-c1016 Glycine max cDNA clone... 121 1e-47
 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 190 3e-47
 emb|AF220602|AF220602 Lycopersicon pimpinellifolium Rio Grande 7... 111 3e-47
 gb|U59317|LPU59317 Lycopersicon pimpinellifolium serine/threonine... 107 3e-47
 5 gb|U13923|LEU13923 Lycopersicon pimpinellifolium serine/threonine... 107 3e-47
 emb|AW034993|AW034993 EST279222 tomato callus, TAMU Lycopersicon... 178 4e-47
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 emb|AW053331|AW053331 L30-1528T3 Ice plant Lambda Uni-Zap XR exp... 126 1e-46
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 10 emb|Z18861|BOSRK RPA B.oleracea encoding S-receptor kinase relate... 118 2e-46
 emb|AI729170|AI729170 BNLGHi12834 Six-day Cotton fiber Gossypium... 128 3e-46
 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 108 7e-46
 emb|AF220603|AF220603 Lycopersicon esculentum VFNT Cherry Pto lo... 109 1e-45
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 15 gb|U59318|LEU59318 Lycopersicon esculentum serine/threonine prot... 105 1e-45
 emb|AW775756|AW775756 EST334821 DSIL Medicago truncatula cDNA cl... 135 2e-45
 emb|Z73295|CRPK1 C.roseus mRNA for receptor-like protein kinase. 68 3e-45
 gb|U59316|LEU59316 Lycopersicon esculentum serine/threonine prot... 103 1e-44

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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005662|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005662|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005662|/ncgi)
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 (966 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

35

Score E

Sequences producing significant alignments: (bits) Value

- emb|AW685935|AW685935 NF031H09NR1F1000 Nodulated root Medicago t... 299 1e-83
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 emb|AI489097|AI489097 EST247436 tomato ovary, TAMU Lycopersicon ... 310 1e-83
 emb|AI781847|AI781847 EST262726 tomato susceptible, Cornell Lyco... 309 2e-83
 emb|AW442260|AW442260 EST311656 tomato fruit red ripe, TAMU Lyco... 308 4e-83
 emb|AI781496|AI781496 EST262375 tomato susceptible, Cornell Lyco... 308 4e-83
 45 emb|AI898923|AI898923 EST268366 tomato ovary, TAMU Lycopersicon ... 307 8e-83
 emb|AI894834|AI894834 EST264277 tomato callus, TAMU Lycopersicon... 306 2e-82
 emb|AW033760|AW033760 EST277331 tomato callus, TAMU Lycopersicon... 306 2e-82
 emb|AI490417|AI490417 EST248743 tomato ovary, TAMU Lycopersicon ... 304 7e-82
 emb|AW686492|AW686492 NF042A07NR1F1000 Nodulated root Medicago t... 299 8e-82
 50 emb|AI898538|AI898538 EST267981 tomato ovary, TAMU Lycopersicon ... 303 1e-81
 emb|AI488586|AI488586 EST246925 tomato ovary, TAMU Lycopersicon ... 303 2e-81
 emb|AI775239|AI775239 EST256339 tomato resistant, Cornell Lycope... 302 4e-81
 emb|AI771731|AI771731 EST252831 tomato ovary, TAMU Lycopersicon ... 301 5e-81
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 55 emb|AW029697|AW029697 EST272952 tomato callus, TAMU Lycopersicon... 299 2e-80
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 emb|AI897802|AI897802 EST267245 tomato ovary, TAMU Lycopersicon ... 297 6e-80
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 60 emb|AW684608|AW684608 NF018H07NR1F1000 Nodulated root Medicago t... 292 3e-78
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5	emb AI488011 AI488011 EST246333 tomato ovary, TAMU Lycopersicon ...	286	2e-76
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15	emb AI485145 AI485145 EST243449 tomato ovary, TAMU Lycopersicon ...	266	2e-70
	emb AW708004 AW708004 EST0051 Grape berries Lambda Zap II Librar...	266	2e-70
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	emb AI898224 AI898224 EST267667 tomato ovary, TAMU Lycopersicon ...	245	1e-69
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	emb AW222134 AW222134 EST298945 tomato fruit red ripe, TAMU Lyco...	243	2e-63
	emb AW625379 AW625379 EST319202 tomato radicle, 5 d post-imbibit...	242	4e-63
	emb AI485781 AI485781 EST244102 tomato ovary, TAMU Lycopersicon ...	240	1e-62
25	emb AW728861 AW728861 GA_Ea0028O02 Gossypium arboreum 7-10 dpa ...	189	2e-59
	emb AI489435 AI489435 EST247774 tomato ovary, TAMU Lycopersicon ...	224	7e-58
	emb AI485480 AI485480 EST243801 tomato ovary, TAMU Lycopersicon ...	221	5e-57
	emb AW030923 AW030923 EST274230 tomato callus, TAMU Lycopersicon...	219	3e-56
	emb AI771831 AI771831 EST252931 tomato ovary, TAMU Lycopersicon ...	219	3e-56
30	emb AI488694 AI488694 EST247033 tomato ovary, TAMU Lycopersicon ...	216	2e-55
	emb AI897044 AI897044 EST266487 tomato ovary, TAMU Lycopersicon ...	216	2e-55
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35	emb AW310620 AW310620 sg22b10.x1 Gm-c1024 Glycine max cDNA clone...	138	4e-49
	emb AA660966 AA660966 00863 MtRHE Medicago truncatula cDNA 5' si...	193	2e-48
	emb AI488052 AI488052 EST246374 tomato ovary, TAMU Lycopersicon ...	191	6e-48
	emb AI483934 AI483934 EST249805 tomato ovary, TAMU Lycopersicon ...	190	2e-47
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40	emb AI488394 AI488394 EST246716 tomato ovary, TAMU Lycopersicon ...	189	3e-47
	emb AW687876 AW687876 NF014D11RT1F1093 Developing root Medicago ...	179	2e-44
	emb AW031053 AW031053 EST274360 tomato callus, TAMU Lycopersicon...	175	6e-43
	emb AI771906 AI771906 EST253006 tomato ovary, TAMU Lycopersicon ...	174	1e-42
	emb AI771730 AI771730 EST252830 tomato ovary, TAMU Lycopersicon ...	171	5e-42
45	emb AI895638 AI895638 EST265081 tomato callus, TAMU Lycopersicon...	164	9e-40
	emb AW441823 AW441823 EST311219 tomato fruit red ripe, TAMU Lyco...	164	9e-40
	emb AW981333 AW981333 EST392486 DSIL Medicago truncatula cDNA cl...	156	3e-37
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50	emb AW563884 AW563884 LG1_272_D05.b1_A002 Light Grown 1 (LG1) So...	136	3e-31
	emb AI489302 AI489302 EST247641 tomato ovary, TAMU Lycopersicon ...	129	4e-29
	emb AI967559 AI967559 Ljirnp05-409-e8 Ljirnp Lambda HybriZap ...	120	2e-26
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55	emb AI725304 AI725304 1170 PtIFG2 Pinus taeda cDNA clone 9256r, ...	78	2e-18
	emb AW096566 AW096566 EST289746 tomato mixed elicitor, BTI Lycop...	90	3e-17
	emb AI899609 AI899609 EST269052 tomato susceptible, Cornell Lyco...	90	3e-17
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- emb|AW032431|AW032431 EST275970 tomato callus, TAMU Lycopersicon... 87 2e-16
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 emb|AW185076|AW185076 se86d10.y1 Gm-cl023 Glycine max cDNA clone... 69 4e-14
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 gb|U00029|YSCH9177 Saccharomyces cerevisiae chromosome VIII cosm... 35 2e-05
 emb|AW670960|AW670960 LG1_278_A08.b1_A002 Light Grown 1 (LG1) So... 50 3e-05
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 10 emb|AW443870|AW443870 EST308800 tomato mixed elicitor, BTI Lycop... 41 0.011
 emb|AW678240|AW678240 WS1_14_G12.b1_A002 Water-stressed 1 (WS1) ... 37 0.26
 emb|AL034559|PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq... 36 0.50
 gb|U10549|ANU10549 Aspergillus niger protein kinase C (pkcA) gen... 35 0.94
 gb|U74447|ZAU74447 Zinnia angustifolia internal transcribed spac... 33 0.95
 15 emb|AZ217616|AZ217616 Sheared DNA-90G1.TF Sheared DNA Trypanosom... 31 2.1

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 (159 letters)

25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AQ940444 AQ940444 Sheared DNA-35C4.TF Sheared DNA Trypanosom...	24	0.40
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40	emb AW266254 AW266254 L30-2966T3 Ice plant Lambda Uni-Zap XR exp...	27	1.6
	emb AL355929 NCB21J21 Neurospora crassa DNA linkage group II BAC...	27	1.6
	emb AW726145 AW726145 GA_Ea0020M12 Gossypium arboreum 7-10 dpa ...	26	2.2
	emb AW661015 AW661015 832009D11.y1 C. reinhardtii CC-125 nutrien...	23	2.7
	emb AV391625 AV391625 AV391625 Chlamydomonas reinhardtii C9 Chla...	23	2.7
45	emb AI055219 AI055219 coau0003G03 Cotton Boll Abscission Zone cD...	23	2.7
	emb AL354533 LMFL6294 Leishmania major Friedlin chromosome 21 co...	26	4.1
	gb N98018 N98018 2045C3 czapPFDd2.1, Debopam Chakrabarti Plasmod...	26	4.1
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	emb AA519224 AA519224 TgESTzz39g08.s1 TgME49 invivo Bradyzoite c...	26	4.1
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	emb AA531994 AA531994 TgESTzz46c10.r1 TgME49 invivo Bradyzoite c...	26	4.1
	emb AA520816 AA520816 TgESTzz64d11.r1 TgME49 invivo Bradyzoite c...	26	4.1
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55	emb AL136536 SPBC1703 S.pombe chromosome II cosmid c1703.	26	4.1
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	emb Z81402 CAZ81402 C.aeruginosa 28S rRNA gene.	26	4.1
	emb AW979496 AW979496 EST310517 tomato root deficiency, Cornell ...	26	4.1
	emb AW671199 AW671199 LG1_330_F04.b1_A002 Light Grown 1 (LG1) So...	25	5.7
60	emb Z74775 SCYOL033W S.cerevisiae chromosome XV reading frame OR...	25	5.7
	emb AA897901 AA897901 NCP4C5T3 Perithecial Neurospora crassa cDN...	25	5.7

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 5 gb|BE054352|BE054352 GA_Ea0035E11f Gossypium arboreum 7-10 dpa ... 25 5.7
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 emb|X87148|VPPPCGEN V.planifolia mRNA for phosphoenolpyruvate ca... 25 5.7
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 10 emb|AI730886|AI730886 BNLGHi8147 Six-day Cotton fiber Gossypium ... 25 5.7
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 15 emb|Z49821|SCPDR10 S.cerevisiae PDR10, MYO2, PDR10, SCD5, MIP1, ... 25 7.8
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 20 emb|AJ131048|CAR131048 Cicer arietinum mRNA for protein kinase, ... 25 7.8
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 25 emb|AI068528|AI068528 mgae0002dE03f Magnaporthe grisea Appressor... 25 7.8
 emb|AI068407|AI068407 mgae0002aH09f Magnaporthe grisea Appressor... 25 7.8
 emb|AL109846|SPBC17G9 S.pombe chromosome II cosmid c17G9. 23 9.1
 emb|Z72244|CNIGRITS1 C.nigricans DNA for internal transcribed sp... 21 9.5
- 30 Query= AL035528.279_i_at 14110_i_at /id_source genbank /description
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 /chip nova /gb_link
 http://www3.ncbi.nlm.nih.gov/htbin-
 35 post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035528| /ncgi
 http://www.ncgr.org/cgi-bin/ff?al035528
 (2508 letters)
- Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters
- Searching.....done
- Score E
 45 Sequences producing significant alignments: (bits) Value
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 50 emb|AJ002236|LPJ002236 Lycopersicon pimpinellifolium Cf-9 resist... 103 2e-57
 gb|U42444|U42444 Lycopersicon pimpinellifolium leucine rich repe... 122 4e-57
 emb|A57130|A57130 Sequence 1 from Patent WO9531564. 122 4e-57
 gb|U42445|U42445 Lycopersicon pimpinellifolium leucine rich repe... 122 4e-57
 emb|A57133|A57133 Sequence 4 from Patent WO9531564. 122 4e-57
 55 emb|AF053995|AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ... 121 2e-56
 emb|AF053997|AF053997 Lycopersicon esculentum Hcr2-5B (Hcr2-5B) ... 109 1e-52
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 emb|AF053996|AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr... 101 5e-49
 emb|AF053998|AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ... 127 7e-49
 60 emb|A67434|A67434 Sequence 7 from Patent WO9743429. 127 7e-49
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- emb|A67429|A67429 Sequence 2 from Patent WO9743429. 127 7e-49
emb|A67428|A67428 Sequence 1 from Patent WO9743429. 127 7e-49
emb|AB029327|AB029327 Nicotiana tabacum mRNA for elicitor-induci... 102 3e-48
emb|AF053994|AF053994 Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ... 103 2e-42
5 emb|Y12640|LECF4A L.esculentum Cf-4A gene. 100 1e-40
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20 emb|AZ044600|AZ044600 Gm_UMB001_116_G01.R UMN Soybean BAC Librar... 106 8e-22
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35 emb|AW030004|AW030004 EST273259 tomato callus, TAMU Lycopersicon... 95 2e-18
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emb|AF159167|AF159167 Eucalyptus grandis polygalacturonase-inhib... 74 3e-18
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40 emb|X81370|TAAWJL236 T.aestivum (subclone pAWJL236) AWJL236 gene. 78 4e-18
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emb|AW399097|AW399097 EST309597 L. pennellii trichome, Cornell U... 69 2e-16
55 emb|AI443128|AI443128 sa84f10.y1 Gm-cl004 Glycine max cDNA clone... 81 2e-16
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emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 87 5e-16
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60 emb|AV419297|AV419297 AV419297 Lotus japonicus young plants (two... 63 7e-16
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- emb|AA557055|AA557055 897 Loblolly pine N Pinus taeda cDNA clone... 86 1e-15
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 5 emb|AW164782|AW164782 se77g01.y1 Gm-c1023 Glycine max cDNA clone... 85 2e-15
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 (2508 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

35 Searching.....done

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| | emb AF119041 AF119041 | Lycopersicon esculentum haplotype Southern... | 105 | 4e-61 |
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| | emb AJ002235 LHJ002235 | Lycopersicon hirsutum Cf-4 resistance gen... | 103 | 1e-59 |
| | emb AJ002236 LPJ002236 | Lycopersicon pimpinellifolium Cf-9 resist... | 103 | 2e-57 |
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| | gb U42445 U42445 | Lycopersicon pimpinellifolium leucine rich repe... | 122 | 4e-57 |
| | emb A57133 A57133 | Sequence 4 from Patent WO9531564. | 122 | 4e-57 |
| | emb AF053995 AF053995 | Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ... | 121 | 2e-56 |
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| | emb A67432 A67432 | Sequence 5 from Patent WO9743429. | 109 | 1e-52 |
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| | emb AF053998 AF053998 | Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ... | 127 | 7e-49 |
| | emb A67434 A67434 | Sequence 7 from Patent WO9743429. | 127 | 7e-49 |
| 55 | emb AF053993 AF053993 | Lycopersicon esculentum disease resistance... | 127 | 7e-49 |
| | emb A67429 A67429 | Sequence 2 from Patent WO9743429. | 127 | 7e-49 |
| | emb A67428 A67428 | Sequence 1 from Patent WO9743429. | 127 | 7e-49 |
| | emb AB029327 AB029327 | Nicotiana tabacum mRNA for elicitor-induci... | 102 | 3e-48 |
| | emb AF053994 AF053994 | Lycopersicon esculentum Hcr2-0A (Hcr2-0A) ... | 103 | 2e-42 |
| 60 | emb Y12640 LECF4A | L.esculentum Cf-4A gene. | 100 | 1e-40 |
| | emb AJ002237 LEJ002237 | Lycopersicon esculentum haplotype of the ... | 100 | 8e-39 |

- emb|A58270|A58270 Sequence 1 from Patent WO9635790. 93 6e-37
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 20 emb|AW398661|AW398661 EST309161 L. pennellii trichome, Cornell U... 85 2e-20
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 30 emb|AF159171|AF159171 Eucalyptus nitens polygalacturonase-inhibi... 74 3e-18
 emb|AF159170|AF159170 Eucalyptus saligna polygalacturonase-inhib... 74 3e-18
 emb|AF159167|AF159167 Eucalyptus grandis polygalacturonase-inhib... 74 3e-18
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 35 emb|Z49063|ADPGIP A.deliciosa pgip mRNA for polygalacturonase in... 74 5e-18
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 5 emb|AW671867|AW671867 LG1_352_F06.b1_A002 Light Grown 1 (LG1) So... 84 5e-15
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 10 emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 66 9e-15
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 emb|AW616567|AW616567 EST322978 L. hirsutum trichome, Cornell Un... 83 9e-15
 emb|AW697060|AW697060 NF111H11ST1F1095 Developing stem Medicago ... 77 1e-14
 15 emb|X81369|TAAWJL218 T.aestivumn (subclone pAWJL218) AWJL218 gene. 83 1e-14
 emb|AI776963|AI776963 EST251989 tomato callus, TAMU Lycopersicon... 83 1e-14
 emb|AW443205|AW443205 EST308135 tomato mixed elicitor, BTI Lycop... 83 1e-14
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- 20 Query= AF077407.30_at 14116_at /id_source genbank /description
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 25 http://www3.ncbi.nlm.nih.gov/htbin-
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- 30 Database: plantfungal
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- emb|AJ132224|LES132224 Lycopersicon esculentum mRNA for hexose t... 819 0.0
 emb|AJ010942|LES010942 Lycopersicon esculentum mRNA for hexose t... 815 0.0
 40 gb|L21753|SCFGLUTRAB Saccharum hybrid cultivar H65-7052 glucose ... 222 e-176
 gb|U38651|MTU38651 Medicago truncatula sugar transporter mRNA, co... 354 e-174
 gb|L08196|RCCSCP Ricinus communis (clone PST293) sugar carrier p... 371 e-173
 emb|Y09590|VVHEXTRAN V.vinifera mRNA for hexose transporter. 356 e-170
 emb|AF061106|AF061106 Petunia x hybrida putative monosaccharide ... 255 e-170
 45 gb|L08188|RCCHCP Ricinus communis (clone ST330) hexose carrier p... 203 e-163
 emb|Z83829|PAMST1 P.abies mRNA for monosaccharide transporter Ms... 211 e-154
 emb|Z93775|VFZ93775 V.faba mRNA for hexose transporter. 362 e-129
 emb|X66856|NTMST1 N.tabacum MST1 mRNA. 215 e-129
 gb|L08197|RCCSCPS Ricinus communis (clone PST9) sugar carrier pr... 210 e-114
 50 emb|AI775535|AI775535 EST256635 tomato resistant, Cornell Lycop... 401 e-111
 gb|L21752|SCFGLUTRAA Saccharum hybrid cultivar H65-7052 glucose ... 193 2e-99
 emb|AI775204|AI775204 EST256304 tomato resistant, Cornell Lycop... 352 7e-98
 emb|AI772312|AI772312 EST253412 tomato resistant, Cornell Lycop... 214 6e-82
 emb|AJ132225|LES132225 Lycopersicon esculentum mRNA for hexose t... 188 5e-79
 55 emb|AF173655|AF173655 Beta vulgaris clone GTRTUNI glucose transp... 156 1e-73
 emb|AJ001061|VVHEXOSET Vitis vinifera hexose transporter gene. 276 3e-73
 emb|AI778344|AI778344 EST259223 tomato susceptible, Cornell Lyco... 259 1e-70
 emb|AV407522|AV407522 AV407522 Lotus japonicus young plants (two... 253 2e-66
 gb|L31352|RCCHEX9HC Ricinus communis hexose carrier (Hex9) mRNA,... 253 2e-66
 60 emb|AW684560|AW684560 NF018C12NR1F1000 Nodulated root Medicago t... 208 9e-61
 emb|AI727659|AI727659 BNLGHi8536 Six-day Cotton fiber Gossypium ... 229 5e-59

- emb|AW737777|AW737777 EST339204 tomato flower buds, anthesis, Co... 223 3e-57
 emb|AI772048|AI772048 EST253148 tomato resistant, Cornell Lycopen... 206 1e-55
 emb|AI772049|AI772049 EST253149 tomato resistant, Cornell Lycopen... 206 1e-55
 5 emb|AJ132223|LES132223 Lycopersicon esculentum mRNA for hexose t... 196 2e-54
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 10 emb|AW349933|AW349933 GM210006A20H11R Gm-r1021 Glycine max cDNA ... 189 2e-49
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 15 emb|AW705527|AW705527 sk61c02.y1 Gm-cl016 Glycine max cDNA clone... 193 1e-48
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 20 emb|AW691511|AW691511 NF045G06ST1F1000 Developing stem Medicago ... 125 3e-46
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 emb|AI731272|AI731272 BNLGHi9072 Six-day Cotton fiber Gossypium ... 172 3e-45
 emb|AW092826|AW092826 EST286006 tomato mixed elicitor, BTI Lycop... 173 6e-45
 25 emb|AI730904|AI730904 BNLGHi8171 Six-day Cotton fiber Gossypium ... 156 2e-43
 emb|AW737195|AW737195 EST338622 tomato flower buds, anthesis, Co... 173 3e-42
 gb|L31353|RCCHX10HC Ricinus communis hexose carrier (Hex10) mRNA... 173 4e-42
 emb|AW680072|AW680072 WS1_3_B09.g1_A002 Water-stressed 1 (WS1) S... 170 2e-41
 emb|AI938772|AI938772 sb58g08.y1 Gm-cl018 Glycine max cDNA clone... 104 3e-41
 30 emb|AI930883|AI930883 sb43g12.y1 Gm-cl015 Glycine max cDNA clone... 117 4e-38
 gb|L08189|RCCSCPB Ricinus communis (clone PDG15) sugar carrier p... 158 1e-37
 gb|L08191|RCCSCPD Ricinus communis (clone PDG19) sugar carrier p... 157 2e-37
 emb|AW774154|AW774154 EST333237 KV3 Medicago truncatula cDNA clo... 153 4e-37
 gb|L08194|RCCSCPG Ricinus communis (clone PDGK4) sugar carrier p... 155 6e-37
 35 gb|U22525|KLU22525 Kluyveromyces lactis high affinity glucose tr... 109 3e-36
 emb|AW234900|AW234900 sf20e02.y1 Gm-cl028 Glycine max cDNA clone... 152 8e-36
 emb|AW455278|AW455278 EST311938 tomato root during/after fruit s... 152 8e-36
 emb|AW040775|AW040775 EST283639 tomato mixed elicitor, BTI Lycop... 141 2e-35
 emb|X96876|SCCHRIVFY S.cerevisiae DNA of cosmid from chromosome ... 81 2e-35
 40 emb|Z74186|SCYDL138W S.cerevisiae chromosome IV reading frame OR... 81 2e-35
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 emb|AW687897|AW687897 NF014F11RT1F1094 Developing root Medicago ... 124 3e-35
 emb|AW185053|AW185053 se86b03.y1 Gm-cl023 Glycine max cDNA clone... 149 4e-35
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 45 emb|AI780094|AI780094 EST260973 tomato susceptible, Cornell Lyco... 139 7e-35
 emb|AF149282|AF149282 Phaseolus vulgaris clone pBHEX2 hexose car... 148 1e-34
 emb|AW756300|AW756300 sl18g04.y1 Gm-cl036 Glycine max cDNA clone... 140 2e-33
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 50 gb|BE126141|BE126141 DG1_66_B09.b1_A002 Dark Grown 1 (DG1) Sorgh... 114 2e-32
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 55 emb|AW432874|AW432874 sh99b03.y1 Gm-cl016 Glycine max cDNA clone... 130 5e-31
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 60 emb|AV407618|AV407618 AV407618 Lotus japonicus young plants (two... 78 2e-24
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- emb|AI728506|AI728506 BNLGHi10921 Six-day Cotton fiber Gossypium... 98 1e-23
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 emb|AF215852|AF215852 Nicotiana tabacum hexose transporter (pGlc... 69 3e-23
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 5 emb|AV425362|AV425362 AV425362 Lotus japonicus young plants (two... 109 7e-23
 gb|U43629|BVU43629 Beta vulgaris integral membrane protein mRNA,... 68 1e-22
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 10 emb|AW255633|AW255633 ML692 peppermint glandular trichome Mentha... 101 1e-20
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 emb|AI778758|AI778758 EST259637 tomato susceptible, Cornell Lyco... 89 1e-19
 15 emb|AI778757|AI778757 EST259636 tomato susceptible, Cornell Lyco... 89 1e-19
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| | Sequences producing significant alignments: | | (bits) Value |
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| | emb X70981 SMCYPEG2 S.melongena CYP71A1 mRNA for P450 hydroxylase. | 127 | 6e-99 |
| | emb Y09423 NRCYP71A5 Nepeta racemosa mRNA for cytochrome P450, C... | 136 | 8e-98 |
| | emb X71654 SMCYP71B3 S.melongena CYP71A2 mRNA for hydroxylase. | 124 | 9e-95 |
| | dbj D14990 POTCPEG4 Eggplant mRNA for cytochrome P-450EG4, compl... | 124 | 9e-95 |
| 40 | emb Y10489 GMC450CP1 G.max mRNA for putative cytochrome P450, cl... | 90 | 1e-84 |
| | emb X70982 SMCYPEG3 S.melongena CYP71A3 mRNA for P450 hydroxylase. | 126 | 3e-74 |
| | emb Y09424 NRCYP71A6 N.racemosa mRNA for cytochrome P450, CYP71A... | 154 | 3e-65 |
| | dbj E13663 E13663 cDNA encoding cytochrome P450 which is induced... | 71 | 9e-63 |
| | dbj D83968 SOYCYP93A1 Soybean mRNA for cytochrome P450 (CYP93A1)... | 71 | 9e-63 |
| 45 | emb AF022157 AF022157 Glycine max cytochrome P450 monooxygenase ... | 126 | 3e-61 |
| | emb AW053855 AW053855 L30-2274T3 Ice plant Lambda Uni-Zap XR exp... | 103 | 1e-53 |
| | emb Y09920 HT7EC0DET Helianthus tuberosus mRNA for 7-ethoxycouma... | 94 | 1e-50 |
| | emb Y10098 HTCYP76B1 H.tuberosus mRNA for 7-ethoxycoumarin O-dee... | 94 | 1e-50 |
| | emb AF022459 AF022459 Glycine max cytochrome P450 monooxygenase ... | 105 | 4e-50 |
| 50 | emb AJ238612 CRO238612 Catharanthus roseus mRNA for cytochrome P... | 89 | 2e-49 |
| | emb AF029858 AF029858 Sorghum bicolor cytochrome P450 CYP71E1 (C... | 139 | 3e-49 |
| | gb U48434 SCU48434 Solanum chacoense cytochrome P450 mRNA, compl... | 117 | 2e-48 |
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| | emb AW223719 AW223719 EST300530 tomato fruit red ripe, TAMU Lyco... | 88 | 4e-46 |
| 55 | emb Y10490 GMC450CP3 G.max mRNA for putative cytochrome P450, cl... | 104 | 6e-46 |
| | emb X71658 SMCYPEG8 S.melongena CYP76A1 mRNA. | 88 | 2e-45 |
| | emb AF122821 AF122821 Capsicum annuum cytochrome P450 (PepCYP) m... | 118 | 4e-45 |
| | emb Z33875 CYMPCP450 M.piperita gene for cytochrome P-450 oxidase. | 88 | 7e-45 |
| | emb AI897763 AI897763 EST267206 tomato ovary, TAMU Lycopersicon ... | 84 | 1e-44 |
| 60 | emb AW830233 AW830233 sm24f03.y1 Gm-c1028 Glycine max cDNA clone... | 139 | 5e-44 |
| | gb U48435 SCU48435 Solanum chacoense putative cytochrome P450 ge... | 95 | 2e-43 |

- emb|AF029857|AF029857 Sorghum bicolor cytochrome P450 CYP99A1 (C... 127 2e-43
emb|X71657|SMCYPEG7 S.melongena CYP76A2 mRNA for hydroxylase. 87 3e-43
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emb|X96784|NTP450GEN N.tabacum cytochrome P-450 gene. 105 1e-42
5 emb|AW034502|AW034502 EST278118 tomato callus, TAMU Lycopersicon... 107 2e-42
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emb|AF124816|AF124816 Mentha x piperita cytochrome p450 isoform ... 87 3e-41
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15 dbj|D14590|D14590 Campanula medium mRNA for flavonoid 3',5'-hydr... 82 2e-39
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25 emb|AW132351|AW132351 se03a02.y1 Gm-c1013 Glycine max cDNA clone... 159 5e-38
emb|AW832652|AW832652 sm15g02.y1 Gm-c1027 Glycine max cDNA clone... 159 5e-38
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emb|AF022460|AF022460 Glycine max cytochrome P450 monooxygenase ... 113 1e-37
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30 emb|AF014801|AF014801 Eschscholzia californica (S)-N-methylcocla... 75 2e-37
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emb|AI730111|AI730111 BNLGHi6162 Six-day Cotton fiber Gossypium ... 84 4e-37
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35 emb|AI896171|AI896171 EST265614 tomato callus, TAMU Lycopersicon... 89 7e-37
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50 emb|AW728587|AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ... 82 5e-34
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gb|BE125733|BE125733 DG1_54_G12.g1_A002 Dark Grown 1 (DG1) Sorgh... 145 1e-33
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55 emb|AJ010324|PAJ10324 Populus trichocarpa cv trichobel mRNA for ... 95 2e-33
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60 emb|AB032833|AB032833 Cicer arietinum CYP76D1 mRNA for cytochrom... 77 4e-33
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- emb|AF134590|AF134590 Papaver somniferum (S)-N-methylcoclaurine ... 83 6e-33
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 5 dbj|D85184|D85184 Gentiana triflora mRNA for flavonoid 3',5'-hyd... 72 2e-32
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 10 emb|AW255299|AW255299 ML307 peppermint glandular trichome Menth... 88 2e-32
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 35 emb|AB013598|AB013598 Verbena hybrida HGT8 mRNA for UDP-glucose:... 104 2e-34
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 40 emb|AW398421|AW398421 EST298268 L. pennellii trichome, Cornell U... 84 6e-32
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 emb|AB027455|AB027455 Petunia x hybrida PH1 mRNA for anthocyanin... 89 6e-30
 emb|AW459258|AW459258 sh22f07.y1 Gm-c1016 Glycine max cDNA clone... 69 4e-29
 emb|AW928895|AW928895 EST337683 tomato flower buds 8 mm to pre-a... 90 4e-29
 50 emb|X85138|LETW11 L.esculentum twil mRNA. 81 1e-28
 emb|AB033758|AB033758 Citrus unshiu LGTase mRNA for limonoid UDP... 89 2e-28
 emb|X72729|LEERT1B L.esculentum (ERT 1b) ripening-related mRNA. 87 9e-28
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 55 emb|AQ580287|AQ580287 T135903b shotgun sub-library of BAC clone ... 93 1e-27
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 60 emb|AQ368131|AQ368131 tox0001H06r CUGI Tomato BAC Library Lycop... 84 7e-27
 emb|AF199453|AF199453 Sorghum bicolor UDP-glucose glucosyltransf... 76 9e-27

- emb|AI488782|AI488782 EST247121 tomato ovary, TAMU Lycopersicon ... 80 1e-26
emb|AI729108|AI729108 BNLGH12670 Six-day Cotton fiber Gossypium... 82 1e-26
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5 emb|X77369|SMGT S.melongena GT mRNA for glycosyltransferase. 97 5e-26
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emb|AQ580273|AQ580273 T135889b shotgun sub-library of BAC clone ... 93 2e-23
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45 emb|AB012114|AB012114 Vigna mungo UFGlyT mRNA for UDP-glucose:fl... 73 2e-21
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- emb|AW781424|AW781424 sl78a07.y1 Gm-c1037 Glycine max cDNA clone... 95 9e-19
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 45 gb|U63534|FXU63534 Fragaria x ananassa cinnamyl alcohol dehydrog... 251 9e-89
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 50 emb|X92855|LEMTD L.esculentum exon 1 of MTD gene. 130 6e-77
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 60 emb|AW350274|AW350274 GM210007B20B7R Gm-r1021 Glycine max cDNA 3... 262 1e-69
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- emb|AW031628|AW031628 EST275082 tomato callus, TAMU Lycopersicon... 182 7e-69
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15 emb|AI488134|AI488134 EST246456 tomato ovary, TAMU Lycopersicon ... 210 2e-53
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35 emb|AV412798|AV412798 AV412798 Lotus japonicus young plants (two... 137 6e-40
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emb|AW775594|AW775594 EST334659 DSIL Medicago truncatula cDNA cl... 98 8e-40
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gb|BE124304|BE124304 EST394429 DSIL Medicago truncatula cDNA clo... 94 7e-39
40 emb|AW776649|AW776649 EST335714 DSIL Medicago truncatula cDNA cl... 94 1e-38
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Database: plantfungal
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 10 emb|AQ361816|AQ361816 mgxb0005A07f CUGI Rice Blast BAC Library P... 30 5.1
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 emb|AF148676|AF148676 Zizaniopsis villanensis maturase (matK) ge... 30 7.1
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 15 emb|AZ216404|AZ216404 Sheared DNA-121G9.TF Sheared DNA Trypanoso... 30 7.1
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 gb|BE058445|BE058445 sn16b09.y1 Gm-c1016 Glycine max cDNA clone ... 30 7.1
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 20 emb|AZ220034|AZ220034 Sheared DNA-63D11.TR Sheared DNA Trypanoso... 30 7.1
 emb|AI110319|AI110319 TENU3289 T. cruzi epimastigote normalized ... 30 7.1
 emb|AW870077|AW870077 NXNV_123_G11_F Nsf Xylem Normal wood Verti... 30 7.1
 emb|AI057841|AI057841 TENU1932 T. cruzi epimastigote normalized ... 30 7.1
 emb|X83851|NTPAR1B N.tabacum mRNA for PAR-1b. 30 7.1
 25 gb|M18538|POPP03A Populus balsamifera subsp. trichocarpa X Popu... 30 7.1
 emb|AW203632|AW203632 sf36d11.y1 Gm-c1028 Glycine max cDNA clone... 30 7.1
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 emb|AI779122|AI779122 EST260001 tomato susceptible, Cornell Lyco... 27 8.3
 emb|AW096641|AW096641 EST289821 tomato mixed elicitor, BTI Lycop... 27 8.9
 30 gb|N98085|N98085 2245C3 czapPFDd2.1, Debopam Chakrabarti Plasmod... 29 9.7
 emb|AW929160|AW929160 EST337948 tomato flower buds 8 mm to pre-a... 29 9.7
 emb|AW037807|AW037807 EST279436 tomato mixed elicitor, BTI Lycop... 29 9.7
 emb|AW729409|AW729409 GA_Ea0024O24 Gossypium arboreum 7-10 dpa ... 29 9.7
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 emb|cab45069.1| (al078637) putative protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 40 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al078637|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al078637>
 (990 letters)

- 45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- 50 Score E
 Sequences producing significant alignments: (bits) Value
- emb|AW092074|AW092074 EST285350 tomato mixed elicitor, BTI Lycop... 145 1e-69
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 55 gb|BE035944|BE035944 MO22E07 MO Mesembryanthemum crystallinum cD... 120 9e-49
 emb|AW618184|AW618184 EST314234 L. pennellii trichome, Cornell U... 138 2e-46
 emb|AI778761|AI778761 EST259640 tomato susceptible, Cornell Lyco... 133 6e-45
 emb|AW618179|AW618179 EST314229 L. pennellii trichome, Cornell U... 114 3e-39
 gb|S59422|S59422 Populus x canadensis major storage protein mRNA... 99 6e-32
 60 gb|M77504|POPBS Populus deltoides bark storage protein mRNA, co... 99 3e-30
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- emb|AW733452|AW733452 sk73g05.y1 Gm-c1016 Glycine max cDNA clone... 122 3e-27
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 emb|AW394463|AW394463 sh32h06.y1 Gm-c1017 Glycine max cDNA clone... 111 4e-26
 emb|AW563817|AW563817 LG1_261_C02.g1_A002 Light Grown 1 (LG1) So... 104 4e-25
 5 emb|AI822191|AI822191 L0-668T3 Ice plant Lambda Uni-Zap XR expre... 114 1e-24
 gb|BE036341|BE036341 MO23E06 MO Mesembryanthemum crystallinum cD... 112 3e-24
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 15 emb|AW929488|AW929488 EST338276 tomato flower buds 8 mm to pre-a... 92 3e-19
 emb|AI778197|AI778197 EST259076 tomato susceptible, Cornell Lyco... 92 3e-19
 emb|AW648720|AW648720 EST327090 tomato germinating seedlings, TA... 92 3e-19
 emb|AW625287|AW625287 EST319290 tomato radicle, 5 d post-imbibit... 92 3e-19
 emb|AW648718|AW648718 EST327088 tomato germinating seedlings, TA... 92 3e-19
 20 emb|AW928879|AW928879 EST337667 tomato flower buds 8 mm to pre-a... 92 3e-19
 gb|L20233|POPVEGSTRA P.trichocarpa x P.deltoides vegetative stor... 94 2e-18
 emb|AW733620|AW733620 sk75h08.y1 Gm-c1016 Glycine max cDNA clone... 86 3e-18
 emb|AW677327|AW677327 DG1_5_D03.g1_A002 Dark Grown 1 (DG1) Sorgh... 93 4e-18
 emb|AI163910|AI163910 A051P26U Hybrid aspen plasmid library Popu... 56 1e-17
 25 emb|AW156195|AW156195 se20g08.y1 Gm-c1015 Glycine max cDNA clone... 90 2e-17
 emb|AW775932|AW775932 EST334997 DSIL Medicago truncatula cDNA cl... 84 2e-17
 emb|AW692820|AW692820 NF056A09ST1F1000 Developing stem Medicago ... 84 2e-17
 emb|AW685340|AW685340 NF027C09NR1F1000 Nodulated root Medicago t... 83 4e-17
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 30 gb|BE037208|BE037208 MP18A03 MP Mesembryanthemum crystallinum cD... 84 2e-15
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 emb|AW286123|AW286123 LG1_261_F11.b1_A002 Light Grown 1 (LG1) So... 64 5e-13
 emb|AW626069|AW626069 EST319976 tomato radicle, 5 d post-imbibit... 69 1e-12
 35 gb|BE095283|BE095283 00344 leafy spurge Lambda HybriZAP 2.1 two-... 62 1e-12
 emb|AW677160|AW677160 DG1_5_D03.b1_A002 Dark Grown 1 (DG1) Sorgh... 62 2e-12
 emb|AW677332|AW677332 DG1_5_F03.g1_A002 Dark Grown 1 (DG1) Sorgh... 70 2e-11
 gb|BE022753|BE022753 sm88a02.y1 Gm-c1015 Glycine max cDNA clone ... 61 5e-11
 emb|AW424028|AW424028 sh59f09.y1 Gm-c1015 Glycine max cDNA clone... 62 8e-11
 40 emb|X70064|PDBSPA P.deltoides gene for poplar bark storage protein. 63 3e-09
 emb|AW119934|AW119934 sd54g12.y1 Gm-c1016 Glycine max cDNA clone... 54 4e-09
 emb|AW677125|AW677125 DG1_5_F03.b1_A002 Dark Grown 1 (DG1) Sorgh... 43 5e-07
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 45 gb|BE037054|BE037054 MP13H01 MP Mesembryanthemum crystallinum cD... 55 1e-06
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 gb|BE035382|BE035382 MO03G01 MO Mesembryanthemum crystallinum cD... 54 2e-06
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 gb|BE095282|BE095282 00343 leafy spurge Lambda HybriZAP 2.1 two-... 52 5e-06
 50 emb|AW287592|AW287592 LG1_244_A09.b1_A002 Light Grown 1 (LG1) So... 40 6e-06
 emb|AA557101|AA557101 943 Loblolly pine N Pinus taeda cDNA clone... 47 2e-04
 gb|BE037091|BE037091 MP14F10 MP Mesembryanthemum crystallinum cD... 47 2e-04
 gb|M25340|POPCHIC Populus sp. chitinase mRNA fragment, clone 4. 46 6e-04
 gb|BE036753|BE036753 MP04H07 MP Mesembryanthemum crystallinum cD... 46 6e-04
 55 gb|BE037437|BE037437 MP21A08 MP Mesembryanthemum crystallinum cD... 34 8e-04
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 60 emb|AW458345|AW458345 sh86h01.y1 Gm-c1016 Glycine max cDNA clone... 30 0.052
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 emb|Z00044|CHNTXX Nicotiana tabacum chloroplast genome DNA. 35 0.70
 5 emb|AL160939|L1356CX Leishmania major Friedlin cosmid L1356.3 t3... 34 1.8
 gb|BE036897|BE036897 MP08B09 MP Mesembryanthemum crystallinum cD... 34 1.8
 emb|AI730722|AI730722 BNLGHi7729 Six-day Cotton fiber Gossypium ... 34 1.8
 emb|AB030726|AB030726 Nicotiana tabacum mRNA for DNA (cytosine-5... 34 2.5
 emb|AW397331|AW397331 sg77e08.y1 Gm-c1007 Glycine max cDNA clone... 34 2.5
 10 emb|AI210350|AI210350 i0c03a1.r1 Aspergillus nidulans 24hr asexu... 34 2.5
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 20 emb|AL354532|LMFL1177 Leishmania major Friedlin chromosome 21 co... 30 6.9
 emb|AJ243516|NCR243516 Neurospora crassa partial nca-3 gene for ... 32 8.8
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 25 /blast_score 0 /ec_number /family /chip nova /gb_link /ncgi
 (1236 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

30

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

35

gb|M60729|HRAHRPCC A.rusticana peroxidase isoenzyme C (HPR C) ge... 744 0.0
 emb|A00741|A00741 A.rusticana synthetic gene (reverse complement... 692 0.0
 emb|A00740|A00740 A.rusticana synthetic gene for peroxidase. 692 0.0
 dbj|E01651|E01651 cDNA encoding horseradish peroxidase. 692 0.0
 40 gb|M37157|HRAHRPCB A.rusticana peroxidase isoenzyme C (HPR C) ge... 371 e-133
 emb|X97349|PTXP2PER P.trichocarpa mRNA for anionic peroxidase P... 473 e-132
 emb|X97350|PTXP3PER P.trichocarpa mRNA for anionic peroxidase P... 469 e-131
 dbj|D83224|POPP01 Populus nigra mRNA for peroxidase, complete cds. 468 e-131
 gb|M37156|HRAHRPCA A.rusticana peroxidase isoenzyme C (HPR C) ge... 363 e-130
 45 emb|X97348|PTXP1PER P.trichocarpa mRNA for anionic peroxidase P... 463 e-129
 dbj|D30652|POPPA Populus kitakamiensis mRNA for peroxidase, part... 441 e-123
 emb|X97351|PTXP4PER P.trichocarpa mRNA for anionic peroxidase P... 383 e-120
 dbj|D30653|POPPB Populus kitakamiensis mRNA for peroxidase, part... 356 e-112
 emb|AF149277|AF149277 Phaseolus vulgaris peroxidase 1 precursor ... 227 e-107
 50 gb|L36157|ALFPXDC Medicago sativa peroxidase (pxdC) mRNA, comple... 229 e-107
 emb|AF007211|AF007211 Glycine max peroxidase precursor (GMIPER1)... 229 e-106
 gb|L07554|LINPEROX Linum usitatissimum peroxidase (FLXPER1) mRNA... 381 e-105
 emb|X90692|MSRNAPE1A M.sativa mRNA for peroxidase 1A. 211 e-105
 dbj|D90115|HRAPRXC2 Horseradish prxC2 gene encoding peroxidase i... 296 e-103
 55 emb|AJ242742|IBA242742 Ipomoea batatas mRNA for peroxidase (pod ... 138 2e-97
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 60 emb|AI959837|AI959837 sc94h07.y1 Gm-c1019 Glycine max cDNA clone... 228 6e-89
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- emb|AW559660|AW559660 EST314772 DSIR *Medicago truncatula* cDNA cl... 236 1e-87
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5 emb|AW981426|AW981426 EST392579 DSIL *Medicago truncatula* cDNA cl... 236 2e-85
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emb|AF244923|AF244923 *Spinacia oleracea* peroxidase prx14 precurs... 205 9e-85
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emb|AW775762|AW775762 EST334827 DSIL *Medicago truncatula* cDNA cl... 236 6e-83
10 emb|Y10466|SOPR XR5 *S. oleracea* mRNA for peroxidase, clone PC18. 218 3e-82
emb|AW775425|AW775425 EST334490 DSIL *Medicago truncatula* cDNA cl... 208 1e-81
emb|AW685437|AW685437 NF029D09NR1F1000 Nodulated root *Medicago* t... 230 9e-80
emb|AB024439|AB024439 *Scutellaria baicalensis* mRNA for peroxidase... 209 2e-79
emb|AF244922|AF244922 *Spinacia oleracea* peroxidase prx13 precurs... 212 3e-79
emb|X57564|ARNEUPERO *A. rusticana* mRNA for neutral peroxidase. 115 6e-78
15 emb|AW776273|AW776273 EST335338 DSIL *Medicago truncatula* cDNA cl... 222 1e-77
emb|AW267813|AW267813 EST305941 DSIR *Medicago truncatula* cDNA cl... 200 1e-76
emb|X91232|MARNAPRX *M. annua* mRNA for peroxidase. 196 5e-76
emb|AF049881|AF049881 *Linum usitatissimum* peroxidase FLXPER4 (PE... 207 7e-76
emb|AW256487|AW256487 EST304624 KV2 *Medicago truncatula* cDNA clo... 200 9e-76
20 emb|AW775890|AW775890 EST334955 DSIL *Medicago truncatula* cDNA cl... 200 3e-74
emb|AW257195|AW257195 EST305332 KV2 *Medicago truncatula* cDNA clo... 214 5e-74
gb|M91373|CUSPREPER *Cucumis sativus* peroxidase mRNA, complete cds. 86 2e-73
gb|U41657|GMU41657 *Glycine max* seed coat peroxidase isozyme (SPO... 159 3e-73
emb|AB027752|AB027752 *Nicotiana tabacum* mRNA for peroxidase, com... 197 5e-73
25 gb|L36110|SSNPEROXIA *Stylosanthes humilis* peroxidase mRNA. 199 5e-73
gb|M37636|ARCPNC1 *Arachis hypogaea* cationic peroxidase (PNC1) mR... 204 7e-73
emb|AW685235|AW685235 NF027H10NR1F1000 Nodulated root *Medicago* t... 236 9e-73
emb|AW278775|AW278775 sf97d02.y1 Gm-c1019 *Glycine max* cDNA clone... 155 1e-72
emb|X71593|LECEV11A *L. esculentum* CEVI-1 mRNA. 99 2e-72
30 gb|J02979|TOBPXDLF *Nicotiana tabacum* lignin-forming peroxidase m... 100 2e-72
emb|AW559945|AW559945 EST314993 DSIR *Medicago truncatula* cDNA cl... 233 2e-72
emb|AW980744|AW980744 EST391897 GVN *Medicago truncatula* cDNA clo... 235 5e-70
emb|Y10467|SOPR XR6 *S. oleracea* mRNA for peroxidase, clone PC23. 105 1e-69
dbj|D83225|POPP02 *Populus nigra* peroxidase gene, complete cds. 196 2e-69
35 gb|M74103|TOBANPER *Nicotiana sylvestris* anionic peroxidase mRNA,... 205 6e-69
emb|AF043234|AF043234 *Striga asiatica* ferriprotein porphyrin-con... 211 1e-68
gb|BE034991|BE034991 MM01A12 MM *Mesembryanthemum crystallinum* cD... 202 6e-68
emb|AW574244|AW574244 EST316835 GVN *Medicago truncatula* cDNA clo... 202 1e-67
emb|Y10465|SOPR XR4 *S. oleracea* mRNA for peroxidase, clone PC44. 98 3e-67
40 emb|AW686084|AW686084 NF038B07NR1F1000 Nodulated root *Medicago* t... 236 5e-67
emb|AW561032|AW561032 EST316080 DSIR *Medicago truncatula* cDNA cl... 203 7e-67
emb|X56011|TAPERO Wheat mRNA for peroxidase. 111 2e-66
emb|AW185769|AW185769 se59d08.y1 Gm-c1019 *Glycine max* cDNA clone... 219 4e-65
emb|Y17192|CPY17192 *Cucurbita pepo* mRNA for peroxidase. 96 2e-64
45 gb|BE033422|BE033422 ME01E09 ME *Mesembryanthemum crystallinum* cD... 184 4e-64
emb|AB024438|AB024438 *Scutellaria baicalensis* mRNA for peroxidase... 205 7e-64
gb|M91374|CUSPREPERA *Cucumis sativus* peroxidase mRNA, complete cds. 76 2e-63
gb|L24120|LINFLXP *Linum usitatissimum* peroxidase precursor (FLXP... 167 2e-63
gb|M91372|CUSPREPERB *Cucumis sativus* peroxidase mRNA, complete cds. 134 2e-63
50 emb|AF043235|AF043235 *Striga asiatica* ferriprotein porphyrin-con... 199 3e-63
emb|AW288002|AW288002 N100846e rootphos(-) *Medicago truncatula* c... 182 7e-63
emb|AW126121|AW126121 N100318e rootphos(-) *Medicago truncatula* c... 216 1e-62
gb|L36093|BLYPRX Barley peroxidase mRNA, complete cds. 133 5e-62
emb|AW687443|AW687443 NF009F07RT1F1062 Developing root *Medicago* ... 235 1e-61
55 emb|AW687957|AW687957 NF001D11ST1F1000 Developing stem *Medicago* ... 236 3e-61
emb|AB024437|AB024437 *Scutellaria baicalensis* mRNA for peroxidase... 163 3e-61
emb|X58396|HVPEROXI Barley mRNA for peroxidase (EC=1.11.1.7). 133 5e-61
emb|AI496388|AI496388 sb04a11.y1 Gm-c1004 *Glycine max* cDNA clone... 224 6e-61
emb|AW686765|AW686765 NF042E07NR1F1000 Nodulated root *Medicago* t... 222 8e-61
60 dbj|D38050|POPP1 Aspen prxA3a gene for peroxidase, complete cds. 121 9e-61
emb|AW704659|AW704659 sk54h10.y1 Gm-c1019 *Glycine max* cDNA clone... 149 9e-61

emb|Y10464|SOPRXR3 *S.oleracea* mRNA for peroxidase, clone PC42. 80 3e-60
 emb|AW705730|AW705730 sk51b02.y1 Gm-c1019 Glycine max cDNA clone... 149 8e-60
 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 100 9e-60
 gb|U12314|CCU12314 *Cenchrus ciliaris* clone PX7 peroxidase mRNA, ... 105 9e-60
 5 emb|A1938533|A1938533 sb46h09.y1 Gm-c1015 Glycine max cDNA clone... 145 1e-59
 emb|AW705617|AW705617 sk50d03.y1 Gm-c1019 Glycine max cDNA clone... 149 2e-59
 emb|A1781859|A1781859 EST262738 tomato susceptible, Cornell Lyco... 102 2e-59
 emb|AF149278|AF149278 *Phaseolus vulgaris* peroxidase 3 precursor ... 90 3e-59
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 10 emb|AW441632|AW441632 EST311028 tomato fruit red ripe, TAMU Lyco... 105 7e-59
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 gb|M32742|CUSCUPER *C.sativus* peroxidase (put.) (CuPer2) mRNA, 3'... 107 2e-58
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<http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x68592|/ncgi>
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 (1530 letters)

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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

30

Score E

Sequences producing significant alignments: (bits) Value

emb|AF006489|AF006489 *Gossypium hirsutum* adenine nucleotide tran... 325 0.0
 emb|X62123|STANTG *S.tuberosum* ant gene for ADP/ATP translocator. 328 0.0
 35 gb|U89839|LEU89839 *Lycopersicon esculentum* ADP/ATP translocator ... 327 0.0
 emb|X57557|STANT1 *S.tuberosum* PANT1 mRNA for adenine nucleotide ... 635 0.0
 emb|AJ003197|LAAJ3197 *Lupinus albus* mRNA for adenine nucleotide ... 331 e-175
 emb|X80023|TTADPATP *T.turgidum* mRNA for ADP/ATP carrier. 322 e-172
 emb|X65194|CRANT *C.reinhardtii* mRNA CRANT for mitochondrial ADP/... 348 e-149
 40 emb|AL023634|SPBC530 *S.pombe* chromosome II cosmid c530. 265 e-139
 emb|Z49974|SPANC1GN *S.pombe* ANC1 gene for adenine nucleotide car... 265 e-139
 emb|AF085429|AF085429 *Candida parapsilosis* ADP/ATP carrier prote... 311 e-134
 dbj|D89102|D89102 *Schizosaccharomyces pombe* mRNA, partial cds, c... 265 e-133
 gb|L33797|YSKAAC *Kluyveromyces lactis* ADP/ATP translocase (AAC) ... 259 e-132
 45 emb|AF237675|AF237675 *Yarrowia lipolytica* ADP/ATP carrier protei... 247 e-132
 emb|AJ277099|CUT277099 *Candida utilis* anc gene for mitochondrial... 253 e-131
 emb|AJ277098|CUT277098 *Candida utilis* anc gene for mitochondrial... 253 e-131
 gb|M34075|YSCAAC3 *S.cerevisiae* ADP/ATP-translocator protein (AAC... 252 e-129
 emb|X77291|SCIILDNA *S.cerevisiae* YBL0421, YBL0438, YBL0418, YBL0... 252 e-129
 50 emb|Z35791|SCYBL030C *S.cerevisiae* chromosome II reading frame OR... 252 e-129
 emb|X74427|SCADNUCA *S.cerevisiae* gene for adenine nucleotide car... 252 e-129
 gb|J04021|YSCAAC2 *S.cerevisiae* ADP/ATP carrier protein (AAC2) ge... 252 e-129
 emb|X00363|NCADPATP *Neurospora crassa* mRNA for mitochondrial ADP... 280 e-126
 emb|Z49703|SC9796 *S.cerevisiae* chromosome XIII cosmid 9796. 248 e-125
 55 gb|M12514|YSCPET9 *S.cerevisiae* ADP/ATP translocator protein (AAC... 248 e-125
 emb|Z35954|SCYBR085W *S.cerevisiae* chromosome II reading frame OR... 247 e-125
 gb|M34076|YSCAAC2A *S.cerevisiae* ADP/ATP-translocator protein (AA... 247 e-125
 emb|AW774326|AW774326 EST333477 *Medicago truncatula* cDNA clo... 288 e-124
 emb|AL111975|CNS019QN *Botrytis cinerea* strain T4 cDNA library un... 254 e-122
 60 emb|AW647699|AW647699 EST307178 tomato germinating seedlings, TA... 299 e-120

- emb|AW349848|AW349848 GM210006A11G9R Gm-r1021 Glycine max cDNA 3... 326 e-118
- emb|AW624842|AW624842 EST313671 tomato radicle, 5 d post-imbibit... 229 e-116
- emb|X95863|TTANT1 T.turgidum ant gene (1549bp). 195 e-114
- 5 emb|AW041186|AW041186 EST284050 tomato mixed elicitor, BTI Lycop... 239 e-114
- emb|X95864|TTANT2 T.turgidum ant gene (1494bp). 191 e-112
- emb|AW706324|AW706324 sj54h05.y1 Gm-cl033 Glycine max cDNA clone... 245 e-110
- emb|AL157416|LMFL6066 Leishmania major Friedlin chromosome 19 co... 233 e-108
- emb|AW160172|AW160172 EST290029 L. pennellii trichome, Cornell U... 328 e-108
- 10 emb|AW928728|AW928728 EST337516 tomato flower buds 8 mm to pre-a... 247 e-107
- emb|AW218544|AW218544 EST303727 tomato radicle, 5 d post-imbibit... 325 e-105
- emb|AW830381|AW830381 sm26a12.y1 Gm-cl028 Glycine max cDNA clone... 268 e-105
- emb|AW201674|AW201674 sf05h11.y1 Gm-cl027 Glycine max cDNA clone... 309 e-104
- emb|AI812944|AI812944 22G12 Pine Lambda Zap Xylem library Pinus ... 251 e-103
- 15 emb|AI777865|AI777865 EST258744 tomato susceptible, Cornell Lyco... 284 e-102
- emb|AW234033|AW234033 sf33d01.y1 Gm-cl028 Glycine max cDNA clone... 237 e-101
- emb|AW831587|AW831587 sm28b02.y1 Gm-cl028 Glycine max cDNA clone... 300 e-101
- emb|AW668198|AW668198 GA_Ea0013C13 Gossypium arboreum 7-10 dpa ... 331 e-100
- emb|AF049130|AF049130 Trypanosoma brucei brucei ADP/ATP carrier ... 238 1e-98
- 20 emb|AI898886|AI898886 EST268329 tomato ovary, TAMU Lycopersicon ... 213 2e-98
- gb|U32987|TBU32987 Trypanosoma brucei rhodesiense ADP/ATP carrie... 238 3e-98
- emb|AW223982|AW223982 EST300793 tomato fruit red ripe, TAMU Lyco... 327 1e-96
- emb|AW624951|AW624951 EST313780 tomato radicle, 5 d post-imbibit... 327 1e-96
- emb|AW348348|AW348348 GM210002A13A5R Gm-r1021 Glycine max cDNA 3... 328 2e-96
- 25 emb|AW441243|AW441243 EST310639 tomato fruit red ripe, TAMU Lyco... 324 1e-95
- emb|AW223973|AW223973 EST300784 tomato fruit red ripe, TAMU Lyco... 321 7e-95
- emb|AW931569|AW931569 EST357412 tomato fruit mature green, TAMU ... 328 2e-94
- emb|AW218871|AW218871 EST301353 tomato root during/after fruit s... 327 8e-94
- 30 emb|AL116444|CNS01D6S Botrytis cinerea strain T4 cDNA library un... 267 4e-93
- emb|AW831561|AW831561 sm34f06.y1 Gm-cl028 Glycine max cDNA clone... 312 2e-92
- emb|AI484151|AI484151 EST248958 tomato resistant, Cornell Lycope... 264 3e-91
- emb|AW925414|AW925414 HVSMEg0001L02 Hordeum vulgare pre-anthesis... 299 6e-91
- emb|AI731594|AI731594 BNLGHi10182 Six-day Cotton fiber Gossypium... 335 7e-91
- 35 emb|AW730597|AW730597 GA_Ea0027H02 Gossypium arboreum 7-10 dpa ... 333 1e-90
- emb|AW647665|AW647665 EST307143 tomato germinating seedlings, TA... 317 1e-90
- emb|AW395111|AW395111 sh40a06.y1 Gm-cl017 Glycine max cDNA clone... 303 6e-90
- emb|AI725588|AI725588 BNLGHi12376 Six-day Cotton fiber Gossypium... 288 1e-89
- emb|AW934656|AW934656 EST353548 tomato flower buds 0-3 mm, Corne... 328 2e-89
- 40 emb|AW757478|AW757478 874001D11.y1 C. reinhardtii CC-1690, Lambd... 202 3e-89
- emb|AW725897|AW725897 GA_Ea0020B06 Gossypium arboreum 7-10 dpa ... 328 8e-89
- emb|AW647757|AW647757 EST326211 tomato germinating seedlings, TA... 301 1e-88
- emb|AW509174|AW509174 sh92b04.y1 Gm-cl016 Glycine max cDNA clone... 297 4e-88
- emb|AW666654|AW666654 GA_Ea0005E11 Gossypium arboreum 7-10 dpa ... 279 7e-88
- 45 emb|AL114553|CNS01BQ9 Botrytis cinerea strain T4 cDNA library un... 231 3e-87
- gb|BE021489|BE021489 sm59b05.y1 Gm-cl028 Glycine max cDNA clone ... 322 5e-87
- emb|AW507801|AW507801 si45c02.y1 Gm-r1030 Glycine max cDNA clone... 259 2e-86
- emb|AW733916|AW733916 sk85a11.y1 Gm-cl035 Glycine max cDNA clone... 306 2e-86
- emb|AW096468|AW096468 EST289648 tomato mixed elicitor, BTI Lycop... 292 6e-86
- 50 emb|AW156741|AW156741 se30b08.y1 Gm-cl015 Glycine max cDNA clone... 184 1e-85
- emb|AI729625|AI729625 BNLGHi13824 Six-day Cotton fiber Gossypium... 276 4e-85
- emb|AW034214|AW034214 EST277785 tomato callus, TAMU Lycopersicon... 304 5e-85
- emb|AJ273864|AJ273864 AJ273864 Metarhizium anisopliae ARSEF 2575... 184 1e-84
- emb|AI775647|AI775647 EST256747 tomato resistant, Cornell Lycope... 297 1e-84
- 55 emb|AI822682|AI822682 L0-1204T3 Ice plant Lambda Uni-Zap XR expr... 314 2e-84
- emb|AW625107|AW625107 EST313924 tomato radicle, 5 d post-imbibit... 314 2e-84
- emb|AI726147|AI726147 BNLGHi5085 Six-day Cotton fiber Gossypium ... 263 6e-83
- emb|AW755396|AW755396 sl03d11.y1 Gm-cl036 Glycine max cDNA clone... 306 3e-82
- emb|AI728088|AI728088 BNLGHi9938 Six-day Cotton fiber Gossypium ... 259 5e-82
- 60 emb|AW979992|AW979992 EST310378 tomato root deficiency, Cornell ... 285 8e-82
- emb|AW333018|AW333018 S16C3 AGS-1 Pneumocystis carinii f. sp. ca... 278 1e-81

- emb|AI780394|AI780394 EST261273 tomato susceptible, Cornell Lyco... 284 2e-81
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 5 emb|AW760027|AW760027 sl57b04.y1 Gm-cl027 Glycine max cDNA clone... 301 1e-80
 emb|AW667101|AW667101 GA_Ea0007F21 Gossypium arboreum 7-10 dpa ... 300 2e-80
 emb|AW622023|AW622023 EST312821 tomato root during/after fruit s... 280 4e-80
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 emb|AW650428|AW650428 EST328882 tomato germinating seedlings, TA... 278 4e-79
 10 emb|AI775628|AI775628 EST256728 tomato resistant, Cornell Lycopers... 295 7e-79
 gb|BE024093|BE024093 sm96f04.y1 Gm-cl015 Glycine max cDNA clone ... 293 2e-78
 emb|AJ273749|AJ273749 AJ273749 Metarhizium anisopliae ARSEF 2575... 256 1e-77
 emb|AW737446|AW737446 EST338789 tomato flower buds, anthesis, Co... 290 2e-77
- 15 Query= Y14251.4_i at 16053_i at /id_source genbank /description
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 thaliana] /blast_score 1.00e-110 /ec_number /family transferase /chip
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 20 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|y14251|/ncgi)
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 (630 letters)
- 25 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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- 30 Score E
 Sequences producing significant alignments: (bits) Value
- emb|X78203|HMGST H.muticus mRNA for glutathione S-transferase. 271 4e-72
 emb|AW727692|AW727692 GA_Ea0015I24 Gossypium arboreum 7-10 dpa ... 146 9e-71
 35 emb|AF002692|AF002692 Solanum commersonii glutathione S-transfer... 264 3e-70
 dbj|D10524|TOBPARB Nicotiana tabacum mRNA for glutathione S-tran... 262 2e-69
 emb|AW731360|AW731360 GA_Ea0030G14 Gossypium arboreum 7-10 dpa ... 142 3e-69
 dbj|D29680|TOBAP12B Tobacco api2 mRNA (which expression is induc... 261 4e-69
 emb|AW220064|AW220064 EST302547 tomato root during/after fruit s... 260 5e-69
 40 emb|Z71749|NPGSTMR N.plumbaginifolia mRNA for glutathione S-tran... 260 8e-69
 emb|AI774583|AI774583 EST255683 tomato resistant, Cornell Lycopers... 258 3e-68
 emb|AW728413|AW728413 GA_Ea0016J18 Gossypium arboreum 7-10 dpa ... 142 7e-68
 emb|AI725552|AI725552 BNLGHi12077 Six-day Cotton fiber Gossypium... 142 4e-67
 emb|AI728937|AI728937 BNLGHi12090 Six-day Cotton fiber Gossypium... 142 4e-67
 45 gb|BE033971|BE033971 MG02G09 MG Mesembryanthemum crystallinum cD... 228 2e-65
 emb|AW735791|AW735791 EST336559 tomato flower buds 0-3 mm, Corne... 248 2e-65
 emb|AF242309|AF242309 Euphorbia esula glutathione S-transferase ... 130 3e-62
 emb|AW726844|AW726844 GA_Ea0022O11 Gossypium arboreum 7-10 dpa ... 140 5e-61
 emb|AI726215|AI726215 BNLGHi5300 Six-day Cotton fiber Gossypium ... 142 5e-61
 50 emb|AW218151|AW218151 EST303332 tomato radicle, 5 d post-imbibit... 232 1e-60
 emb|AW728876|AW728876 GA_Ea0028P14 Gossypium arboreum 7-10 dpa ... 147 2e-60
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 emb|AF133894|AF133894 Persea americana glutathione S-transferase... 220 8e-57
 emb|AI352770|AI352770 MB58-4B PZ204.BNlib Brassica napus cDNA cl... 174 7e-55
 55 emb|AW040790|AW040790 EST283654 tomato mixed elicitor, BTI Lycopers... 210 6e-54
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 emb|AW862639|AW862639 00097 leafy spurge Lambda HybriZAP 2.1 two... 128 2e-48
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 60 emb|AW684286|AW684286 NF015A06NR1F1000 Nodulated root Medicago t... 186 1e-46
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10 emb|AI486597|AI486597 EST244918 tomato ovary, TAMU Lycopersicon ... 173 1e-42
emb|AV417605|AV417605 AV417605 Lotus japonicus young plants (two... 172 2e-42
emb|AW667380|AW667380 GA_Ea0009C08 Gossypium arboreum 7-10 dpa ... 147 2e-42
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15 dbj|D49526|TOBPBARBA Tobacco chimeric parB promoter/beta-glucuron... 163 1e-39
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20 emb|Y07721|PHGLSTRAN P.hybrida mRNA for glutathione S-transferase. 151 5e-36
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25 emb|AW926756|AW926756 HVSMeg0008B23 Hordeum vulgare pre-anthesis... 92 3e-35
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emb|AV427165|AV427165 AV427165 Lotus japonicus young plants (two... 142 3e-33
emb|AJ010451|AMY010451 Alopecurus myosuroides mRNA for glutathio... 97 4e-33
emb|AF184059|AF184059 Triticum aestivum glutathione S-transferase... 81 5e-33
30 emb|AW164336|AW164336 se71b09.y1 Gm-c1023 Glycine max cDNA clone... 139 1e-32
emb|AJ010454|AMY010454 Alopecurus myosuroides mRNA for glutathio... 95 2e-32
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35 emb|AW561921|AW561921 IPPGHZ0010 Cotton fiber and embryo Lambda ... 137 7e-32
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40 emb|AI823131|AI823131 L30-1014T3 Ice plant Lambda Uni-Zap XR exp... 112 4e-31
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emb|AI773198|AI773198 EST254298 tomato resistant, Cornell Lycopersicon... 133 1e-30
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45 emb|AW279568|AW279568 sf95d06.y1 Gm-c1019 Glycine max cDNA clone... 131 4e-30
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60 emb|AW689646|AW689646 NF022G04ST1F1000 Developing stem Medicago ... 66 3e-25
gb|BE060798|BE060798 HVSMeg0013G13f Hordeum vulgare pre-anthesis... 92 6e-25

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 5 emb|AI352728|AI352728 MB47-17 PZ204.BNlib Brassica napus cDNA cl... 110 1e-23
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 10 emb|AW459151|AW459151 sh21c07.y1 Gm-cl016 Glycine max cDNA clone... 66 6e-23

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 (1619 letters)

20 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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emb AJ007574 RCO7574 Ricinus communis mRNA for amino acid carrier.	410	0.0		
30 emb Y09591 VFAMACTRA V.faba mRNA for amino acid transporter.	392	0.0		
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emb AF080543 AF080543 Nepenthes alata amino acid transporter (AA...	641	0.0		
emb Y09826 STAAP2 S.tuberosum mRNA for amino acid transporter AA...	354	0.0		
emb AF080544 AF080544 Nepenthes alata amino acid transporter (AA...	596	0.0		
35 emb Y09825 STAAP1 S.tuberosum mRNA for amino acid transporter AA...	288	e-158		
emb Z68759 RCAACMR R.communis mRNA for amino acid carrier.	334	e-155		
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45 emb AW648039 AW648039 EST326493 tomato germinating seedlings, TA...	226	2e-67		
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emb AW720246 AW720246 LjNEST17f12r Lotus japonicus nodule librar...	235	6e-61		
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55 emb AW737124 AW737124 EST338551 tomato flower buds, anthesis, Co...	217	2e-55		
emb AW691461 AW691461 NF045C01ST1F1000 Developing stem Medicago ...	206	7e-55		
emb AW432416 AW432416 sh73f10.y1 Gm-cl015 Glycine max cDNA clone...	89	8e-51		
emb AW255060 AW255060 ML1355 peppermint glandular trichome Menth...	111	1e-50		
emb AW685782 AW685782 NF035B03NR1F1000 Nodulated root Medicago t...	201	1e-50		
60 gb BE125804 BE125804 DG1_57_F07.b1_A002 Dark Grown 1 (DG1) Sorgh...	178	3e-50		
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- emb|AW349599|AW349599 GM210005A21G12R Gm-r1021 Glycine max cDNA ... 140 5e-49
- emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 122 2e-48
- emb|AW737784|AW737784 EST339211 tomato flower buds, anthesis, Co... 192 6e-48
- 5 emb|AW309945|AW309945 sf27a03.x1 Gm-c1028 Glycine max cDNA clone... 149 5e-47
- emb|AW738557|AW738557 EST339984 tomato flower buds, anthesis, Co... 188 8e-47
- emb|AQ842052|AQ842052 T134338 Soybean RFLP probe Glycine max gen... 148 2e-44
- emb|AF074703|AF074703 Glycine max pA381 marker, sequence tagged ... 149 1e-43
- emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 127 3e-43
- 10 gb|BE022301|BE022301 sm73b09.y1 Gm-c1028 Glycine max cDNA clone ... 176 4e-43
- emb|AW597381|AW597381 si92b03.y1 Gm-c1031 Glycine max cDNA clone... 175 1e-42
- emb|AW310916|AW310916 sg29h08.x1 Gm-c1024 Glycine max cDNA clone... 172 5e-42
- emb|AW306512|AW306512 se51h04.y1 Gm-c1017 Glycine max cDNA clone... 140 1e-41
- emb|AW395873|AW395873 sh01d01.y1 Gm-c1026 Glycine max cDNA clone... 112 4e-41
- 15 emb|AW201454|AW201454 sf03c12.y1 Gm-c1027 Glycine max cDNA clone... 127 9e-41
- emb|AW684816|AW684816 NF021D09NR1F1000 Nodulated root Medicago t... 164 2e-39
- emb|AZ051221|AZ051221 Gm_UMB001_166_P11R UMN Soybean BAC Library... 159 7e-38
- emb|AI779305|AI779305 EST260184 tomato susceptible, Cornell Lyco... 155 1e-36
- emb|AI779304|AI779304 EST260183 tomato susceptible, Cornell Lyco... 155 1e-36
- 20 emb|AW830977|AW830977 sm31a10.y1 Gm-c1028 Glycine max cDNA clone... 149 4e-35
- emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 147 3e-34
- emb|AJ004829|STAJ4829 Solanum tuberosum fdh3 pseudogene. 110 3e-33
- emb|AQ841805|AQ841805 T134055 Soybean RFLP probe Glycine max gen... 140 2e-32
- emb|AW736648|AW736648 EST333140 KV3 Medicago truncatula cDNA clo... 138 1e-31
- 25 emb|AV418629|AV418629 AV418629 Lotus japonicus young plants (two... 130 3e-29
- emb|AW442349|AW442349 EST311745 tomato fruit red ripe, TAMU Lyco... 130 3e-29
- emb|AW738564|AW738564 EST339991 tomato flower buds, anthesis, Co... 104 7e-29
- emb|AW561095|AW561095 EST316143 DSIR Medicago truncatula cDNA cl... 126 6e-28
- emb|AW234791|AW234791 sf19c06.y1 Gm-c1028 Glycine max cDNA clone... 124 2e-27
- 30 gb|U31932|NSU31932 Nicotiana sylvestris amino acid permease 1 (N... 61 3e-27
- emb|AI441371|AI441371 sa64f02.y1 Gm-c1004 Glycine max cDNA clone... 72 2e-26
- emb|AW438003|AW438003 ST83D04 Pine TriplEx shoot tip library Pin... 111 2e-23
- emb|AW056573|AW056573 ST52G03 Pine TriplEx shoot tip library Pin... 109 8e-23
- emb|AW923686|AW923686 DG1_57_F07.g1_A002 Dark Grown 1 (DG1) Sorg... 107 3e-22
- 35 emb|AW924285|AW924285 WS1_52_F10.b1_A002 Water-stressed 1 (WS1) ... 106 5e-22
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- emb|AW102174|AW102174 sd84c08.y1 Gm-c1009 Glycine max cDNA clone... 100 6e-20
- emb|AW102244|AW102244 sd85c02.y1 Gm-c1009 Glycine max cDNA clone... 92 1e-17
- emb|AW620352|AW620352 sj04b02.y1 Gm-c1032 Glycine max cDNA clone... 92 1e-17
- 40 emb|AW288077|AW288077 N100921e rootphos(-) Medicago truncatula c... 84 2e-15
- emb|AW396191|AW396191 sh02e09.y1 Gm-c1026 Glycine max cDNA clone... 57 2e-14
- emb|AI773761|AI773761 EST254861 tomato resistant, Cornell Lycop... 65 2e-12
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- emb|AF014810|AF014810 Lycopersicon esculentum proline transporte... 54 9e-12
- 45 emb|AI728355|AI728355 BNLGH10544 Six-day Cotton fiber Gossypium... 70 4e-11
- emb|AW780460|AW780460 sl71b05.y1 Gm-c1027 Glycine max cDNA clone... 70 6e-11
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- emb|AF014809|AF014809 Lycopersicon esculentum proline transporte... 52 2e-08
- emb|AW832495|AW832495 sm11e04.y1 Gm-c1027 Glycine max cDNA clone... 60 2e-08
- 50 emb|AW563318|AW563318 LG1_228_A07.g1_A002 Light Grown 1 (LG1) So... 48 2e-07
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- emb|AV417239|AV417239 AV417239 Lotus japonicus young plants (two... 52 1e-05
- emb|AI772468|AI772468 EST253568 tomato resistant, Cornell Lycop... 52 1e-05
- 55 gb|BE023644|BE023644 sm83e05.y1 Gm-c1015 Glycine max cDNA clone ... 51 2e-05
- emb|AW102341|AW102341 sd86d12.y1 Gm-c1009 Glycine max cDNA clone... 49 9e-05
- emb|AW560837|AW560837 EST315885 DSIR Medicago truncatula cDNA cl... 47 3e-04
- emb|AW720608|AW720608 LjNEST20d11rc Lotus japonicus nodule libra... 47 4e-04
- emb|AW720138|AW720138 LjNEST15d10r Lotus japonicus nodule librar... 47 4e-04
- 60 emb|AV409658|AV409658 AV409658 Lotus japonicus young plants (two... 47 4e-04
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5 emb|X87611|SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83). 44 0.003
emb|AW677443|AW677443 DG1_7_D10.b1_A002 Dark Grown 1 (DG1) Sorgh... 44 0.004
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(735 letters)

15 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

20 Score E
Sequences producing significant alignments: (bits) Value

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25 emb|AW573922|AW573922 EST316513 GVN Medicago truncatula cDNA clo... 409 e-113
emb|AW685184|AW685184 NF026H08NR1F1000 Nodulated root Medicago t... 338 e-105
emb|AW348587|AW348587 GM210002B22C8R Gm-r1021 Glycine max cDNA 3... 365 e-101
emb|AW685583|AW685583 NF029C04NR1F1000 Nodulated root Medicago t... 320 e-100
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30 emb|X12739|NTPRRMAJ N. tabacum mRNA for pathogenesis-related pro... 201 4e-99
emb|AF003007|AF003007 Vitis vinifera thaumatin-like protein VVTL... 214 7e-98
emb|X15223|NTE2TLP Tobacco E2 gene for a thaumatin-like protein. 195 2e-97
emb|X03913|NTTHAUR Tobacco mRNA for TMV induced protein homolog... 195 2e-97
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35 emb|AV428977|AV428977 AV428977 Lotus japonicus young plants (two... 343 7e-94
emb|Y10992|VVOSM1 V. vinifera mRNA for osmotin-like protein. 224 3e-90
emb|AF199508|AF199508 Fragaria x ananassa osmotin-like protein (... 220 1e-89
emb|X72928|SC13OLP S.commersonii (pOSML13) gene for osmotin-like... 200 1e-88
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40 emb|X70787|LEPRPA L.esculentum pr p23 mRNA for pathogenesis-rela... 200 1e-88
emb|AW039873|AW039873 EST282346 tomato mixed elicitor, BTI Lycop... 200 1e-88
emb|X66416|LETPM1M L.esculentum tpm 1 mRNA. 199 1e-88
emb|AW218786|AW218786 EST301266 tomato root during/after fruit s... 197 9e-88
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45 emb|X95308|NTOSPR N.tabacum osmotin gene. 195 8e-87
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gb|S44889|S44889 osmotin=pathogenesis-related protein homolog [N... 195 1e-86
50 emb|A16782|A16782 osmotin-like protein gene without 20 C- termin... 195 1e-86
emb|A16780|A16780 osmotin-like protein gene seq ID No: 5. 195 1e-86
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55 emb|X72927|SC81OLP S.commersonii (pOSML81) gene for osmotin-like... 193 7e-86
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60 emb|AW223970|AW223970 EST300781 tomato fruit red ripe, TAMU Lyco... 193 1e-85
emb|AW223507|AW223507 EST300318 tomato fruit red ripe, TAMU Lyco... 193 1e-85

- emb|AW222204|AW222204 EST299015 tomato fruit red ripe, TAMU Lyco... 193 1e-85
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10 emb|AF001528|AF001528 Musa acuminata ripening-associated protein... 307 8e-85
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emb|AW033829|AW033829 EST277400 tomato callus, TAMU Lycopersicon... 193 2e-84
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15 emb|AW621924|AW621924 EST312722 tomato root during/after fruit s... 192 2e-83
emb|AW650675|AW650675 EST329129 tomato germinating seedlings, TA... 193 1e-82
emb|AW034088|AW034088 EST277583 tomato callus, TAMU Lycopersicon... 193 1e-81
emb|AW219330|AW219330 EST301812 tomato root during/after fruit s... 193 1e-81
emb|AW034433|AW034433 EST278004 tomato callus, TAMU Lycopersicon... 175 2e-80
20 emb|AI895910|AI895910 EST265353 tomato callus, TAMU Lycopersicon... 177 3e-80
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25 emb|AW029746|AW029746 EST273001 tomato callus, TAMU Lycopersicon... 168 2e-78
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30 emb|AW686653|AW686653 NF043G01NR1F1000 Nodulated root Medicago t... 265 1e-76
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emb|AW458142|AW458142 sh78g09.y1 Gm-c1016 Glycine max cDNA clone... 185 2e-75
35 emb|AJ131731|PME131731 Pseudotsuga menziesii mRNA for Thaumatin-... 237 3e-74
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40 gb|J01209|TDATHAU2 T.daniellii preprothaumatin-2 mRNA, complete ... 116 4e-72
emb|A15673|A15673 proprothaumatin and the coding strand of its ... 116 4e-72
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45 emb|A15660|A15660 Mature thaumatin. 116 2e-71
emb|A46806|A46806 Sequence 3 from Patent EP0684312. 115 5e-71
emb|AF121776|AF121776 Juniperus ashei allergen Jun a 3 mRNA, com... 144 1e-70
emb|AF016327|AF016327 Hordeum vulgare Barperml (perml) mRNA, par... 221 3e-70
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50 emb|AI896554|AI896554 EST265997 tomato callus, TAMU Lycopersicon... 140 5e-70
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emb|AV423642|AV423642 AV423642 Lotus japonicus young plants (two... 263 1e-69
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55 emb|A46810|A46810 Sequence 7 from Patent EP0684312. 108 1e-68
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60 emb|AI895353|AI895353 EST264796 tomato callus, TAMU Lycopersicon... 193 1e-68
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 (357 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10

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15			emb X89759 BOPC17 B.oleracea mRNA for thioredoxin h-like, pollen... 194 2e-49
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			emb AB010434 AB010434 Brassica rapa PEC-2 mRNA for Thioredoxin, ... 192 9e-49
			emb AW255457 AW255457 ML480 peppermint glandular trichome Mentha... 190 3e-48
20			emb AW569018 AW569018 si74e02.yl Gm-cl031 Glycine max cDNA clone... 185 1e-46
			emb AI988470 AI988470 sd02f07.yl Gm-cl020 Glycine max cDNA clone... 185 1e-46
			emb Z70677 RCTHIORXN R.communis mRNA for thioredoxin. 183 5e-46
			emb AI161830 AI161830 A007P52U Hybrid aspen plasmid library Popu... 182 9e-46
			gb BE053835 BE053835 GA_Ea0009P21f Gossypium arboreum 7-10 dpa ... 182 9e-46
25			emb AW677726 AW677726 WS1_10_F03.g1_A002 Water-stressed 1 (WS1) ... 181 2e-45
			emb AW924685 AW924685 WS1_71_B11.b1_A002 Water-stressed 1 (WS1) ... 181 2e-45
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30			emb AW349345 AW349345 GM210007A20B10R Gm-r1021 Glycine max cDNA ... 179 6e-45
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			emb AI461219 AI461219 sa76f11.yl Gm-cl004 Glycine max cDNA clone... 179 6e-45
			emb AJ009762 TAE9762 Triticum aestivum mRNA for thioredoxin H. 179 9e-45
35			emb AW164730 AW164730 se77a02.yl Gm-cl023 Glycine max cDNA clone... 179 9e-45
			gb T24347 T24347 crs1466 lambdaZAPST Ricinus communis cDNA clone... 177 3e-44
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40			emb AW329521 AW329521 N200767e rootphos(-) Medicago truncatula c... 176 6e-44
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			gb U59380 BNU59380 Brassica napus thioredoxin-h-like-2 (THL-2) m... 101 5e-43
60			gb C95504 C95504 C95504 Citrus unshiu Miyagawa-wase maturation s... 172 7e-43
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- emb|AI441505|AI441505 sa87c03.y1 Gm-cl004 Glycine max cDNA clone... 171 1e-42
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- 5 emb|AW096472|AW096472 EST289652 tomato mixed elicitor, BTI Lycop... 171 3e-42
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emb|AI776110|AI776110 EST257198 tomato resistant, Cornell Lycop... 171 3e-42
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- 10 emb|AW040001|AW040001 EST282492 tomato mixed elicitor, BTI Lycop... 171 3e-42
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emb|AW037831|AW037831 EST279460 tomato mixed elicitor, BTI Lycop... 171 3e-42
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- 20 emb|AI778940|AI778940 EST259819 tomato susceptible, Cornell Lyco... 171 3e-42
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- 25 emb|AW038564|AW038564 EST280247 tomato mixed elicitor, BTI Lycop... 168 1e-41
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emb|AW217307|AW217307 EST296026 tomato flower buds 0-3 mm, Corne... 165 2e-40
emb|AW289622|AW289622 NXNV003H05F Nsf Xylem Normal wood Vertical... 164 2e-40
- 30 emb|AW064893|AW064893 ST37B02 Pine TriplEx shoot tip library Pin... 162 8e-40
emb|AW065132|AW065132 ST40A08 Pine TriplEx shoot tip library Pin... 162 1e-39
emb|AF051206|AF051206 Picea mariana probable thioredoxin H (Sb09... 162 1e-39
emb|AW010199|AW010199 ST03C05 Pine TriplEx shoot tip library Pin... 162 1e-39
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- 35 emb|AW043214|AW043214 ST30F08 Pine TriplEx shoot tip library Pin... 162 1e-39
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- 45 emb|AW290231|AW290231 NXNV015E05F Nsf Xylem Normal wood Vertical... 159 1e-38
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- 50 emb|AW706540|AW706540 sj57g11.y1 Gm-cl033 Glycine max cDNA clone... 156 7e-38
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- 55 emb|AW681036|AW681036 WS1_8_D05.b1_A002 Water-stressed 1 (WS1) S... 154 2e-37
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 (1896 letters)

5

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E
 Sequences producing significant alignments: (bits) Value

emb|AF123503|AF123503 Nicotiana tabacum Nt-gh3 deduced protein m... 484 0.0
 15 emb|X60033|GMGH3G G.max GH3 gene for auxin-regulated protein. 406 0.0
 emb|AI489187|AI489187 EST247526 tomato ovary, TAMU Lycopersicon ... 421 e-116
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 emb|AW223544|AW223544 EST300355 tomato fruit red ripe, TAMU Lyco... 385 e-106
 emb|AI729810|AI729810 BNLGHi5260 Six-day Cotton fiber Gossypium ... 225 e-103
 20 emb|AW455302|AW455302 EST311840 tomato root during/after fruit s... 358 6e-98
 emb|AW307114|AW307114 sf52h11.y1 Gm-cl009 Glycine max cDNA clone... 357 2e-97
 emb|AW730905|AW730905 GA_Ea0029G23 Gossypium arboreum 7-10 dpa ... 321 2e-95
 emb|AW737090|AW737090 EST338517 tomato flower buds, anthesis, Co... 228 3e-94
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 emb|AW686313|AW686313 NF040C09NR1F1000 Nodulated root Medicago t... 211 7e-78
 emb|AW035201|AW035201 EST280463 tomato callus, TAMU Lycopersicon... 153 2e-77
 emb|AW720296|AW720296 LjNEST20d3r Lotus japonicus nodule library... 290 3e-77
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emb|AW568731|AW568731 si72d08.yl Gm-c1031 Glycine max cDNA clone... 104 1e-33
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10 emb|AV408894|AV408894 AV408894 Lotus japonicus young plants (two... 132 1e-29
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emb|AI777312|AI777312 EST258277 tomato resistant, Cornell Lycop... 103 6e-21
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Database: plantfungal

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	emb AW832427 AW832427 sm10c03.y1 Gm-cl027 Glycine max cDNA clone...	233	3e-60	
20	emb AW760284 AW760284 sl48d01.y1 Gm-cl027 Glycine max cDNA clone...	206	6e-55	
	emb AW620771 AW620771 sj09d03.y1 Gm-cl032 Glycine max cDNA clone...	209	5e-53	
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25	emb AW459166 AW459166 sh21e03.y1 Gm-cl016 Glycine max cDNA clone...	170	3e-41	
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35	emb AW928458 AW928458 EST337246 tomato flower buds 8 mm to pre-a...	85	3e-23	
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40	emb AW221912 AW221912 EST298723 tomato fruit red ripe, TAMU Lyco...	70	9e-19	
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	emb AI562604 AI562604 TENS2761 T. cruzi epimastigote normalized ...	95	2e-18	
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50	emb Z73261 SCYLR089C S.cerevisiae chromosome XII reading frame O...	51	2e-14	
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(460 letters)

Database: plantfungal
60 661,018 sequences; 426,114,510 total letters

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5	emb AW035239 AW035239	EST280501	tomato callus, TAMU Lycopersicon...	274	3e-73
	emb AW035958 AW035958	EST282817	tomato callus, TAMU Lycopersicon...	274	3e-73
	emb X94943 LECEVI16G	L.esculentum mRNA for peroxidase.		274	3e-73
	emb AW032485 AW032485	EST276044	tomato callus, TAMU Lycopersicon...	272	1e-72
10	gb M37637 ARCPNC2	A.hypogaea cationic peroxidase mRNA, complete ...		271	2e-72
	emb AF149279 AF149279	Phaseolus vulgaris peroxidase 4 precursor ...		265	1e-70
	emb AI777064 AI777064	EST252031	tomato callus, TAMU Lycopersicon...	261	3e-69
	emb AW216562 AW216562	EST295276	tomato callus, TAMU Lycopersicon...	259	9e-69
	emb AW035446 AW035446	EST281184	tomato callus, TAMU Lycopersicon...	258	2e-68
15	emb AB027753 AB027753	Nicotiana tabacum mRNA for peroxidase, com...		255	1e-67
	emb AW216873 AW216873	EST295587	tomato callus, TAMU Lycopersicon...	251	2e-66
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	emb AI773788 AI773788	EST254888	tomato resistant, Cornell Lycope...	246	9e-65
	gb L36112 SSNPEROXIC	Stylosanthes humilis peroxidase mRNA.		193	3e-64
20	emb Y10468 SOPRXR7	S.oleracea mRNA for peroxidase, clone PC36.		242	8e-64
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25	emb AW219926 AW219926	EST302409	tomato root during/after fruit s...	235	2e-61
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	emb AW030052 AW030052	EST273307	tomato callus, TAMU Lycopersicon...	186	8e-47
45	emb AF145349 AF145349	Glycine max peroxidase (Prx3) mRNA, partia...		143	2e-46
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50	emb AW569733 AW569733	si79g02.y1	Gm-c1031 Glycine max cDNA clone...	175	2e-43
	emb AW621545 AW621545	EST312343	tomato root during/after fruit s...	108	2e-43
	emb AW694946 AW694946	NF081G11ST1F1087	Developing stem Medicago ...	142	4e-43
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55	emb AW622066 AW622066	EST312864	tomato root during/after fruit s...	111	4e-42
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	gb L13654 TOMTPX1A	Lycopersicon esculentum peroxidase (TPX1) mRN...		112	5e-42
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	emb AW219925 AW219925	EST302408	tomato root during/after fruit s...	168	2e-41
60	emb AW622012 AW622012	EST312810	tomato root during/after fruit s...	111	2e-41
	emb AW621198 AW621198	EST311996	tomato root during/after fruit s...	111	2e-41

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 5 emb|AW928514|AW928514 EST337302 tomato flower buds 8 mm to pre-a... 95 5e-41
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 10 emb|AF244921|AF244921 Spinacia oleracea peroxidase prx12 precurs... 103 2e-40
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 20 emb|Y10470|SOPR XR9 S.oleracea mRNA for peroxidase, clone PC56. 151 1e-39
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 25 emb|AW625780|AW625780 EST319687 tomato radicle, 5 d post-imbibit... 105 2e-39
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 http://www3.ncbi.nlm.nih.gov/htbin-
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 http://www.ncgr.org/cgi-bin/ff?ac000132
 (2766 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

60 Searching.....done

Score E.

	Sequences producing significant alignments:	(bits) Value
	emb AF053127 AF053127 <i>Malus domestica</i> leucine-rich receptor-like... 333 2e-91	
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	emb A57130 A57130 Sequence 1 from Patent WO9531564. 198 1e-70	
	gb U42445 U42445 <i>Lycopersicon pimpinellifolium</i> leucine rich repe... 198 1e-70	
	emb A57133 A57133 Sequence 4 from Patent WO9531564. 198 1e-70	
10	emb AF053998 AF053998 <i>Lycopersicon esculentum</i> Hcr2-5D (Hcr2-5D) ... 194 3e-68	
	emb A67434 A67434 Sequence 7 from Patent WO9743429. 194 3e-68	
	gb U77888 INU77888 <i>Ipomoea nil</i> receptor-like protein kinase (inr... 174 2e-66	
	emb AF053995 AF053995 <i>Lycopersicon esculentum</i> Hcr2-0B (Hcr2-0B) ... 195 1e-65	
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15	emb A67429 A67429 Sequence 2 from Patent WO9743429. 198 2e-65	
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	emb AI485090 AI485090 EST243394 tomato ovary, TAMU Lycopersicon ... 177 9e-64	
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	emb AW727470 AW727470 GA_Ea0012H16 <i>Gossypium arboreum</i> 7-10 dpa ... 86 5e-41	
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45	emb AW267958 AW267958 EST306300 DSIR <i>Medicago truncatula</i> cDNA cl... 125 2e-34	
	emb AW667985 AW667985 GA_Ea0012C15 <i>Gossypium arboreum</i> 7-10 dpa ... 117 1e-33	
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	emb Z73295 CRPK1 <i>C.roseus</i> mRNA for receptor-like protein kinase. 125 2e-32	
	emb AW618736 AW618736 EST320722 <i>L. pennellii</i> trichome, Cornell U... 141 2e-32	
50	emb AA557073 AA557073 915 Loblolly pine N <i>Pinus taeda</i> cDNA clone... 85 6e-32	
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55	emb AW034426 AW034426 EST277997 tomato callus, TAMU Lycopersicon... 119 1e-30	
	emb AW224303 AW224303 EST301030 tomato fruit red ripe, TAMU Lyco... 128 1e-30	
	emb AW035394 AW035394 EST281132 tomato callus, TAMU Lycopersicon... 136 1e-30	
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	emb AW932515 AW932515 EST358358 tomato fruit mature green, TAMU ... 78 1e-30	
60	emb AI166936 AI166936 xylem.est.719 Poplar xylem Lambda ZAPII li... 85 1e-30	
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 5 gb|BE060551|BE060551 HVSMEg0012J19f *Hordeum vulgare* pre-anthesis... 88 1e-29
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 20 emb|AJ727547|AJ727547 BNLGHi8389 Six-day Cotton fiber *Gossypium* ... 75 9e-28
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 30 emb|AW587497|AW587497 IPPGHZ0085 Cotton fiber and embryo Lambda ... 123 3e-27
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 40 emb|AW685504|AW685504 NF030H04NR1F1000 Nodulated root *Medicago t*... 122 1e-26
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 (921 letters)

50 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

55 Score E
 Sequences producing significant alignments: (bits) Value

gb|U22147|HBU22147 *Hevea brasiliensis* beta-1,3-glucanase (HGN1) ... 279 e-123
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 60 emb|A26453|A26453 Recombinant soya beta-1,3-glucanase plasmid. 259 e-117
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- emb|A26447|A26447 Soya beta-1,3-glucanase cDNA HindIII-HindIII f... 259 e-117
emb|A26451|A26451 Soya beta-1,3-glucanase plasmid pBR59 NdeI-Hin... 259 e-117
emb|X53129|PV13BDGL P. vulgaris mRNA for 1,3-beta-D-glucanase. 244 e-111
emb|X89717|PVB13GLUC P. vulgaris beta-1,3-glucanase gene. 247 e-110
5 emb|X07280|NPGLUCB Nicotiana plumbaginifolia mRNA for beta-glucanase... 245 e-108
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gb|S51479|S51479 beta-1,3-glucanase [Pisum sativum=peas, cultiva... 246 e-106
10 gb|U27179|MSU27179 Medicago sativa acidic glucanase mRNA, comple... 232 e-104
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20 emb|AF004838|AF004838 Musa acuminata beta-1,3-glucanase mRNA, pa... 205 8e-95
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emb|AF034117|AF034117 Glycine max beta-1,3-glucanase 12 (SGlu12)... 180 3e-94
gb|M59442|TOBGLUCA N. tabacum basic-1,3-glucanase gene, complete cds. 236 7e-94
emb|A16121|A16121 Intracellular Beta-1, 3 glucanase gene (SEQ ID... 236 7e-94
25 gb|M59443|TOBGLUCB N. tabacum acidic beta-1,3-glucanase gene, com... 150 2e-92
emb|A16120|A16120 Extracellular Beta-1, 3 glucanase gene (SEQ ID... 150 2e-92
gb|M60460|TOBPR2A Tobacco PR2 protein mRNA, complete cds. 149 4e-91
emb|AJ277900|VVI277900 Vitis vinifera mRNA for beta 1-3 glucanas... 221 8e-91
gb|U01902|U01902 Solanum tuberosum Datura endo-1,3-beta-D-glucan... 238 3e-90
30 gb|U49454|PPU49454 Prunus persica beta-1,3-glucanase (Gns1) gene... 211 2e-89
emb|AF227953|AF227953 Capsicum annuum basic beta-1,3-glucanase (... 224 4e-89
emb|AF034106|AF034106 Glycine max beta-1,3-glucanase 1 (SGlu1) g... 221 2e-88
emb|AF141654|AF141654 Nicotiana tabacum beta-1,3-glucanase (GGL4... 139 3e-88
gb|M60463|TOBGL153A Tobacco GL153 protein mRNA, complete cds. 139 3e-88
35 gb|M20620|TOBGLUBC N. tabacum beta-1,3-glucanase mRNA, clone pGL43. 238 4e-88
emb|AF034113|AF034113 Glycine max beta-1,3-glucanase 8 (SGlu8) g... 222 1e-87
emb|X54431|NTSP41B Tobacco sp41b mRNA for (1-3)-beta-glucanase. 136 6e-87
emb|AF141653|AF141653 Nicotiana tabacum beta-1,3-glucanase (GGL1... 136 1e-86
gb|M60464|TOBB13G Tobacco beta-1,3-glucanase mRNA, complete cds. 136 1e-86
40 emb|AJ000081|CSAJ81 Citrus sinensis mRNA for beta-1,3-glucanase. 113 2e-86
emb|X81560|NTSP41AGN N. tabacum Sp41a gene. 136 4e-86
emb|X54430|NTSP41A Tobacco sp41a mRNA for (1-3)-beta-glucanase. 135 8e-86
dbj|E03985|E03985 DNA encoding beta-1,3-endoglucanase. 167 3e-84
dbj|E02108|E02108 cDNA sequence coding for beta-1,3-endoglucanase. 167 3e-84
45 gb|M37753|SOYB13ENDG Soybean beta-1,3-endoglucanase mRNA, comple... 167 3e-84
emb|AJ009932|STAJ9932 Solanum tuberosum mRNA for beta-1,3-glucan... 144 4e-84
emb|AW034632|AW034632 EST278316 tomato callus, TAMU Lycopersicon... 188 1e-82
gb|U41323|GMU41323 Glycine max beta-1,3-glucanase (SGN1) gene, c... 169 3e-82
emb|AW033770|AW033770 EST277341 tomato callus, TAMU Lycopersicon... 186 5e-82
50 gb|M80604|TOMB13GLUA Lycopersicon esculentum beta-1,3-glucanase ... 142 5e-82
emb|X74905|LEQA L. esculentum TomQ'a mRNA for beta(1,3)glucanase. 128 4e-79
emb|AI896001|AI896001 EST265444 tomato callus, TAMU Lycopersicon... 175 9e-79
emb|AW034584|AW034584 EST278268 tomato callus, TAMU Lycopersicon... 226 9e-79
emb|X54456|NTEC32139 N. tabacum mRNA for acidic beta-1,3 glucana... 127 2e-78
55 emb|AJ012751|CAR012751 Cicer arietinum mRNA for glucan endo-beta... 126 2e-78
emb|AW034478|AW034478 EST278049 tomato callus, TAMU Lycopersicon... 227 8e-78
emb|AW031078|AW031078 EST274385 tomato callus, TAMU Lycopersicon... 169 4e-77
emb|AW035235|AW035235 EST280497 tomato callus, TAMU Lycopersicon... 179 5e-77
gb|M60462|TOBPRNA Tobacco PRN protein mRNA, 3' end. 117 5e-76
60 emb|AW775271|AW775271 EST334336 DSIL Medicago truncatula cDNA cl... 163 6e-76
emb|AW776932|AW776932 EST335997 DSIL Medicago truncatula cDNA cl... 156 7e-76

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	emb AW032447 AW032447 EST276006 tomato callus, TAMU Lycopersicon...	227	2e-74
	emb AW156463 AW156463 se26e04.y1 Gm-c1015 Glycine max cDNA clone...	256	3e-74
	emb Z68154 GHBGLUCS G.hirsutum mRNA for 1,3-beta-glucanase.	152	1e-73
5	gb M63634 TOBGCBREG Nicotiana plumbaginifolia beta(1,3)-glucanas...	250	9e-73
	emb AW032644 AW032644 EST276203 tomato callus, TAMU Lycopersicon...	189	1e-71
	emb AF230109 AF230109 Populus alba x Populus tremula beta-1,3 gl...	173	3e-71
	gb M20618 TOBGLUBA N.tabacum beta-1,3-glucanase mRNA, clones pGL...	238	3e-71
	emb AI894445 AI894445 EST263900 tomato callus, TAMU Lycopersicon...	231	3e-71
10	emb AF034107 AF034107 Glycine max beta-1,3-glucanase 2 (SGlu2) g...	142	7e-71
	emb AW031387 AW031387 EST274841 tomato callus, TAMU Lycopersicon...	237	7e-71
	emb AW035366 AW035366 EST280928 tomato callus, TAMU Lycopersicon...	237	7e-71
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15	emb AW030447 AW030447 EST273702 tomato callus, TAMU Lycopersicon...	236	3e-70
	emb AF034116 AF034116 Glycine max beta-1,3-glucanase 11 (SGlu11)...	124	9e-70
	emb AW030277 AW030277 EST273532 tomato callus, TAMU Lycopersicon...	144	2e-69
	emb AF034110 AF034110 Glycine max beta-1,3-glucanase 5 (SGlu5) g...	122	3e-69
	emb AW035160 AW035160 EST280422 tomato callus, TAMU Lycopersicon...	142	6e-69
20	emb AW032444 AW032444 EST276003 tomato callus, TAMU Lycopersicon...	142	6e-69
	emb X74906 LEQB L.esculentum TomQ'b mRNA for beta(1,3)glucanase.	101	1e-68
	emb AJ011769 CIN011769 Cichorium intybus X Cichorium endivia sub...	97	1e-68
	emb AW030283 AW030283 EST273538 tomato callus, TAMU Lycopersicon...	140	2e-68
	gb M13237 BLYGLUCB Barley beta glucanase mRNA.	158	7e-68
25	emb Z15131 ASBGLUCAN A.sativa mRNA for beta glucanase.	158	9e-68
	emb AI896042 AI896042 EST265485 tomato callus, TAMU Lycopersicon...	237	1e-67
	gb M62740 BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan...	158	2e-67
	emb AW031259 AW031259 EST274634 tomato callus, TAMU Lycopersicon...	136	3e-67
	emb AW035840 AW035840 EST281994 tomato callus, TAMU Lycopersicon...	136	3e-67
30	emb AW032451 AW032451 EST276010 tomato callus, TAMU Lycopersicon...	136	3e-67
	emb AW031353 AW031353 EST274807 tomato callus, TAMU Lycopersicon...	136	3e-67
	emb AI895981 AI895981 EST265424 tomato callus, TAMU Lycopersicon...	136	3e-67
	gb U73709 VVU73709 Vitis vinifera beta-1,3-glucanase mRNA, parti...	244	3e-67
	emb Z22874 TABETGLUB T.aestivum (1,3;1,4) beta glucanase mRNA, c...	160	3e-67
35	emb AF034114 AF034114 Glycine max beta-1,3-glucanase 9 (SGlu9) p...	119	7e-67

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 40 thaliana] /blast_score 1.00e-158 /ec_number /family /chip nova
 /gb_link /ncgi
 (939 letters)

Database: plantfungal

45 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
 50 Sequences producing significant alignments: (bits) Value

	emb AW730233 AW730233 GA_Ea0014B16 Gossypium arboreum 7-10 dpa ...	352	5e-98
	emb AW649960 AW649960 EST328414 tomato germinating seedlings, TA...	308	4e-83
	emb AW621664 AW621664 EST312462 tomato root during/after fruit s...	290	1e-77
55	emb AW031327 AW031327 EST274781 tomato callus, TAMU Lycopersicon...	282	3e-75
	gb U38804 PPU38804 Porphyra purpurea chloroplast, complete genome.	271	4e-72
	emb AW775853 AW775853 EST334918 DSIL Medicago truncatula cDNA cl...	264	9e-70
	emb Z21642 CHASTRNAA Antithamnion sp. Chloroplast trnK, trnE, trpA...	255	4e-67
	gb BE124387 BE124387 EST393422 GVN Medicago truncatula cDNA clon...	227	9e-59
60	gb BE121873 BE121873 894015F07.y1 C. reinhardtii CC-1690, normal...	227	1e-58
	emb AF022186 AF022186 Cyanidium caldarium strain RK1 chloroplast...	220	1e-56

- emb|AI782364|AI782364 EST263243 tomato susceptible, Cornell Lyco... 210 1e-53
 emb|AW691298|AW691298 NF040B01ST1F1000 Developing stem Medicago ... 193 1e-49
 dbj|D63675|D63675 Cyanidioschyzon merolae trnK, trpA, trnT, rps4... 130 1e-49
 emb|AV392084|AV392084 AV392084 Chlamydomonas reinhardtii C9 Chla... 195 5e-49
 5 emb|AA660642|AA660642 00530 MtRHE Medicago truncatula cDNA 5' si... 190 1e-47
 dbj|D17791|CYNPLTRNK C.caldarium chloroplast gene for trnK and g... 121 1e-46
 emb|AW034248|AW034248 EST277819 tomato callus, TAMU Lycopersicon... 184 9e-46
 dbj|D63676|D63676 Cyanidium caldarium trnK, trpA, trnT, rps4, tr... 122 1e-45
 gb|L38526|L38526 BNAF0168E Mustard flower buds Brassica rapa cDN... 177 1e-43
 10 emb|V01342|SCTRP5A Yeast gene (trp5) for tryptophan synthetase. 86 9e-42
 emb|Z72548|SCYGL026C S.cerevisiae chromosome VII reading frame O... 86 9e-42
 emb|AW398861|AW398861 EST309361 L. pennellii trichome, Cornell U... 158 5e-38
 emb|AU090244|AU090244 AU090244 Hordeum vulgare subsp. vulgare Up... 149 7e-38
 emb|AW650911|AW650911 EST329365 tomato germinating seedlings, TA... 141 1e-32
 15 emb|AI773494|AI773494 EST254594 tomato resistant, Cornell Lycopersicon... 138 5e-32
 emb|Z98974|SPAC19A8 S.pombe chromosome I cosmid c19A8. 74 3e-30
 emb|V01343|SCTRP5B Part of the yeast gene for tryptophan synthet... 86 2e-26
 emb|AI165371|AI165371 A082p39u Hybrid aspen plasmid library Popu... 81 1e-21
 emb|AU090028|AU090028 AU090028 Hordeum vulgare subsp. vulgare Up... 97 2e-19
 20 gb|J04594|NEUTRP3A N.crassa tryptophan synthetase (trp3) alpha-2... 78 1e-17
 emb|AF084886|AF084886 Neurospora crassa 314-448A mutant tryptoph... 68 9e-11
 emb|AF084890|AF084890 Neurospora crassa TD 554-6A mutant tryptop... 53 4e-10
 emb|AF084880|AF084880 Neurospora crassa EMSG9-9A mutant tryptoph... 66 5e-10
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 25 emb|AF084884|AF084884 Neurospora crassa 314-722A mutant tryptoph... 64 1e-09
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 30 gb|M29094|CCITRP01 Mushroom (C.cinereus) tryptophan synthetase (... 59 4e-08
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 emb|AW693052|AW693052 NF059C08ST1F1065 Developing stem Medicago ... 51 1e-05
 emb|AV390244|AV390244 AV390244 Chlamydomonas reinhardtii C9 Chla... 49 4e-05
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 35 emb|AL354022|P761R Leishmania major Friedlin PAC P761 right end... 44 0.002
 gb|M91656|CCITRP05 Coprinus cinereus tryptophan synthetase (TRP1... 43 0.005
 emb|AQ903789|AQ903789 GSSTc04230 Trypanosome cruzi random genomi... 35 0.24
 emb|AW727215|AW727215 GA_Ea0023N23 Gossypium arboreum 7-10 dpa ... 36 0.52
 gb|M91654|CCITRP03 Coprinus cinereus tryptophan synthetase (TRP1... 36 0.52
 40 emb|AW728975|AW728975 GA_Ea0018P19 Gossypium arboreum 7-10 dpa ... 35 0.64
 emb|AL139794|LMPF1105 Leishmania major Friedlin chromosome 4 PAC... 35 0.87
 emb|AW926438|AW926438 HVSMeg0007D14 Hordeum vulgare pre-anthesis... 34 1.2
 emb|AA965348|AA965348 e9d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
 gb|U12630|ENU12630 Emericella nidulans R153 core histone H3 (H3)... 34 1.3
 45 emb|AI007494|AI007494 e9c09a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
 emb|AA787433|AA787433 n3d04a1.r1 Aspergillus nidulans 24hr asexu... 34 1.3
 emb|X55548|ANH3GENE A.nidulans gene for core histone for H3. 34 1.3
 emb|AQ396426|AQ396426 mgxb0013C24f CUGI Rice Blast BAC Library P... 34 1.6
 emb|AF262997|AF262997 Ricinus communis NADP-dependent malic prot... 34 1.6
 50 gb|M19025|CFUCPOR C.fumago cpo gene encoding chloroperoxidase, c... 34 1.6
 emb|AF084888|AF084888 Neurospora crassa 656-2A mutant tryptophan... 31 1.7
 emb|AF084887|AF084887 Neurospora crassa TDA78(1-A)9A(TD201) muta... 31 1.7
 emb|AW694774|AW694774 NF080A05ST1F1036 Developing stem Medicago ... 34 1.8
 emb|Y18012|TVE18012 Trametes versicolor mRNA for laccase. 33 2.3
 55 emb|AQ500614|AQ500614 V35B5 mTn-3xHA/lacZ Insertion Library Sacc... 33 2.5
 emb|AW187498|AW187498 BNLGHi6414 Six-day Cotton fiber Gossypium ... 33 3.1
 emb|AW187530|AW187530 BNLGHi6944 Six-day Cotton fiber Gossypium ... 33 3.1
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 emb|AW186883|AW186883 BNLGHi6498 Six-day Cotton fiber Gossypium ... 33 3.1
 60 emb|AW187537|AW187537 BNLGHi7006 Six-day Cotton fiber Gossypium ... 33 3.1
 emb|AW187474|AW187474 BNLGHi5936 Six-day Cotton fiber Gossypium ... 33 3.1

	emb AA167859 AA167859 CpEST.053 uniZAPCpIOWAsporoLib1 Cryptospor...	33	3.5
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	emb AF129874 AF129874 Pichia angusta peroxin-6 (PEX6) gene, comp...	33	4.3
	emb AL112679 CNS01AA7 Botrytis cinerea strain T4 cDNA library un...	33	4.7
5	gb BE028433 BE028433 EtESTea78d07.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI166784 AI166784 xylem.est.582 Poplar xylem Lambda ZAPII li...	32	5.9
	emb AQ941624 AQ941624 Sheared DNA-53E1.TF Sheared DNA Trypanosom...	32	5.9
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10	emb AI757375 AI757375 EtESTea32d03.y1 Eimeria S5-2 Sporozoite st...	32	5.9
	gb BE027843 BE027843 EtESTea88c05.y1 Eimeria M5-6 Merozoite stag...	32	5.9
	emb AI973878 AI973878 sd13a09.y1 Gm-c1020 Glycine max cDNA clone...	32	5.9
	dbj D85261 D85261 Plasmodium vivax clone TD439B DNA for merozoit...	32	5.9
	dbj D85251 D85251 Plasmodium vivax clone TD207B DNA for merozoit...	32	5.9
15	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	32	6.5
	emb Z71509 SCYNL233W S.cerevisiae chromosome XIV reading frame O...	32	6.5
	emb AW707662 AW707662 832011E08.y1 C. reinhardtii CC-125 nutrien...	28	7.3
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20	emb AW703740 AW703740 sk23g09.y1 Gm-c1028 Glycine max cDNA clone...	32	8.1
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35 http://www3.ncbi.nlm.nih.gov/htbin-
post/entrez/query?db=n&form=6&dopt=g&uid=gb|z97339|/ncgi
http://www.ncgr.org/cgi-bin/ff?z97339
(441 letters)

40 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

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	emb AW685774 AW685774 NF035A03NR1F1000 Nodulated root Medicago t...	123 6e-28
	emb AW687017 AW687017 NF005A10RT1F1072 Developing root Medicago ...	123 6e-28
50	emb AW687794 AW687794 NF013E08RT1F1066 Developing root Medicago ...	89 3e-23
	emb AW310121 AW310121 sf31d07.x1 Gm-c1028 Glycine max cDNA clone...	68 3e-19
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	emb AW395252 AW395252 sh45g06.y1 Gm-c1017 Glycine max cDNA clone...	68 3e-19
	emb AW704612 AW704612 sk54c11.y1 Gm-c1019 Glycine max cDNA clone...	68 3e-19
55	emb AT000508 AT000508 AT000508 Brassica rapa guard cell Brassica...	50 2e-18
	emb AW704218 AW704218 sk17c12.y1 Gm-c1028 Glycine max cDNA clone...	63 3e-17
	emb AW423428 AW423428 sh66f08.y1 Gm-c1015 Glycine max cDNA clone...	63 1e-16
	emb AW687188 AW687188 NF006H09RT1F1079 Developing root Medicago ...	82 3e-15
	emb AW684973 AW684973 NF023G04NR1F1000 Nodulated root Medicago t...	68 1e-13
60	emb AW233878 AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone...	69 3e-13
	emb AW687098 AW687098 NF006A02RT1F1007 Developing root Medicago ...	72 2e-12

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 emb|AI437669|AI437669 sa38a11.y1 Gm-cl004 Glycine max cDNA clone... 48 1e-11
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 5 emb|AW687565|AW687565 NF011A04RT1F1024 Developing root Medicago ... 48 2e-11
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 10 emb|AW394608|AW394608 sh33e11.y1 Gm-cl017 Glycine max cDNA clone... 46 2e-07
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 emb|AI960446|AI960446 sc84a10.y1 Gm-cl018 Glycine max cDNA clone... 48 4e-06
 emb|AI794716|AI794716 sb68b06.y1 Gm-cl019 Glycine max cDNA clone... 48 5e-06
 gb|BE024111|BE024111 sm96h03.y1 Gm-cl015 Glycine max cDNA clone ... 48 9e-06
 emb|Z99969|MAZ99969 Musa acuminata mRNA for putative beta-1,3-gl... 41 6e-05
 15 emb|AV412437|AV412437 AV412437 Lotus japonicus young plants (two... 47 9e-05
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 emb|AW277478|AW277478 sf82e11.y1 Gm-cl019 Glycine max cDNA clone... 37 4e-04
 emb|AW775954|AW775954 EST335019 DSIL Medicago truncatula cDNA cl... 42 7e-04
 20 gb|BE122569|BE122569 Ljirmp29-344-g6 Ljirmp Lambda HybriZap t... 43 0.001
 emb|AW299135|AW299135 EST305809 KV2 Medicago truncatula cDNA clo... 43 0.002
 emb|AW423359|AW423359 sh06g04.y1 Gm-cl016 Glycine max cDNA clone... 41 0.004
 emb|AW171748|AW171748 N100642e rootphos(-) Medicago truncatula c... 40 0.014
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 25 emb|AW747074|AW747074 WS1_65_A07.g1_A002 Water-stressed 1 (WS1) ... 39 0.026
 emb|AW649685|AW649685 EST328139 tomato germinating seedlings, TA... 38 0.036
 emb|AW299176|AW299176 EST305986 KV2 Medicago truncatula cDNA clo... 38 0.036
 emb|AW220014|AW220014 EST302497 tomato root during/after fruit s... 38 0.050
 gb|C96140|C96140 Marchantia polymorpha immature sex organ... 38 0.050
 30 emb|AW625648|AW625648 EST319555 tomato radicle, 5 d post-imbibit... 38 0.050
 emb|AW926780|AW926780 HVSMEG0008D23 Hordeum vulgare pre-anthesis... 37 0.094
 gb|L05906|PMCMSGF Pneumocystis carinii (clone GP3) major surface... 36 0.18
 emb|AW333354|AW333354 S20F5 AGS-1 Pneumocystis carinii f. sp. ca... 36 0.18
 emb|Z98595|SPAC11E3 S.pombe chromosome I cosmid c11E3. 35 0.24
 35 emb|AW725520|AW725520 GA_Ea0018G22 Gossypium arboreum 7-10 dpa ... 35 0.46
 gb|BE052896|BE052896 GA_Ea0025I06f Gossypium arboreum 7-10 dpa ... 35 0.46
 emb|AW309936|AW309936 sf26g12.x1 Gm-cl028 Glycine max cDNA clone... 35 0.46
 emb|AW310120|AW310120 sf31d06.x1 Gm-cl028 Glycine max cDNA clone... 35 0.46
 emb|AW233798|AW233798 sf26g12.y1 Gm-cl028 Glycine max cDNA clone... 35 0.46
 40 gb|BE053040|BE053040 GA_Ea0015D14f Gossypium arboreum 7-10 dpa ... 35 0.46
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 gb|BE054609|BE054609 GA_Ea0006A14f Gossypium arboreum 7-10 dpa ... 35 0.46
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 45 emb|AC013353|AC013353 Trypanosoma brucei chromosome VI clone RPC... 34 0.63
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 emb|AW691828|AW691828 NF044F04ST1F1000 Developing stem Medicago ... 34 0.63
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 emb|AI731500|AI731500 BNLGHi9982 Six-day Cotton fiber Gossypium ... 34 0.63
 50 emb|AQ660279|AQ660279 Sheared DNA-3L23.TF Sheared DNA Trypanoso... 34 0.63
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 emb|AI725456|AI725456 BNLGHi12219 Six-day Cotton fiber Gossypium... 34 0.63
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 emb|AI731231|AI731231 BNLGHi8954 Six-day Cotton fiber Gossypium ... 34 0.87
 55 emb|AL035477|PFMAL4P4 Plasmodium falciparum chromosome 4 strain ... 34 0.87
 gb|BE033791|BE033791 MF06E10 MF Mesembryanthemum crystallinum cD... 34 0.87
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 60 emb|AW620830|AW620830 sj47b03.y1 Gm-cl033 Glycine max cDNA clone... 28 1.1
 dbj|D63449|YSCATF1A Yeast ATF1 gene for alcohol acetyltransferas... 33 1.2

- dbj|E08050|E08050 cDNA encoding beer yeast alcohol acetyltransfe... 33 1.2
 dbj|E06817|E06817 DNA encoding alcohol acetyltransferase 1. 33 1.2
 dbj|D26554|YSCATF1 Yeast ATF1 gene for alcohol acetyltransferase... 33 1.2
 dbj|E08049|E08049 cDNA encoding sake yeast alcohol acetyltransfe... 33 1.2
 5 dbj|E06816|E06816 DNA encoding alcohol acetyltransferase 1. 33 1.2
 emb|Z75285|SCYOR377W *S.cerevisiae* chromosome XV reading frame OR... 33 1.2
 emb|AW725476|AW725476 GA_Ea0018C14 *Gossypium arboreum* 7-10 dpa ... 33 1.6
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 10 emb|X01777|HVB3HORD Barley mRNA fragment for B3-hordein. 33 1.6
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 emb|AL031261|SPBC3H7 *S.pombe* chromosome II cosmid c3H7. 32 2.2
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 15 emb|AI728744|AI728744 BNLGHi11492 Six-day Cotton fiber *Gossypium...* 32 2.2
 gb|BE036189|BE036189 MO20F12 *Mesembryanthemum crystallinum* cD... 32 3.1
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 emb|AL160371|LMFLCHR15 *Leishmania major* Friedlin assembled chrom... 31 4.2
 emb|AL122012|LMFL8342 *Leishmania major* Friedlin chromosome 23 co... 31 4.2
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(592 letters)

Database: plantfungal

- 35 661,018 sequences; 426,114,510 total letters

Searching.....done

- 40 Sequences producing significant alignments: (bits) Value

- emb|X90695|MSRNAPE02 *M.sativa* mRNA for peroxidase 2. 339 1e-92
 emb|AJ011939|TRE011939 *Trifolium repens* mRNA for peroxidase. 335 2e-91
 emb|Y10469|SOPRXR8 *S.oleracea* mRNA for peroxidase, clone PC55. 332 2e-90
 45 emb|AI487510|AI487510 EST245832 tomato ovary, TAMU *Lycopersicon* ... 327 5e-89
 emb|AI486784|AI486784 EST245106 tomato ovary, TAMU *Lycopersicon* ... 327 5e-89
 emb|AI895842|AI895842 EST265285 tomato callus, TAMU *Lycopersicon...* 325 1e-88
 emb|AW032442|AW032442 EST276001 tomato callus, TAMU *Lycopersicon...* 325 2e-88
 gb|L36158|ALFPXDD *Medicago sativa* peroxidase (pxdD) mRNA, 3' end. 320 6e-87
 50 emb|AW216351|AW216351 EST295095 tomato callus, TAMU *Lycopersicon...* 319 1e-86
 emb|AW691003|AW691003 NF040C11ST1F1000 Developing stem *Medicago* ... 319 2e-86
 emb|AW625601|AW625601 EST319508 tomato radicle, 5 d post-imbibit... 318 3e-86
 gb|BE124281|BE124281 EST394406 *DSIL Medicago truncatula* cDNA clo... 314 4e-85
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 emb|AI897419|AI897419 EST266862 tomato ovary, TAMU *Lycopersicon* ... 295 2e-79
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50	emb AW832025 AW832025 sm30b11.y1 Gm-c1028 Glycine max cDNA clone...	210 1e-53
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 15 emb|AW622012|AW622012 EST312810 tomato root during/after fruit s... 106 1e-43
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	emb AI485651 AI485651 EST243972 tomato ovary, TAMU Lycopersicon ...	62 4e-20
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	dbj D16416 WHTWZF1B Wheat mRNA for WZF1, complete cds.	62 7e-20
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 emb|AI484099|AI484099 EST249970 tomato ovary, TAMU Lycopersicon ... 62 5e-14
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(940 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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 gb|U68763|GMU68763 Glycine max putative transcription factor SCO... 72 2e-39
 dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 69 4e-38
 emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 125 7e-38
 35 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 62 3e-36
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 40 emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 67 4e-32
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 45 dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 59 8e-29
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(426 letters)

15 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Score E
Sequences producing significant alignments: (bits) Value

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emb|AW568285|AW568285 si69g11.y1 Gm-r1030 Glycine max cDNA clone... 240 5e-63
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emb|AW335287|AW335287 S45D10 AGS-1 Pneumocystis carinii f. sp. c... 76 5e-35
60 emb|AI026521|AI026521 TENU0733 T. cruzi epimastigote normalized ... 124 3e-31
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 emb|AW933878|AW933878 EST359721 tomato fruit mature green, TAMU ... 89 7e-25
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 5 emb|X59720|SCCHRIII S.cerevisiae chromosome III complete DNA seq... 80 8e-25
 emb|AW617209|AW617209 EST323620 L. hirsutum trichome, Cornell Un... 89 1e-24
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 10 emb|AW222638|AW222638 EST299449 tomato fruit red ripe, TAMU Lyco... 89 2e-22
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 20 emb|AW220746|AW220746 EST297215 tomato fruit mature green, TAMU ... 89 2e-17
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 25 emb|AT000681|AT000681 AT000681 Brassica rapa guard cell Brassica... 61 3e-12
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 emb|AW907238|AW907238 EST343361 potato stolon, Cornell Universit... 63 9e-10
 30 emb|AZ215418|AZ215418 Sheared DNA-79B7.TF Sheared DNA Trypanosom... 54 2e-09
 emb|AA842826|AA842826 CFB57 Floral bud cDNA library of Hot peppe... 59 2e-08
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Score E

Sequences producing significant alignments: (bits) Value

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	emb AF082028 AF082028 Hemerocallis hybrid cultivar senescence-as...	194 3e-67
	emb AW775904 AW775904 EST334969 DSIL Medicago truncatula cDNA cl...	223 9e-66
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50	emb AF014802 AF014802 Eschscholzia californica (S)-N-methylcocla...	165 7e-47
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55	gb U29333 PSU29333 Pisum sativum novel wound-inducible cytochrom...	161 6e-45
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 45 emb|AF195804|AF195804 *Lens culinaris* isoflavone synthase 1 (ifs1)... 96 6e-40
 emb|AF195816|AF195816 *Beta vulgaris* isoflavone synthase 1 (ifs1)... 99 6e-40
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- Database: plantfungal
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	gb U21801 LEU21801 Lycopersicon esculentum alcohol dehydrogenase...	111	1e-64	
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10	emb AW625848 AW625848 EST319755 tomato radicle, 5 d post-imbibit...	125	2e-54	
	emb AW096560 AW096560 EST289740 tomato mixed elicitor, BTI Lycop...	117	5e-52	
	emb AI494929 AI494929 sa92g06.y1 Gm-cl004 Glycine max cDNA clone...	203	1e-51	
	emb AB018559 AB018559 Citrullus lanatus mRNA for wts2L, complete...	74	1e-50	
	emb AF053638 AF053638 Pisum sativum short-chain alcohol dehydrog...	103	3e-50	
15	emb AF097651 AF097651 Pisum sativum short-chain alcohol dehydrog...	103	8e-50	
	emb AF053639 AF053639 Pisum sativum short-chain alcohol dehydrog...	103	2e-49	
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	emb AJ223177 NTAJ3177 Nicotiana tabacum mRNA for short chain alc...	93	7e-49	
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	emb AW698458 AW698458 g412 glandular-haired subtracted cDNA libr...	75	3e-22
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(1056 letters)

55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments: (bits) Value

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 5 emb|AW668121|AW668121 GA_Ea0012N05 Gossypium arboreum 7-10 dpa ... 167 3e-62
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 (1216 letters)

50 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

55 Searching.....done

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 Sequences producing significant alignments: (bits) Value

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- emb|AW775409|AW775409 EST334474 DSIL *Medicago truncatula* cDNA cl... 304 9e-94
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 (1716 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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60 emb AW695003 AW695003 NF082C07ST1F1053 Developing stem Medicago ...	88	2e-16		
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- emb|AW736154|AW736154 EST332140 KV3 Medicago truncatula cDNA clo... 88 2e-16
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 (2403 letters)

- 40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 50 emb|Y18932|LES18932 Lycopersicon esculentum p69F gene. 142 e-152
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 55 emb|AJ006379|LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
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 emb|AJ006786|LES6786 Lycopersicon esculentum p69d gene. 141 e-136
 emb|AJ005171|LEAJ5171 Lycopersicon esculentum p69c gene, complete... 142 e-136
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 60 emb|Y10149|LESUBTILI L.esculentum mRNA for subtilisin-like protein. 138 e-130
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- emb|X95270|LESUBENDO L.esculentum mRNA for subtilisin-like endop... 138 e-126
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 20 emb|AJ012164|CGL012164 Casuarina glauca mRNA for cg12 gene fragm... 114 4e-62
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 emb|AW030462|AW030462 EST273717 tomato callus, TAMU Lycopersicon... 173 4e-51
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35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 45 emb|Y18932|LES18932 Lycopersicon esculentum p69F gene. 142 e-152
 emb|Y17278|LES17278 Lycopersicon esculentum p69d gene, complete ... 141 e-146
 emb|AJ005173|LEAJ5173 Lycopersicon esculentum p69f gene, complet... 141 e-146
 emb|AJ005172|LEAJ5172 Lycopersicon esculentum p69e gene, complet... 142 e-146
 emb|Y18931|LES18931 Lycopersicon esculentum p69E gene. 144 e-144
 50 emb|AJ006379|LES6379 Lycopersicon esculentum sbt2 gene. 163 e-142
 emb|X98930|LESBT2 L.esculentum mRNA for serine protease, SBT2. 163 e-142
 emb|AJ006786|LES6786 Lycopersicon esculentum p69d gene. 141 e-136
 emb|AJ005171|LEAJ517 Lycopersicon esculentum p69c gene, complete... 142 e-136
 emb|Y17276|LES17276 Lycopersicon esculentum p69b gene, complete ... 138 e-130
 55 emb|Y10149|LESUBTILI L.esculentum mRNA for subtilisin-like protein. 138 e-130
 emb|Y17275|LES17275 Lycopersicon esculentum p69a gene, complete ... 138 e-126
 emb|X95270|LESUBENDO L.esculentum mRNA for subtilisin-like endop... 138 e-126
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- dbj|D86598|D86598 Norway spruce mRNA for antifreeze-like protein... 135 6e-77
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 35 emb|AW221342|AW221342 EST297811 tomato fruit mature green, TAMU ... 154 7e-52
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 30 (2002 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| gb U43542 NTU43542 Nicotiana tabacum diphenol oxidase mRNA, comp... | 379 | e-104 |
| gb U73103 LTU73103 Liriodendron tulipifera high-pI laccase (LAC2... | 363 | e-103 |
| gb U12757 APU12757 Acer pseudoplatanus laccase mRNA, complete cds. | 368 | e-100 |
| 50 gb U73104 LTU73104 Liriodendron tulipifera high-pI laccase (LAC2... | 353 | 3e-99 |
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 35 emb|AI167003|AI167003 xylem.est.78 Poplar xylem Lambda ZAPII lib... 204 3e-51
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 55 emb|AW887962|AW887962 NXNV_127_D08_F Nsf Xylem Normal wood Verti... 176 7e-43
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- emb|AW693471|AW693471 NF065C09ST1F1000 Developing stem Medicago ... 169 8e-41
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 10 emb|AW695246|AW695246 NF092G11ST1F1087 Developing stem Medicago ... 92 5e-37
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 (965 letters)

Database: plantfungal
 30 661,018 sequences; 426,114,510 total letters

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Score E
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 40 emb|AF149279|AF149279 Phaseolus vulgaris peroxidase 4 precursor ... 220 2e-94
 gb|L36112|SSNPEROXIC Stylosanthes humilis peroxidase mRNA. 157 2e-86
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 emb|Y10468|SOPRXX7 S.oleracea mRNA for peroxidase, clone PC36. 196 6e-78
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 45 emb|AW216873|AW216873 EST295587 tomato callus, TAMU Lycopersicon... 212 3e-73
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 50 emb|AW032353|AW032353 EST275807 tomato callus, TAMU Lycopersicon... 137 1e-61
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20 emb|X56011|TAPERO Wheat mRNA for peroxidase. 102 2e-48
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25 gb|M74103|TOBANPER *Nicotiana sylvestris* anionic peroxidase mRNA,... 100 2e-47
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35 gb|M91372|CUSPREPERB *Cucumis sativus* peroxidase mRNA, complete cds. 89 2e-45
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45 emb|AI772237|AI772237 EST253337 tomato resistant, Cornell Lycop... 180 2e-44
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gb|U12315|CCU12315 Cenchrus ciliaris clone PX18 peroxidase mRNA,... 106 9e-41
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(1025 letters)

25 Database: plantfungal
661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E
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50 emb|AW729695|AW729695 GA_Ea0025M09 Gossypium arboreum 7-10 dpa ... 394 e-109
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- gb|BE036915|BE036915 MP09A12 MP Mesembryanthemum crystallinum cD... 368 e-101
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15 emb|AI773291|AI773291 EST254391 tomato resistant, Cornell Lycopersicon... 293 1e-95
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25 emb|AI485855|AI485855 EST244176 tomato ovary, TAMU Lycopersicon ... 343 1e-93
emb|AW432541|AW432541 sh75f05.yl Gm-cl015 Glycine max cDNA clone... 342 3e-93
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dbj|E06964|E06964 Anti-sense RNA of xyloglucan endotransferase g... 310 4e-93
30 emb|AI489962|AI489962 EST248301 tomato ovary, TAMU Lycopersicon ... 341 4e-93
emb|AI898758|AI898758 EST268201 tomato ovary, TAMU Lycopersicon ... 286 7e-93
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35 dbj|D16458|VIREXT5 V.angularis mRNA for endo-xyloglucan transfer... 314 1e-90
gb|L43094|TRUXET1G Tropaeolum majus xyloglucan endotransglycosyl... 324 1e-90
dbj|E06968|E06968 DNA encoding xyloglucan endotransferase. 314 1e-90
dbj|E06963|E06963 Anti-sense RNA of xyloglucan endotransferase g... 314 1e-90
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40 emb|AJ004917|CAAJ4917 Cicer arietinum mRNA for endoxyloglucan tr... 310 1e-89
emb|X91659|HVEXTGENE H.vulgare mRNA for endoxyloglucan transferase. 318 1e-89
dbj|D16457|WHTEXT4 Wheat mRNA for endo-xyloglucan transferase, c... 319 2e-89
dbj|E06972|E06972 DNA encoding xyloglucan endotransferase. 319 6e-89
dbj|E06967|E06967 Anti-sense RNA of xyloglucan endotransferase g... 319 6e-89
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emb|AI488724|AI488724 EST247063 tomato ovary, TAMU Lycopersicon ... 273 2e-88
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55 emb|AI487338|AI487338 EST245660 tomato ovary, TAMU Lycopersicon ... 265 3e-87
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 10 emb|AW216790|AW216790 EST295504 tomato callus, TAMU Lycopersicon... 312 3e-84
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- emb|AI130885|FSY130885 Fagus sylvatica mRNA for xyloglucan endot... 424 e-134
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 emb|AW218856|AW218856 EST301338 tomato root during/after fruit s... 413 e-115
 35 emb|AW031139|AW031139 EST274446 tomato callus, TAMU Lycopersicon... 380 e-115
 emb|AI725820|AI725820 BNLGHi13219 Six-day Cotton fiber Gossypium... 413 e-114
 emb|AI938507|AI938507 sb46e06.y1 Gm-c1015 Glycine max cDNA clone... 407 e-112
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 emb|AI488729|AI488729 EST247068 tomato ovary, TAMU Lycopersicon ... 406 e-112
 40 emb|AI485531|AI485531 EST243852 tomato ovary, TAMU Lycopersicon ... 402 e-111
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 emb|AW729695|AW729695 GA_Ea0025M09 Gossypium arboreum 7-10 dpa ... 394 e-109
 45 emb|X93175|HVXETXEB H. vulgare mRNA for xyloglucan endotransglyco... 387 e-109
 emb|AW651314|AW651314 EST329768 tomato germinating seedlings, TA... 390 e-108
 emb|AW218734|AW218734 EST301214 tomato root during/after fruit s... 388 e-107
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- emb|AW031478|AW031478 EST274932 tomato callus, TAMU Lycopersicon... 360 1e-98
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 20 emb|AW432541|AW432541 sh75f05.y1 Gm-cl015 Glycine max cDNA clone... 342 3e-93
 dbj|D16455|SOYEXT2 Soybean mRNA for endo-xyloglucan transferase,... 310 4e-93
 dbj|E06969|E06969 DNA encoding xyloglucan endotransferase. 310 4e-93
 dbj|E06964|E06964 Anti-sense RNA of xyloglucan endotransferase g... 310 4e-93
 emb|AI489962|AI489962 EST248301 tomato ovary, TAMU Lycopersicon ... 341 4e-93
 25 emb|AI898758|AI898758 EST268201 tomato ovary, TAMU Lycopersicon ... 286 7e-93
 emb|AW394832|AW394832 sh35h09.y1 Gm-cl017 Glycine max cDNA clone... 341 7e-93
 dbj|E06959|E06959 Anti-sense DNA of xyloglucan endotransferase g... 306 6e-92
 gb|L46792|ACTXET Actinidia deliciosa clone AdXET-5 xyloglucan en... 320 8e-92
 dbj|D16458|VIREXT5 V.angularis mRNA for endo-xyloglucan transfer... 314 1e-90
 30 gb|L43094|TRUXET1G Tropaeolum majus xyloglucan endotransglycosyl... 324 1e-90
 dbj|E06968|E06968 DNA encoding xyloglucan endotransferase. 314 1e-90
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 35 emb|X91659|HVEXTGENE H.vulgare mRNA for endoxyloglucan transferase. 318 1e-89
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 40 emb|AW687253|AW687253 NF007F05RT1F1046 Developing root Medicago ... 292 1e-88
 emb|AI488724|AI488724 EST247063 tomato ovary, TAMU Lycopersicon ... 273 2e-88
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 45 emb|AW038999|AW038999 EST280972 tomato mixed elicitor, BTI Lycop... 303 3e-88
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 55 emb|AI489200|AI489200 EST247539 tomato ovary, TAMU Lycopersicon ... 274 2e-85
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 emb|AI729066|AI729066 BNLGHi12528 Six-day Cotton fiber Gossypium... 315 4e-85
 dbj|D16456|TOMEXT3 Tomato mRNA for endo-xyloglucan transferase, ... 295 4e-85
 dbj|E06971|E06971 DNA encoding xyloglucan endotransferase. 295 4e-85
 60 dbj|E06966|E06966 Anti-sense RNA of xyloglucan endotransferase g... 295 4e-85
 dbj|E06961|E06961 Anti-sense DNA of xyloglucan endotransferase g... 295 4e-85

emb|AW934469|AW934469 EST353373 tomato flower buds 0-3 mm, Corne... 314 7e-85
 emb|AW185234|AW185234 se88f12.y1 Gm-c1023 Glycine max cDNA clone... 314 1e-84
 emb|AI487776|AI487776 EST246098 tomato ovary, TAMU Lycopersicon ... 266 2e-84
 emb|AW216790|AW216790 EST295504 tomato callus, TAMU Lycopersicon... 312 3e-84
 5 emb|AI895031|AI895031 EST264474 tomato callus, TAMU Lycopersicon... 312 4e-84

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 (390 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AW980547 AW980547 EST391700 GVN Medicago truncatula cDNA clo...	95	2e-22	
	emb AW685869 AW685869 NF031B09NR1F1000 Nodulated root Medicago t...	95	2e-22	
25	gb BE124445 BE124445 EST393480 GVN Medicago truncatula cDNA clon...	95	2e-22	
	gb BE124752 BE124752 EST393787 GVN Medicago truncatula cDNA clon...	95	2e-22	
	emb AW684629 AW684629 NF019B05NR1F1000 Nodulated root Medicago t...	95	2e-22	
	emb AW329233 AW329233 N200445e rootphos(-) Medicago truncatula c...	95	2e-22	
	gb BE124520 BE124520 EST393555 GVN Medicago truncatula cDNA clon...	95	4e-22	
30	emb AW125962 AW125962 N100157e rootphos(-) Medicago truncatula c...	92	2e-21	
	emb AW622601 AW622601 EST313401 tomato root during/after fruit s...	101	2e-21	
	emb AW624937 AW624937 EST313766 tomato radicle, 5 d post-imbibit...	101	2e-21	
	emb AW560894 AW560894 EST315942 DSIR Medicago truncatula cDNA cl...	95	3e-21	
	emb AW621250 AW621250 EST312048 tomato root during/after fruit s...	98	9e-21	
35	emb AW626221 AW626221 EST320128 tomato radicle, 5 d post-imbibit...	98	9e-21	
	emb AW035571 AW035571 EST281309 tomato callus, TAMU Lycopersicon...	98	1e-20	
	emb AW217082 AW217082 EST295796 tomato callus, TAMU Lycopersicon...	98	1e-20	
	emb AW032764 AW032764 EST276323 tomato callus, TAMU Lycopersicon...	98	1e-20	
	emb AW443140 AW443140 EST308070 tomato mixed elicitor, BTI Lycop...	98	1e-20	
40	emb AW622645 AW622645 EST313445 tomato root during/after fruit s...	96	1e-20	
	emb AW907202 AW907202 EST343325 potato stolon, Cornell Universit...	99	2e-20	
	emb AI776056 AI776056 EST257156 tomato resistant, Cornell Lycop...	98	3e-20	
	emb AI779211 AI779211 EST260090 tomato susceptible, Cornell Lyco...	98	3e-20	
	emb AW034083 AW034083 EST277578 tomato callus, TAMU Lycopersicon...	98	3e-20	
45	emb AW094444 AW094444 EST287624 tomato mixed elicitor, BTI Lycop...	98	3e-20	
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55	emb AW725519 AW725519 GA_Ea0018G20 Gossypium arboreum 7-10 dpa ...	94	4e-19	
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	emb AI779212 AI779212 EST260091 tomato susceptible, Cornell Lyco...	94	6e-19	
60	emb AV413531 AV413531 AV413531 Lotus japonicus young plants (two...	93	1e-18	
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 emb|AI352845|AI352845 MB69-3F PZ204.BNlib Brassica napus cDNA cl... 68 1e-16
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 emb|AV422321|AV422321 AV422321 Lotus japonicus young plants (two... 70 2e-15
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 15 emb|AW306872|AW306872 sf49g05.y1 Gm-c1009 Glycine max cDNA clone... 62 3e-15
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 (1579 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10

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	emb AW691556 AW691556	NF046C09ST1F1000 Developing stem Medicago ...	178 8e-52
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	emb AW102341 AW102341	sd86d12.y1 Gm-cl009 Glycine max cDNA clone...	186 4e-46
	emb AW063020 AW063020	SBcD66 Sugar beet leaf cDNA library Beta v...	133 3e-44
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	emb AJ004959 CAA004959	Cicer arietinum mRNA for hypothetical pro...	52 9e-06
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55	emb AW396191 AW396191	sh02e09.y1 Gm-cl026 Glycine max cDNA clone...	46 6e-04
	emb AW395873 AW395873	sh01d01.y1 Gm-cl026 Glycine max cDNA clone...	37 0.003
	emb AI166826 AI166826	xylem.est.62 Poplar xylem Lambda ZAPII lib...	44 0.003
	emb AW830239 AW830239	sm24g01.y1 Gm-cl028 Glycine max cDNA clone...	44 0.004
	emb AF074703 AF074703	Glycine max pA381 marker, sequence tagged ...	43 0.005
60	emb AQ842052 AQ842052	T134338 Soybean RFLP probe Glycine max gen...	43 0.005
	gb BE022301 BE022301	sm73b09.y1 Gm-cl028 Glycine max cDNA clone ...	43 0.007

- emb|AW102174|AW102174 sd84c08.y1 Gm-c1009 Glycine max cDNA clone... 42 0.010
 emb|AI166882|AI166882 xylem.est.670 Poplar xylem Lambda ZAPII li... 41 0.019
 emb|Y09826|STAAP2 S.tuberosum mRNA for amino acid transporter AA... 36 0.020
 5 emb|AW307208|AW307208 sf54b08.y1 Gm-c1009 Glycine max cDNA clone... 41 0.026
 emb|AF080543|AF080543 Nepenthes alata amino acid transporter (AA... 40 0.049
 emb|AW096758|AW096758 EST289938 tomato mixed elicitor, BTI Lycop... 40 0.068
 emb|AI727855|AI727855 BNLGHI9274 Six-day Cotton fiber Gossypium ... 29 0.17
 emb|AI487167|AI487167 EST245489 tomato ovary, TAMU Lycopersicon ... 38 0.18
 10 emb|AW649763|AW649763 EST328217 tomato germinating seedlings, TA... 38 0.18
 emb|AW310916|AW310916 sg29h08.x1 Gm-c1024 Glycine max cDNA clone... 38 0.24
 emb|AJ400848|SOL400848 Spinacia oleracea complete chloroplast ge... 37 0.46
 emb|AW203255|AW203255 sf27a03.y1 Gm-c1028 Glycine max cDNA clone... 36 0.63
 emb|AI778004|AI778004 EST258883 tomato susceptible, Cornell Lyco... 36 0.86
 emb|AW649841|AW649841 EST328295 tomato germinating seedlings, TA... 36 0.86
 15 emb|AF061435|AF061435 Vicia faba amino acid transporter b (AAPB)... 35 1.2
 emb|AQ492251|AQ492251 V109G12 mTn-3xHA/lacZ Insertion Library Sa... 35 1.2
 emb|AI779305|AI779305 EST260184 tomato susceptible, Cornell Lyco... 35 1.2
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 20 emb|AQ874703|AQ874703 V113C6 mTn-3xHA/lacZ Insertion Library, st... 35 1.6
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 25 emb|AF061434|AF061434 Vicia faba amino acid transporter a (AAPA)... 35 2.2
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 emb|AQ876104|AQ876104 V133C7 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 30 emb|AQ876111|AQ876111 V133D2 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|AQ875710|AQ875710 V128E8 mTn-3xHA/lacZ Insertion Library, st... 35 2.2
 emb|AW092708|AW092708 EST285888 tomato mixed elicitor, BTI Lycop... 34 3.1
 emb|AI938816|AI938816 sc60f01.y1 Gm-c1016 Glycine max cDNA clone... 34 4.2
 emb|AW704460|AW704460 sk53c11.y1 Gm-c1019 Glycine max cDNA clone... 34 4.2
 35 emb|AI965655|AI965655 sc75b03.y1 Gm-c1018 Glycine max cDNA clone... 34 4.2
 emb|AW010573|AW010573 ST08D02 Pine TriplEx shoot tip library Pin... 34 4.2
 emb|AJ277985|NTA277985 Nicotiana tabacum drepp1 gene, exons 1-4. 33 5.8
 emb|AL049559|SPCC1450 S.pombe chromosome III cosmid c1450. 33 8.0
 emb|Z72791|SCYGR006W S.cerevisiae chromosome VII reading frame O... 33 8.0
 40 emb|Z34930|TV18SRRN T.violaceum (var. violaceum) gene for 18S rRNA. 33 8.0
 gb|U42663|TGU42663 Tuber gibbosum 18S small subunit ribosomal RN... 33 8.0
 emb|AQ940191|AQ940191 Sheared DNA-42C20.TF Sheared DNA Trypanoso... 33 8.0
 emb|AA274279|AA274279 TgESTzz24b06.s1 TgME49 invivo Bradyzoite c... 33 8.0
 emb|AU006886|AU006886 AU006886 Schizosaccharomyces pombe late lo... 33 8.0
 45 emb|AW926892|AW926892 HVSMEg0008N19 Hordeum vulgare pre-anthesis... 33 8.0
 dbj|D64123|D64123 Fibulobasidium inconspicuum DNA for small subu... 33 8.0

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 thaliana] /blast_score 7.00e-40 /ec_number /family /chip nova
 /gb_link [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002335|/ncgi)
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 http://www.ncgr.org/cgi-bin/ff?ac002335
 55 (449 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

60 Searching.....done

	Score	E		(bits)	Value
	Sequences producing significant alignments:				
	emb Y16190 SAMTI2	Sinapsis alba mRNA for trypsin inhibitor 2.	161	2e-39	
5	emb X84208 SSAMTI2	Sinapsis alba mti-2 gene for trypsin inhibitor 2.	161	3e-39	
	emb AT002119 AT002119	AT002119 Flower bud cDNA Brassica rapa sub...	72	5e-14	
	gb L33539 L33539	BNAESTF178 Mustard flower buds Brassica rapa cD...	72	6e-14	
	emb AF025857 AF025857	Aegilops caudata RAPD marker generated by ...	36	0.18	
	emb AI065316 AI065316	TENU2203 T. cruzi epimastigote normalized ...	31	0.42	
10	emb AF066077 AF066077	Helianthus annuus RPL5A-related protein (R...	34	0.89	
	emb AL356173 NCB14D6	Neurospora crassa DNA linkage group II BAC ...	34	0.89	
	emb AF242188 AF242188	Plasmodium falciparum membrane protein Pfl...	34	0.89	
	gb M28889 PFAMEM12A	P.falciparum membrane protein Pfl2 gene, com...	34	0.89	
	emb AL160371 LMFLCHR15	Leishmania major Friedlin assembled chrom...	33	1.2	
15	gb U47092 U47092	DCU47092 Carrot somatic embryos Daucus carota c...	33	1.2	
	emb AL354533 LMFL6294	Leishmania major Friedlin chromosome 21 co...	33	1.2	
	emb AW278233 AW278233	sf41d09.y1 Gm-c1009 Glycine max cDNA clone...	33	1.2	
	emb AQ849793 AQ849793	LMAJFV1_lm49f04.x1 Leishmania major FV1 ra...	33	1.2	
	gb U91982 SHU91982	Stylosanthes hamata EREBP-3 homolog mRNA, com...	33	1.7	
20	emb AW727560 AW727560	GA_Ea0012P04 Gossypium arboreum 7-10 dpa ...	33	1.7	
	emb AQ848503 AQ848503	LMAJFV1_lm10a08.x1 Leishmania major FV1 ra...	33	1.7	
	emb AW668496 AW668496	GA_Ea0014C23 Gossypium arboreum 7-10 dpa ...	33	1.7	
	emb AL136236 SPAPJ696	S.pombe chromosome I PCR product p696.	32	2.3	
	emb AL133359 SPAP696	S.pombe chromosome I PCR product p696.	32	2.3	
25	emb AW728870 AW728870	GA_Ea0028O24 Gossypium arboreum 7-10 dpa ...	32	2.3	
	emb AW099428 AW099428	sd40c12.y1 Gm-c1016 Glycine max cDNA clone...	32	2.3	
	emb AV389315 AV389315	AV389315 Chlamydomonas reinhardtii C9 Chla...	32	2.3	
	emb AW707869 AW707869	832013D08.y1 C. reinhardtii CC-125 nutrien...	32	2.3	
	emb AC068564 AC068564	Filobasidiella neoformans var. neoformans,...	32	3.2	
30	emb Z38058 LMCLPB	L.major (MHOM/SU/5ASKH) DNA for 100 kDa heat s...	32	3.2	
	emb AW932211 AW932211	EST358054 tomato fruit mature green, TAMU ...	32	3.2	
	emb AL356172 NCB23L21	Neurospora crassa DNA linkage group II BAC...	32	3.2	
	emb AQ445563 AQ445563	GSSTc0014 Trypanosoma cruzi random genomic...	32	3.2	
	emb AF263283 AF263283	Filobasidiella neoformans var. neoformans ...	32	3.2	
35	emb X95256 HVXYLISOG	H.vulgare xylose isomerase gene.	32	3.2	
	emb AW217087 AW217087	EST295801 tomato callus, TAMU Lycopersicon...	32	3.2	
	emb X62675 TRMINEX5S	T.rangeli DNA for mini-exon and 5S rRNA.	29	3.5	
	emb AW745480 AW745480	WS1_35_H03.b1_A002 Water-stressed 1 (WS1) ...	31	4.4	
	emb AW705201 AW705201	sk43a03.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
40	emb AI496396 AI496396	sb04b11.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AW694532 AW694532	NF077E02ST1F1017 Developing stem Medicago ...	31	4.4	
	emb AW598155 AW598155	sj89b07.y1 Gm-c1034 Glycine max cDNA clone...	31	4.4	
	emb AW508121 AW508121	si51a09.y1 Gm-r1030 Glycine max cDNA clone...	31	4.4	
	emb AW317929 AW317929	sg59a02.y1 Gm-c1007 Glycine max cDNA clone...	31	4.4	
45	emb AW185756 AW185756	se59c04.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
	emb AW119645 AW119645	sd50d05.y1 Gm-c1016 Glycine max cDNA clone...	31	4.4	
	emb AI522947 AI522947	sa92d09.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	gb L38627 GYNRGNA	Gymnodinium catenatum 24S ribosomal RNA (24S r...	31	4.4	
	emb AW926726 AW926726	HVSMEg0007P17 Hordeum vulgare pre-anthesis...	31	4.4	
50	emb AW307483 AW307483	sf57e09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4	
	emb AW307220 AW307220	sf54c09.y1 Gm-c1009 Glycine max cDNA clone...	31	4.4	
	emb AI437852 AI437852	sa40e07.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AW733531 AW733531	sk74g09.y1 Gm-c1016 Glycine max cDNA clone...	31	4.4	
	emb AW186505 AW186505	se68f10.y1 Gm-c1019 Glycine max cDNA clone...	31	4.4	
55	emb AW099682 AW099682	sd29g03.y2 Gm-c1012 Glycine max cDNA clone...	31	4.4	
	emb AW761228 AW761228	sl64h04.y1 Gm-c1027 Glycine max cDNA clone...	31	4.4	
	emb AI900314 AI900314	sc03h10.y1 Gm-c1012 Glycine max cDNA clone...	31	4.4	
	emb AF031065 AF031065	Dipsacomyces acuminosporus 28S ribosomal R...	31	4.4	
	emb AW099689 AW099689	sd29h03.y2 Gm-c1012 Glycine max cDNA clone...	31	4.4	
60	emb AI494951 AI494951	sa93a10.y1 Gm-c1004 Glycine max cDNA clone...	31	4.4	
	emb AI988406 AI988406	sd01f04.y1 Gm-c1020 Glycine max cDNA clone...	31	4.4	

- emb|AW782121|AW782121 sm01g01.y1 Gm-c1027 Glycine max cDNA clone... 31 4.4
 emb|AW100084|AW100084 sd20b03.y2 Gm-c1012 Glycine max cDNA clone... 31 4.4
 emb|AI939026|AI939026 sc64f02.y1 Gm-c1016 Glycine max cDNA clone... 31 4.4
 emb|AI736322|AI736322 sb27a03.y1 Gm-c1009 Glycine max cDNA clone... 31 4.4
 5 emb|AI965890|AI965890 sc79c09.y1 Gm-c1018 Glycine max cDNA clone... 31 4.4
 emb|AI901200|AI901200 sc22a07.y1 Gm-c1013 Glycine max cDNA clone... 31 4.4
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 10 emb|AW831353|AW831353 sm32e10.y1 Gm-c1028 Glycine max cDNA clone... 31 6.0
 gb|L37877|CPCRL27P *Cryptococcus neoformans* ribosomal protein L2... 31 6.0
 emb|Z75290|SCYOR382W *S.cerevisiae* chromosome XV reading frame OR... 31 6.0
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 emb|AQ847349|AQ847349 LMAJFV1_lm30a04.x1 *Leishmania major* FV1 ra... 31 6.0
 15 emb|AC008241|AC008241 *Leishmania major* clone L952b strain Friedl... 31 6.0
 emb|AW667667|AW667667 GA_Ea0010C24 *Gossypium arboreum* 7-10 dpa ... 31 6.0
 emb|AF031066|AF031066 *Martensiomycetes pterosporus* 28S ribosomal R... 31 6.0
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 emb|AZ215468|AZ215468 Sheared DNA-79C4.TF Sheared DNA Trypanosom... 25 7.1
 20 dbj|D50617|YSCCHRVIN *Saccharomyces cerevisiae* chromosome VI comp... 30 8.3
 dbj|D44598|YSCF4121F *Saccharomyces cerevisiae* chromosome VI phag... 30 8.3
 dbj|D87895|D87895 *Aspergillus nidulans* chiA gene for chitinase, ... 30 8.3
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 35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x99923|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x99923|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x99923|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?x99923>
 (1710 letters)

- 40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

- 45 Score E
 Sequences producing significant alignments: (bits) Value
- emb|AF149917|AF149917 *Simmondsia chinensis* acyl CoA reductase mR... 158 e-144
 emb|X99922|BNMS2PROT *B.napus* mRNA for male sterility protein 2. 137 2e-74
 50 emb|A45743|A45743 Sequence 22 from Patent WO9520668. 137 2e-74
 emb|AW615992|AW615992 EST325442 tomato flower buds 0-3 mm, Corne... 277 2e-73
 emb|AI730540|AI730540 BNLGHi7015 Six-day Cotton fiber *Gossypium* ... 153 4e-59
 emb|AW738637|AW738637 EST340064 tomato flower buds, anthesis, Co... 158 3e-51
 emb|AW931162|AW931162 EST357005 tomato fruit mature green, TAMU ... 201 1e-50
 55 emb|AW616784|AW616784 EST323195 *L. hirsutum* trichome, Cornell Un... 200 3e-50
 emb|AW308800|AW308800 sf72b03.y1 Gm-c1013 Glycine max cDNA clone... 141 7e-50
 emb|AW278653|AW278653 sf63e03.y1 Gm-c1013 Glycine max cDNA clone... 110 1e-46
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 60 emb|AW306151|AW306151 se46e08.y1 Gm-c1017 Glycine max cDNA clone... 145 2e-39
 emb|AW688482|AW688482 NF008B06ST1F1000 Developing stem *Medicago* ... 127 6e-38

- emb|AW648210|AW648210 EST326664 tomato germinating seedlings, TA... 107 1e-37
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5 emb|AW624291|AW624291 EST322152 tomato flower buds 3-8 mm, Corne... 121 1e-32
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emb|Z11889|MITTARRNG T.aestivum mitochondrion rm26 gene for rRN... 88 2e-16
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20 emb|AW980920|AW980920 EST392073 GVN Medicago truncatula cDNA clo... 50 3e-13
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25 emb|AW289724|AW289724 NXNV005H02F Nsf Xylem Normal wood Vertical... 48 2e-04
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emb|AZ050471|AZ050471 GSSTc11316 Trypanosoma cruzi random genom... 48 2e-04
emb|AW758790|AW758790 NXNV_089_G03_F Nsf Xylem Normal wood Verti... 47 5e-04
emb|AA952454|AA952454 TENS1392_T. cruzi epimastigote normalized ... 46 0.001
30 emb|AQ361876|AQ361876 mgxb0005G07r CUGI Rice Blast BAC Library P... 42 0.015
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emb|AW649203|AW649203 EST327657 tomato germinating seedlings, TA... 41 0.021
emb|Y13967|PCLYS2 Penicillium chrysogenum lys2 gene. 41 0.021
emb|AW929360|AW929360 EST338148 tomato flower buds 8 mm to pre-a... 40 0.074
35 emb|AW564691|AW564691 LG1_300_C05.b1_A002 Light Grown 1 (LG1) So... 37 0.50
emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 37 0.50
gb|BE033566|BE033566 MF03E04 MF Mesembryanthemum crystallinum cD... 36 0.69
emb|AI488290|AI488290 EST246612 tomato ovary, TAMU Lycopersicon ... 36 0.94
emb|AW932683|AW932683 EST358526 tomato fruit mature green, TAMU ... 36 0.94
40 emb|AW932440|AW932440 EST358283 tomato fruit mature green, TAMU ... 36 0.94
emb|AQ874417|AQ874417 V108D3 mTn-3xHA/lacZ Insertion Library, st... 35 1.3
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emb|AW720470|AW720470 LjNEST19f2r Lotus japonicus nodule library... 35 1.8
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emb|AL353821|NC68B2 Neurospora crassa DNA linkage group V Cosmid... 35 2.4
emb|AW775233|AW775233 EST331955 GVN Medicago truncatula cDNA clo... 35 2.4
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emb|AW693849|AW693849 NF069G11ST1F1087 Developing stem Medicago ... 35 2.4
50 emb|AW694067|AW694067 NF072D11ST1F1093 Developing stem Medicago ... 35 2.4
emb|AW773778|AW773778 EST332764 KV3 Medicago truncatula cDNA clo... 35 2.4
emb|AW774799|AW774799 EST333950 KV3 Medicago truncatula cDNA clo... 35 2.4
emb|AW774591|AW774591 EST333742 KV3 Medicago truncatula cDNA clo... 35 2.4
emb|AW689574|AW689574 NF021H08ST1F1000 Developing stem Medicago ... 35 2.4
55 emb|AW694736|AW694736 NF079D09ST1F1077 Developing stem Medicago ... 35 2.4
emb|AI075585|AI075585 TENU3007 T. cruzi epimastigote normalized ... 35 2.4
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60 emb|AQ841091|AQ841091 T132045b Medicago truncatula BAC library M... 35 2.4
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- emb|AW299108|AW299108 EST305782 KV2 Medicago truncatula cDNA clo... 35 2.4
 gb|U46545|HAU46545 Helianthus annuus 17.7 kDa heat-shock protein... 34 3.4
 emb|AW309167|AW309167 sg05b03.y1 Gm-cl019 Glycine max cDNA clone... 34 3.4
 emb|AW234839|AW234839 sf19g08.y1 Gm-cl028 Glycine max cDNA clone... 34 3.4
 5 emb|AI960722|AI960722 sc89e06.y1 Gm-cl019 Glycine max cDNA clone... 34 3.4
 emb|AF233374|AF233374 Volvox carteri argininosuccinate lyase (VA... 34 4.6
 emb|AW925731|AW925731 HVSMeg0005F22 Hordeum vulgare pre-anthesis... 34 4.6
 gb|BE053807|BE053807 GA_Ea0014K20f Gossypium arboreum 7-10 dpa ... 34 4.6
 10 emb|AJ213767|AJ213767 z5b08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.6
 gb|U58133|CAU58133 Candida albicans alpha-aminoacidate reductase... 26 6.1
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 emb|Z46881|SC3299 S.cerevisiae chromosome IX cosmid 3299. 33 6.3
 emb|AV391768|AV391768 AV391768 Chlamydomonas reinhardtii C9 Chla... 33 6.3
 emb|AW933793|AW933793 EST359636 tomato fruit mature green, TAMU ... 33 6.3
 15 emb|AW618444|AW618444 EST320430 L. pennellii trichome, Cornell U... 33 6.3
 gb|BE053260|BE053260 GA_Ea0035A01f Gossypium arboreum 7-10 dpa ... 33 6.3
 emb|AF082993|AF082993 Cryptosporidium parvum type I fatty acid s... 33 6.3
 emb|AZ220106|AZ220106 Sheared DNA-63H10.TR Sheared DNA Trypanoso... 33 6.3
 emb|AF072272|AF072272 Lactuca sativa resistance protein candidat... 33 6.3
 20 emb|AB012945|AB012945 Aspergillus oryzae gene for amyRp, complet... 33 8.7
 emb|AF180560|AF180560 Emericella nidulans sgdA gene, partial seq... 33 8.7
 dbj|D29761|YSACSII Candida maltosa gene for chitin synthase 2, p... 33 8.7
 emb|AJ273086|AJ273086 AJ273086 Metarhizium anisopliae ARSEF 2575... 33 8.7
 dbj|E12507|E12507 Promoter region of the agdA gene. 33 8.7
 25 dbj|D50617|YSCCHRVIN Saccharomyces cerevisiae chromosome VI comp... 33 8.7

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 (1467 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

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	emb AI896887 AI896887 EST266330 tomato callus, TAMU Lycopersicon...	178	1e-72
	emb AW030421 AW030421 EST273676 tomato callus, TAMU Lycopersicon...	254	1e-66
50	gb BE059595 BE059595 sn34c09.y1 Gm-cl016 Glycine max cDNA clone ...	177	2e-43
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	emb AW687734 AW687734 NF012H03RT1F1031 Developing root Medicago ...	105	7e-39
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	emb AI166722 AI166722 xylem.est.526 Poplar xylem Lambda ZAPII li...	103	3e-29
	emb AW830251 AW830251 sm33a02.y1 Gm-cl028 Glycine max cDNA clone...	128	8e-29
	emb AW777089 AW777089 M110842e GVSN Medicago truncatula cDNA clo...	126	5e-28
60	emb AT000492 AT000492 AT000492 Brassica rapa guard cell Brassica...	92	6e-28
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emb|AV427085|AV427085 AV427085 Lotus japonicus young plants (two... 111 1e-23
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5 emb|AW685452|AW685452 NF029F12NR1F1000 Nodulated root Medicago t... 104 2e-21
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emb|AW647985|AW647985 EST326439 tomato germinating seedlings, TA... 95 9e-19
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10 emb|AW278350|AW278350 sf43a03.y1 Gm-c1009 Glycine max cDNA clone... 90 3e-17
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20 emb|AW687218|AW687218 NF007C06RT1F1049 Developing root Medicago ... 78 2e-13
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30 emb|AW564851|AW564851 LG1_310_D10.b1_A002 Light Grown 1 (LG1) So... 54 2e-06
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40 emb|AL133468|LMFL3238 Leishmania major Friedlin chromosome 19 co... 35 1.1
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55 gb|U13054|LEU13054 Lycopersicon esculentum endo-1,4-beta-glucana... 33 7.3
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 (1743 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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25	emb AW560039 AW560039	EST315087	DSIR Medicago truncatula cDNA cl... 276 3e-73
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	emb AI486962 AI486962	EST245284	tomato ovary, TAMU Lycopersicon ... 269 4e-71
	emb AW441974 AW441974	EST311370	tomato fruit red ripe, TAMU Lycop... 242 8e-71
30	emb AW099977 AW099977	sd19c07.y2	Gm-c1012 Glycine max cDNA clone... 253 7e-69
	emb AW733661 AW733661	sk83d11.y1	Gm-c1016 Glycine max cDNA clone... 223 4e-65
	emb AW164658 AW164658	se75h05.y1	Gm-c1023 Glycine max cDNA clone... 162 1e-64
	emb AW689466 AW689466	NF019F01ST1F1000	Developing stem Medicago ... 159 1e-62
	emb AI441647 AI441647	sa65a03.y1	Gm-c1004 Glycine max cDNA clone... 212 9e-58
35	emb AI729737 AI729737	BNLGH14077	Six-day Cotton fiber Gossypium... 128 7e-55
	emb AI771313 AI771313	EST252329	tomato ovary, TAMU Lycopersicon ... 137 3e-46
	emb AW033056 AW033056	EST276615	tomato callus, TAMU Lycopersicon... 177 3e-43
	emb AW623019 AW623019	EST320964	tomato flower buds 3-8 mm, Corne... 76 2e-41
	emb AI728350 AI728350	BNLGH10536	Six-day Cotton fiber Gossypium... 76 5e-40
40	emb AW922217 AW922217	DG1_17_D01.b1_A002	Dark Grown 1 (DG1) Sorg... 162 6e-39
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	emb Z98600 SPAC20G4	S.pombe chromosome I	cosmid c20G4. 133 6e-30
45	emb AW056437 AW056437	ST51H06	Pine TriplEx shoot tip library Pin... 68 4e-27
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10 emb|AW266043|AW266043 L30-2716T3 Ice plant Lambda Uni-Zap XR exp... 51 4e-05
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emb|AQ953753|AQ953753 Sheared DNA-52P9.TF Sheared DNA Trypanosom... 49 1e-04
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15 emb|AQ649643|AQ649643 Sheared DNA-16E5.TR Sheared DNA Trypanosom... 33 4e-04
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20 emb|Z97208|SPAC15A10 S.pombe chromosome I cosmid c15A10. 46 9e-04
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 (594 letters)

Database: plantfungal
 10 661,018 sequences; 426,114,510 total letters

Searching.....done

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	emb AW423359 AW423359 sh06g04.y1 Gm-c1016 Glycine max cDNA clone...	38	0.076	
	emb AW649685 AW649685 EST328139 tomato germinating seedlings, TA...	28	0.35	
45	emb AA520781 AA520781 TgESTzz64a03.r1 TgME49 invivo Bradyzoite c...	35	0.37	
	emb AW620830 AW620830 sj47b03.y1 Gm-c1033 Glycine max cDNA clone...	30	0.48	
	emb X65608 SCPDC2G S.cerevisiae PDC2 gene.	35	0.51	
	emb Z74377 SCYDR081C S.cerevisiae chromosome IV reading frame OR...	35	0.51	
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50	emb X82086 SCCHROIV S.cerevisiae DNA for right arm of chromosome...	35	0.51	
	gb L19880 YSCPDC2A Saccharomyces cerevisiae pdc2 gene, complete ...	35	0.51	
	emb AW299176 AW299176 EST305986 KV2 Medicago truncatula cDNA clo...	35	0.70	
	emb AW310120 AW310120 sf31d06.x1 Gm-c1028 Glycine max cDNA clone...	35	0.70	
	emb AW309936 AW309936 sf26g12.x1 Gm-c1028 Glycine max cDNA clone...	35	0.70	
55	emb AW278505 AW278505 sf45c08.y1 Gm-c1009 Glycine max cDNA clone...	35	0.70	
	emb AW310598 AW310598 sg21h03.x1 Gm-c1024 Glycine max cDNA clone...	34	0.96	
	emb AW233878 AW233878 sf31d07.y1 Gm-c1028 Glycine max cDNA clone...	34	0.96	
	gb BE125775 BE125775 DG1_57_B06.b1_A002 Dark Grown 1 (DG1) Sorgh...	34	0.96	
	gb M13237 BLYGLUCB Barley beta glucanase mRNA.	34	0.96	
60	gb M62740 BLYGLB2 Hordeum vulgare 1,3-1,4-beta-D glucan 4-glucan...	34	0.96	
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- emb|AJ228137|NTJ228137 *Nicotiana tomentosiformis* DNA for Tnt1 re... 34 1.3
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 5 emb|AW233798|AW233798 sf26g12.y1 *Gm-c1028* Glycine max cDNA clone... 33 2.5
 emb|AV393790|AV393790 AV393790 *Chlamydomonas reinhardtii* C9 Chla... 33 2.5
 emb|AI920265|AI920265 1795 Pine Lambda Zap Xylem library Pinus t... 32 3.4
 emb|AL157415|LMFL8325 *Leishmania major* Friedlin chromosome 5 cos... 32 3.4
 emb|AQ935443|AQ935443 CpG2473A CplOWAgDNA1 *Cryptosporidium parvu*... 32 3.4
 10 emb|AW686346|AW686346 NF040F08NR1F1000 Nodulated root *Medicago* t... 32 3.4
 emb|AW687188|AW687188 NF006H09RT1F1079 Developing root *Medicago* ... 32 3.4
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 emb|AQ851040|AQ851040 LMAJFV1_lm43g10.x1 *Leishmania major* FV1 ra... 32 3.4
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 emb|AQ855101|AQ855101 CpG1965B CplOWAgDNA1 *Cryptosporidium parvu*... 32 3.4
 15 emb|Y08937|CRNII *Chlamydomonas reinhardtii* mRNA for nitrite red... 32 3.4
 gb|C96140|C96140 C96140 *Marchantia polymorpha* immature sex organ... 32 4.7
 emb|AI162427|AI162427 A017P38U Hybrid aspen plasmid library Popu... 31 6.5
 emb|Z98549|PFSC03014 *Plasmodium falciparum* DNA *** SEQUENCING IN... 31 6.5
 emb|AC013353|AC013353 *Trypanosoma brucei* chromosome VI clone RPC... 31 6.5
 20 emb|AC013484|AC013484 *Trypanosoma brucei* chromosome IX clone RPC... 31 6.5
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 emb|AI213146|AI213146 y8b01a1.r1 *Aspergillus nidulans* 24hr asexu... 31 6.5
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 25 emb|AC007863|AC007863 *Trypanosoma brucei* chromosome VI clone RPC... 31 6.5
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 emb|A85864|A85864 Sequence 523 from Patent EP0866129. 31 6.5
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 30 emb|AQ945249|AQ945249 Sheared DNA-54D15.TR Sheared DNA *Trypanoso*... 31 6.5
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 40 emb|caa66965.1|(x98321) peroxidase [arabidopsis thaliana]
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[post/entrez/query?db=n&form=6&dopt=g&uid=gb|x98321|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|x98321|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?x98321>
 45 (1212 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

50 Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

- 55 gb|U51191|GMU51191 Glycine max peroxidase precursor (sEPa1) mRNA... 388 e-129
 gb|U51192|GMU51192 Glycine max peroxidase precursor (sEPa2) mRNA... 385 e-128
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 gb|L13654|TOMTPX1A *Lycopersicon esculentum* peroxidase (TPX1) mRN... 204 e-118
 emb|Y16776|SOY16776 *Spinacia oleracea* mRNA for peroxidase, prx10... 210 e-113
 60 emb|Z22920|SPPEROXDS *S. polyrrhiza* mRNA for peroxidase. 183 5e-90
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- emb|AW219258|AW219258 EST301740 tomato root during/after fruit s... 212 5e-85
emb|AW621449|AW621449 EST312247 tomato root during/after fruit s... 212 7e-85
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emb|AW622057|AW622057 EST312855 tomato root during/after fruit s... 182 2e-83
5 emb|AW329363|AW329363 N200592e rootphos(-) *Medicago truncatula* c... 307 1e-82
emb|AW647641|AW647641 EST307119 tomato germinating seedlings, TA... 190 9e-82
emb|AW625441|AW625441 EST319348 tomato radicle, 5 d post-imbibit... 187 7e-80
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10 emb|AW704698|AW704698 sk39d06.y1 *Gm-c1028 Glycine max* cDNA clone... 297 1e-79
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15 emb|AW220017|AW220017 EST302500 tomato root during/after fruit s... 197 7e-77
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20 emb|AI771103|AI771103 EST252203 tomato ovary, TAMU *Lycopersicon* ... 190 8e-75
emb|AW218917|AW218917 EST301399 tomato root during/after fruit s... 180 2e-74
emb|AW831524|AW831524 sm27c05.y1 *Gm-c1028 Glycine max* cDNA clone... 279 3e-74
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gb|BE020787|BE020787 sm52h01.y1 *Gm-c1028 Glycine max* cDNA clone ... 274 1e-72
25 emb|AW649146|AW649146 EST327600 tomato germinating seedlings, TA... 178 3e-71
emb|AW219955|AW219955 EST302438 tomato root during/after fruit s... 178 3e-71
gb|BE020269|BE020269 sm42f09.y1 *Gm-c1028 Glycine max* cDNA clone ... 165 3e-71
emb|AW219743|AW219743 EST302225 tomato root during/after fruit s... 173 9e-70
emb|AW218390|AW218390 EST303573 tomato radicle, 5 d post-imbibit... 191 8e-69
30 gb|BE020135|BE020135 sm41f03.y1 *Gm-c1028 Glycine max* cDNA clone ... 184 1e-68
emb|AI895098|AI895098 EST264541 tomato callus, TAMU *Lycopersicon*... 169 2e-68
emb|AW219511|AW219511 EST301909 tomato root during/after fruit s... 193 6e-68
emb|AW154826|AW154826 EST290219 tomato root deficiency, Cornell ... 154 1e-67
gb|L36112|SSNPEROXIC *Stylosanthes humilis* peroxidase mRNA. 105 8e-67
35 emb|AW625509|AW625509 EST319416 tomato radicle, 5 d post-imbibit... 167 2e-65
dbj|D42065|TOBCPI40KB Tobacco mRNA for cationic peroxidase isozy... 122 3e-65
gb|U51193|GMU51193 *Glycine max* peroxidase (sEPb1) mRNA, partial ... 95 5e-65
dbj|D42064|TOBCPI38KA Tobacco mRNA for cationic peroxidase isozy... 119 6e-65
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40 emb|AW621545|AW621545 EST312343 tomato root during/after fruit s... 166 8e-65
emb|AW704193|AW704193 sk17a09.y1 *Gm-c1028 Glycine max* cDNA clone... 244 8e-64
gb|M37637|ARCPNC2 *A.hypogaea* cationic peroxidase mRNA, complete ... 100 2e-63
emb|X90694|MSRNAPE1C *M.sativa* mRNA for peroxidase 1C. 164 3e-63
emb|AW621842|AW621842 EST312640 tomato root during/after fruit s... 151 4e-63
45 emb|X94943|LECEVI16G *L.esculentum* mRNA for peroxidase. 104 4e-63
emb|AI487546|AI487546 EST245868 tomato ovary, TAMU *Lycopersicon* ... 150 5e-63
emb|AW625242|AW625242 EST319245 tomato radicle, 5 d post-imbibit... 149 9e-63
emb|AF149279|AF149279 *Phaseolus vulgaris* peroxidase 4 precursor ... 100 2e-62
emb|AW621971|AW621971 EST312769 tomato root during/after fruit s... 147 6e-62
50 emb|AW218589|AW218589 EST303772 tomato radicle, 5 d post-imbibit... 147 6e-62
emb|AW621728|AW621728 EST312526 tomato root during/after fruit s... 136 8e-62
gb|L36157|ALFPXDC *Medicago sativa* peroxidase (pxdC) mRNA, comple... 151 2e-61
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55 emb|AW621885|AW621885 EST312683 tomato root during/after fruit s... 145 2e-61
gb|J02979|TOBPXDLF *Nicotiana tabacum* lignin-forming peroxidase m... 235 6e-61
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emb|Y16778|SPY16778 *Spinacia oleracea* mRNA for peroxidase, prx11... 109 3e-60
60 emb|X71593|LECEVI1A *L.esculentum* CEVI-1 mRNA. 174 4e-60
emb|X90693|MSRNAPE1B *M.sativa* mRNA for peroxidase 1B. 153 6e-60

- gb|BE057477|BE057477 sm58f06.y1 Gm-c1028 Glycine max cDNA clone ... 231 6e-60
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 5 gb|L36111|SSNPEROXIB Stylosanthes humilis peroxidase mRNA. 161 2e-58
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 10 emb|X56011|TAPERO Wheat mRNA for peroxidase. 146 6e-58
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 15 emb|AB024438|AB024438 Scutellaria baicalensis mRNA for peroxidase... 141 6e-57
 emb|AJ250121|PAB250121 Picea abies mRNA for SPI2 protein (spi2 g... 109 8e-57
 emb|AW559660|AW559660 EST314772 DSIR Medicago truncatula cDNA cl... 154 1e-56
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 20 emb|AW981426|AW981426 EST392579 DSIL Medicago truncatula cDNA cl... 154 1e-56
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 25 emb|AW625144|AW625144 EST319051 tomato radicle, 5 d post-imbibit... 123 8e-55
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 30 emb|AB042103|AB042103 Asparagus officinalis AspPOX1 mRNA for per... 158 2e-54
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 [arabidopsis thaliana] /blast_score 1.00e-118 /ec_number /family
 transferase /chip nova /gb_link
 40 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004561|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac004561>
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 45 Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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 Sequences producing significant alignments: (bits) Value
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- gb|BE021138|BE021138 sm55h05.yl Gm-c1028 Glycine max cDNA clone ... 89 2e-35
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 5 gb|U20809|VRU20809 Vigna radiata clone MII-4 auxin-induced prote... 75 4e-35
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 20 emb|AW981250|AW981250 EST392403 DSIL Medicago truncatula cDNA cl... 84 4e-33
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 25 emb|AW776845|AW776845 EST335910 DSIL Medicago truncatula cDNA cl... 84 2e-31
 emb|AW776620|AW776620 EST335685 DSIL Medicago truncatula cDNA cl... 79 2e-31
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 30 emb|AW684397|AW684397 NF016E02NR1F1000 Nodulated root Medicago t... 84 6e-31
 emb|AW234437|AW234437 sf25b07.yl Gm-c1028 Glycine max cDNA clone... 82 8e-31
 emb|AW307015|AW307015 sf51g02.yl Gm-c1009 Glycine max cDNA clone... 82 2e-30
 emb|AW306150|AW306150 se46e07.yl Gm-c1017 Glycine max cDNA clone... 85 7e-30
 emb|AW397802|AW397802 sg68e08.yl Gm-c1007 Glycine max cDNA clone... 81 1e-29
 35 emb|AW234580|AW234580 sf15h12.yl Gm-c1028 Glycine max cDNA clone... 81 2e-29
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 40 emb|AF239928|AF239928 Euphorbia esula glutathione S-transferase ... 84 4e-29
 emb|AW907271|AW907271 EST343394 potato stolon, Cornell Universit... 81 5e-29
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 45 emb|AW218869|AW218869 EST301351 tomato root during/after fruit s... 62 8e-29
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 50 emb|AJ010448|AMY010448 Alopecurus myosuroides mRNA for glutathio... 63 2e-28
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 55 emb|AW684915|AW684915 NF023A04NR1F1000 Nodulated root Medicago t... 75 4e-28
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- emb|X56268|NTAUX1 N.tabacum gene for an auxin-induced protein (p... 79 4e-27
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 (927 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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emb AF202184 AF202184 Glycine max isoflavone reductase homolog 2...	581	e-165		
emb X92075 STISORED H S.tuberosum mRNA for isoflavone reductase h...	542	e-153		
emb AF135127 AF135127 Betula pendula isoflavone reductase homolo...	534	e-151		
55 emb AF242491 AF242491 Forsythia x intermedia clone 1 phenylcouma...	527	e-149		
emb AF242492 AF242492 Forsythia x intermedia clone 2 phenylcouma...	512	e-144		
emb AJ005806 PTR5806 Populus trichocarpa mRNA for phenylcoumaran...	497	e-140		
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emb AJ005804 PTR5804 Populus trichocarpa mRNA for phenylcoumaran...	497	e-140		
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emb AF201458 AF201458 Medicago sativa isoflavone reductase-like ...	294	e-136		

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 (734 letters)

Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters

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 nova /gb_link
 30 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005770|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005770|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005770|/ncgi)
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 (378 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

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- | | Score | E | (bits) | Value |
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| gb BE057244 BE057244 sm99e04.y1 Gm-c1015 Glycine max cDNA clone ... | 87 | 7e-17 | | |
| 45 gb BE057597 BE057597 sn04d12.y1 Gm-c1015 Glycine max cDNA clone ... | 87 | 7e-17 | | |
| gb BE022905 BE022905 sm89a05.y1 Gm-c1015 Glycine max cDNA clone ... | 87 | 7e-17 | | |
| gb BE022697 BE022697 sm87c09.y1 Gm-c1015 Glycine max cDNA clone ... | 87 | 7e-17 | | |
| emb AW156430 AW156430 se26b01.y1 Gm-c1015 Glycine max cDNA clone... | 87 | 7e-17 | | |
| emb AI938252 AI938252 sc41h01.y1 Gm-c1014 Glycine max cDNA clone... | 87 | 7e-17 | | |
| 50 emb Z46949 SNPR6JT11 S.nigra mRNA for pathogenesis-related prote... | 86 | 9e-17 | | |
| gb BE024084 BE024084 sm96e02.y1 Gm-c1015 Glycine max cDNA clone ... | 85 | 2e-16 | | |
| emb AI938085 AI938085 sc41h07.x1 Gm-c1014 Glycine max cDNA clone... | 84 | 3e-16 | | |
| emb AI930853 AI930853 sb43c07.y1 Gm-c1015 Glycine max cDNA clone... | 84 | 6e-16 | | |
| emb AW156600 AW156600 se27e01.y1 Gm-c1015 Glycine max cDNA clone... | 83 | 1e-15 | | |
| 55 emb AI966712 AI966712 sc55h06.y1 Gm-c1015 Glycine max cDNA clone... | 80 | 6e-15 | | |
| gb BE023986 BE023986 sm95a07.y1 Gm-c1015 Glycine max cDNA clone ... | 78 | 2e-14 | | |
| emb AW433320 AW433320 sh55e08.y1 Gm-c1015 Glycine max cDNA clone... | 78 | 2e-14 | | |
| gb BE057243 BE057243 sm99e03.y1 Gm-c1015 Glycine max cDNA clone ... | 78 | 2e-14 | | |
| emb AI522988 AI522988 sb07e02.y1 Gm-c1004 Glycine max cDNA clone... | 78 | 2e-14 | | |
| 60 emb AI937952 AI937952 sc06b01.y1 Gm-c1012 Glycine max cDNA clone... | 78 | 2e-14 | | |
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- emb|AI938255|AI938255 sc41h04.y1 Gm-c1014 Glycine max cDNA clone... 78 3e-14
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5 emb|AW432522|AW432522 sh75d04.y1 Gm-c1015 Glycine max cDNA clone... 76 1e-13
emb|AW432580|AW432580 sh76c09.y1 Gm-c1015 Glycine max cDNA clone... 75 3e-13
emb|AJ132473|AHY132473 *Amaranthus hypochondriacus* mRNA for tryps... 75 3e-13
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15 gb|J04099|TOMERIP II Tomato fruit-ripening protein (ethylene resp... 52 4e-11
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emb|AW041591|AW041591 EST284455 tomato mixed elicitor, BTI Lycop... 67 8e-11
emb|AW929951|AW929951 EST354221 tomato flower buds 8 mm to pre-a... 50 9e-11
emb|AI483878|AI483878 EST249749 tomato ovary, TAMU Lycopersicon ... 50 9e-11
20 emb|AW944751|AW944751 EST336801 tomato flower buds 3-8 mm, Corne... 50 1e-10
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emb|AW010812|AW010812 ST14C10 Pine TriplEx shoot tip library Pin... 64 4e-10
emb|AI485251|AI485251 EST243555 tomato ovary, TAMU Lycopersicon ... 47 4e-10
25 dbj|D26455|TOBTID44 *Nicotiana glauca* X *Nicotiana langsdorffii* mR... 51 5e-10
emb|Z12623|NTPII3PI *N.tabacum* pre-pro-PI-Ib gene encoding pre-pr... 50 8e-10
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emb|X67075|NTTIMPB *N.tabacum* TIMPB mRNA for inhibitor of microbi... 50 8e-10
emb|X67076|NTTIMPA *N.tabacum* TIMPa mRNA for inhibitor of microbi... 50 9e-10
30 emb|AW929928|AW929928 EST354198 tomato flower buds 8 mm to pre-a... 46 2e-09
emb|AW616209|AW616209 EST307248 *L. hirsutum* trichome, Cornell Un... 48 3e-09
emb|AW432477|AW432477 sh74f01.y1 Gm-c1015 Glycine max cDNA clone... 61 4e-09
emb|AW092750|AW092750 EST285930 tomato mixed elicitor, BTI Lycop... 45 4e-09
gb|M74102|TOBCPII *Nicotiana sylvestris* serine proteinase inhibit... 52 6e-09
35 emb|AW622766|AW622766 EST306752 tomato flower buds 3-8 mm, Corne... 46 1e-08
emb|AI563053|AI563053 EST00177 watermelon lambda zap library Cit... 58 3e-08
emb|AI563140|AI563140 EST00264 watermelon lambda zap library Cit... 58 3e-08
emb|AI723907|AI723907 RHIZ1_32_B07.y1_A001 Rhizome1 Sorghum hale... 57 5e-08
emb|AI724626|AI724626 RHIZ1_11_A01.y1_A001 Rhizome1 Sorghum hale... 57 5e-08
40 emb|AJ250663|HVU250663 *Hordeum vulgare* partial mRNA for putative... 57 5e-08
emb|AI724485|AI724485 RHIZ1_10_F03.y1_A001 Rhizome1 Sorghum hale... 57 5e-08
dbj|D13662|TOBGTI *Nicotiana glauca* X *Nicotiana langsdorffii* mRNA... 51 7e-08
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gb|L06985|POTPINIA *Solanum tuberosum* proteinase inhibitor I mRNA... 43 1e-07
45 gb|M13938|TOMWIPIG Tomato (*L.esculentum*) wound-inducible protein... 42 2e-07
emb|AI771798|AI771798 EST252898 tomato ovary, TAMU Lycopersicon ... 42 2e-07
emb|AI490242|AI490242 EST248568 tomato ovary, TAMU Lycopersicon ... 42 2e-07
emb|AI486930|AI486930 EST245252 tomato ovary, TAMU Lycopersicon ... 42 2e-07
gb|BE049671|BE049671 NXNV_140_C03_F Nsf Xylem Normal wood Vertic... 55 2e-07
50 gb|K03290|TOMWIPI Tomato leaf wound-induced proteinase inhibitor... 42 2e-07
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emb|X67675|STPIN1 *S.tuberosum* mRNA for proteinase inhibitor I. 41 5e-07
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emb|X57035|HVICA2 *H.vulgare* chymotrypsin inhibitor-2 gene. 53 8e-07
55 emb|AI899242|AI899242 EST268685 tomato ovary, TAMU Lycopersicon ... 41 9e-07
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emb|Z12611|STPROINI *S.tuberosum* proteinase inhibitor I. 44 9e-07
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60 emb|AW040832|AW040832 EST283696 tomato mixed elicitor, BTI Lycop... 41 1e-06
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 emb|AI781668|AI781668 EST262547 tomato susceptible, Cornell Lyco... 35 4e-06
 10 emb|AW092485|AW092485 EST285665 tomato mixed elicitor, BTI Lycop... 35 4e-06
 emb|AI772725|AI772725 EST253825 tomato resistant, Cornell Lycop... 35 5e-06
 emb|AI778944|AI778944 EST259823 tomato susceptible, Cornell Lyco... 35 5e-06
 emb|AI774403|AI774403 EST255503 tomato resistant, Cornell Lycop... 35 5e-06
 emb|AI772154|AI772154 EST253254 tomato resistant, Cornell Lycop... 35 5e-06
 emb|AW094311|AW094311 EST287491 tomato mixed elicitor, BTI Lycop... 35 5e-06
 15 emb|AW092125|AW092125 EST285221 tomato mixed elicitor, BTI Lycop... 35 5e-06
 emb|AW039975|AW039975 EST282466 tomato mixed elicitor, BTI Lycop... 35 5e-06
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 emb|AW093509|AW093509 EST286689 tomato mixed elicitor, BTI Lycop... 35 5e-06
 20 emb|AI938012|AI938012 sc40a06.x1 Gm-cl014 Glycine max cDNA clone... 51 5e-06
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 http://www3.ncbi.nlm.nih.gov/htbin-
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 30 http://www.ncgr.org/cgi-bin/ff?aj001809
 (2247 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

35 Searching.....done

	Score	E	(bits) Value
40	Sequences producing significant alignments:		
	emb AL132984 SPAC1556	S.pombe chromosome I cosmid c1556.	637 0.0
	emb Z26877 SCDCHR11	S.cerevisiae (S288C) 36.2kb DNA fragment fro...	408 0.0
	emb Z49320 SCYJL045W	S.cerevisiae chromosome X reading frame ORF...	403 0.0
	gb M86909 YSCSDH1A	Saccharomyces cerevisiae succinate dehydrogen...	408 0.0
45	gb M94874 YSCSDH1B	Saccharomyces cerevisiae succinate dehydrogen...	408 0.0
	emb Z28148 SCYKL148C	S.cerevisiae chromosome XI reading frame OR...	408 0.0
	gb M86746 YSCSDHA	Saccharomyces cerevisiae succinate dehydrogena...	408 0.0
	dbj D86573 D86573	Plasmodium falciparum DNA for flavoprotein sub...	676 0.0
	emb AB031741 AB031741	Trypanosoma cruzi mRNA for succinate dehyd...	456 0.0
50	dbj D89263 D89263	Schizosaccharomyces pombe mRNA, partial cds, c...	637 0.0
	emb Y10377 CATOP2	C.albicans TOP2 gene.	635 0.0
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	emb AW720194 AW720194	LjNEST16f8r Lotus japonicus nodule library...	440 e-122
	emb AI898950 AI898950	EST268393 tomato ovary, TAMU Lycopersicon ...	434 e-121
55	emb AI727777 AI727777	BNLGH19047 Six-day Cotton fiber Gossypium ...	391 e-114
	emb AW775119 AW775119	EST334270 KV3 Medicago truncatula cDNA clo...	407 e-112
	emb AL110721 CNS018RU	Botrytis cinerea strain T4 cDNA library un...	323 e-110
	emb AW729362 AW729362	GA_Ea0024M24 Gossypium arboreum 7-10 dpa ...	314 4e-94
	emb AW687411 AW687411	NF009C11RT1F1085 Developing root Medicago ...	208 2e-85
60	emb AW180257 AW180257	MgA0347f MgA Library Mycosphaerella gramin...	309 4e-83
	emb AA660851 AA660851	00746 MtRHE Medicago truncatula cDNA 5' si...	163 3e-82

- emb|AW760184|AW760184 sl59b01.y1 Gm-c1027 Glycine max cDNA clone... 304 1e-81
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 emb|AW703689|AW703689 sk23b10.y1 Gm-c1028 Glycine max cDNA clone... 298 1e-79
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 emb|AW688181|AW688181 NF004D03ST1F1000 Developing stem Medicago ... 204 5e-67
 10 emb|AW667947|AW667947 GA_Ea0012A06 Gossypium arboreum 7-10 dpa ... 250 4e-65
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 15 emb|AI495497|AI495497 sa98g08.y1 Gm-c1004 Glycine max cDNA clone... 219 8e-56
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 20 emb|AQ659508|AQ659508 Sheared DNA-5G3.TF Sheared DNA Trypanosoma... 140 2e-46
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 25 emb|AW334279|AW334279 S32G2 AGS-1 Pneumocystis carinii f. sp. ca... 158 5e-39
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 30 emb|AV409739|AV409739 AV409739 Lotus japonicus young plants (two... 138 6e-33
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 35 emb|AW736633|AW736633 EST333125 KV3 Medicago truncatula cDNA clo... 128 6e-32
 emb|AA051852|AA051852 Cn0030-5 Cryptococcus neoformans, Stratage... 117 3e-31
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 40 emb|AW991033|AW991033 SsS0224 Suaeda salsa ZAP cDNA library Suae... 95 9e-28
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 45 emb|AW830714|AW830714 sm35c05.y1 Gm-c1028 Glycine max cDNA clone... 81 3e-18
 emb|AW568440|AW568440 si70g12.y1 Gm-c1031 Glycine max cDNA clone... 88 2e-16
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 gb|BE034538|BE034538 MK01A06 MK Mesembryanthemum crystallinum cD... 74 3e-12
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 gb|BE122635|BE122635 Ljirmp30-425-h1 Ljirmp Lambda HybriZap t... 53 5e-12
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 55 gb|L36344|YSC2GGMS Saccharomyces cerevisiae tRNA-Met, tRNA-Ser, ... 47 1e-06
 gb|L26347|YSC2GQA Saccharomyces cerevisiae COR gene cluster, iso... 47 1e-06
 emb|Z49551|SCYJR051W S.cerevisiae chromosome X reading frame ORF... 47 1e-06
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 gb|U18779|SCE8199 Saccharomyces cerevisiae chromosome V cosmid 8... 46 1e-05
 60 emb|AC011017|AC011017 Leishmania major chromosome 35 clone L3184... 45 1e-05
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emb|AL110853|CNS018VI Botrytis cinerea strain T4 cDNA library un... 38 1e-04
 emb|AC022284|AC022284 Leishmania major chromosome 35 clone L3377... 43 2e-04
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 5 emb|AI897849|AI897849 EST267292 tomato ovary, TAMU Lycopersicon ... 46 0.002
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 10 emb|AA785876|AA785876 h8g02a1.r1 Aspergillus nidulans 24hr asexu... 40 0.053
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 emb|AW398425|AW398425 EST298272 L. pennellii trichome, Cornell U... 37 0.49
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 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005727|/ncgi)
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 (2008 letters)

30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

35 Score E
 Sequences producing significant alignments: (bits) Value

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 40 emb|AI782064|AI782064 EST262943 tomato susceptible, Cornell Lyco... 220 4e-56
 emb|AW290802|AW290802 NXNV047A02F Nsf Xylem Normal wood Vertical... 204 2e-51
 emb|AA856223|AA856223 L30-246T3 Ice plant Lambda Uni-Zap XR expr... 182 1e-45
 gb|BE058219|BE058219 sn13b08.y1 Gm-cl016 Glycine max cDNA clone ... 184 2e-45
 emb|AW458125|AW458125 sh78e12.y1 Gm-cl016 Glycine max cDNA clone... 183 5e-45
 45 emb|AW030539|AW030539 EST273794 tomato callus, TAMU Lycopersicon... 163 2e-43
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 50 emb|AW033885|AW033885 EST277456 tomato callus, TAMU Lycopersicon... 108 1e-22
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 emb|AW676943|AW676943 DG1_2_E04.b1_A002 Dark Grown 1 (DG1) Sorgh... 101 2e-20
 emb|AW277624|AW277624 sf84e05.y1 Gm-cl019 Glycine max cDNA clone... 95 2e-18
 emb|AV428005|AV428005 AV428005 Lotus japonicus young plants (two... 91 2e-17
 55 emb|AW399438|AW399438 EST309938 L. pennellii trichome, Cornell U... 64 2e-16
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 emb|AW698259|AW698259 NXNV_070_G08_F Nsf Xylem Normal wood Verti... 83 6e-15
 emb|AW560259|AW560259 EST315307 DSIR Medicago truncatula cDNA cl... 53 2e-14
 60 emb|AW698260|AW698260 NXNV_070_G09_F Nsf Xylem Normal wood Verti... 81 3e-14
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- emb|AW626583|AW626583 NXNV067A10 Nsf Xylem Normal wood Vertical ... 70 6e-14
- emb|AW163982|AW163982 Ljirnp18-406-a10 Ljirnp Lambda HybriZap... 73 6e-14
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- gb|BE058708|BE058708 sn19g01.y1 Gm-cl016 Glycine max cDNA clone ... 51 5e-13
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- emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 50 2e-12
- emb|Z74998|SCYOR090C S.cerevisiae chromosome XV reading frame OR... 50 2e-12
- emb|AJ277744|FSY277744 Fagus sylvatica mRNA for ABA and calcium ... 56 2e-12
- 10 emb|AI485178|AI485178 EST243482 tomato ovary, TAMU Lycopersicon ... 51 3e-12
- emb|AW932792|AW932792 EST358635 tomato fruit mature green, TAMU ... 51 8e-12
- emb|AW676913|AW676913 DG1_2_G04.b1_A002 Dark Grown 1 (DG1) Sorgh... 72 2e-11
- emb|AW164418|AW164418 se72c06.y1 Gm-cl023 Glycine max cDNA clone... 47 3e-11
- emb|AI726381|AI726381 BNLGHi5700 Six-day Cotton fiber Gossypium ... 44 7e-11
- 15 emb|AW348221|AW348221 GM210001B12B8R Gm-r1021 Glycine max cDNA 3... 48 5e-10
- emb|AW650300|AW650300 EST328754 tomato germinating seedlings, TA... 46 6e-10
- gb|BE053500|BE053500 GA_Ea0001P09f Gossypium arboreum 7-10 dpa ... 53 1e-09
- gb|C23895|C23895 C23895 Miyagawa-wase satsuma mandarin orange (M... 65 2e-09
- emb|AI896264|AI896264 EST265707 tomato callus, TAMU Lycopersicon... 53 2e-09
- 20 emb|AW687126|AW687126 NF006C06RT1F1049 Developing root Medicago ... 53 7e-09
- emb|AI897957|AI897957 EST267400 tomato ovary, TAMU Lycopersicon ... 48 1e-08
- emb|AW030242|AW030242 EST273497 tomato callus, TAMU Lycopersicon... 38 2e-08
- emb|AV420315|AV420315 AV420315 Lotus japonicus young plants (two... 52 3e-08
- emb|AW729643|AW729643 GA_Ea0025K03 Gossypium arboreum 7-10 dpa ... 59 8e-08
- 25 emb|AI897759|AI897759 EST267202 tomato ovary, TAMU Lycopersicon ... 54 6e-07
- emb|AI897074|AI897074 EST266517 tomato ovary, TAMU Lycopersicon ... 56 1e-06
- emb|AI899132|AI899132 EST268575 tomato ovary, TAMU Lycopersicon ... 56 1e-06
- emb|AW256742|AW256742 EST304879 KV2 Medicago truncatula cDNA clo... 55 2e-06
- emb|AI489557|AI489557 EST247896 tomato ovary, TAMU Lycopersicon ... 54 3e-06
- 30 emb|AI898184|AI898184 EST267627 tomato ovary, TAMU Lycopersicon ... 54 3e-06
- emb|AI895459|AI895459 EST264902 tomato callus, TAMU Lycopersicon... 54 4e-06
- emb|AW398099|AW398099 EST297982 L. pennellii trichome, Cornell U... 54 5e-06
- emb|AW207933|AW207933 M111162e DSIR Medicago truncatula cDNA clo... 54 5e-06
- emb|AV427908|AV427908 AV427908 Lotus japonicus young plants (two... 54 5e-06
- 35 emb|AL355926|NCB17C10 Neurospora crassa DNA linkage group II BAC... 42 7e-06
- emb|AI486082|AI486082 EST244403 tomato ovary, TAMU Lycopersicon ... 53 7e-06
- emb|AW093348|AW093348 EST286528 tomato mixed elicitor, BTI Lycop... 53 1e-05
- emb|AW746773|AW746773 WS1_55_B12.b1_A002 Water-stressed 1 (WS1) ... 53 1e-05
- emb|AW666538|AW666538 GA_Ea0005H20 Gossypium arboreum 7-10 dpa ... 53 1e-05
- 40 emb|AW309762|AW309762 sf24e02.x1 Gm-cl028 Glycine max cDNA clone... 52 1e-05
- emb|AW624350|AW624350 EST322295 tomato flower buds 3-8 mm, Corne... 51 3e-05
- emb|AV417021|AV417021 AV417021 Lotus japonicus young plants (two... 51 3e-05
- emb|AW290215|AW290215 NXNV015C12F Nsf Xylem Normal wood Vertical... 51 4e-05
- emb|AI484987|AI484987 EST243250 tomato ovary, TAMU Lycopersicon ... 51 4e-05
- 45 emb|AI728047|AI728047 BNLGHi9685 Six-day Cotton fiber Gossypium ... 51 4e-05
- emb|AI771145|AI771145 EST252341 tomato ovary, TAMU Lycopersicon ... 51 4e-05
- emb|AI939275|AI939275 sc69f06.y1 Gm-cl016 Glycine max cDNA clone... 50 5e-05
- emb|AI052977|AI052977 Mpc4 Ice plant seedlings, RT-PCR, pCRII M... 50 5e-05
- emb|AW349802|AW349802 GM210006A20E6R Gm-r1021 Glycine max cDNA 3... 49 9e-05
- 50 emb|AW349791|AW349791 GM210006A20E12R Gm-r1021 Glycine max cDNA ... 49 9e-05
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- emb|AI731667|AI731667 BNLGHi10427 Six-day Cotton fiber Gossypium... 43 1e-04
- emb|AW598662|AW598662 sj94c01.y1 Gm-cl023 Glycine max cDNA clone... 49 2e-04
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- 55 emb|AW328948|AW328948 N200140e rootphos(-) Medicago truncatula c... 48 2e-04
- emb|AI442775|AI442775 sa26c12.x1 Gm-cl1004 Glycine max cDNA clone... 48 2e-04
- emb|AW399213|AW399213 EST309713 L. pennellii trichome, Cornell U... 48 3e-04
- emb|AI779659|AI779659 EST260538 tomato susceptible, Cornell Lyco... 48 3e-04
- emb|AI486266|AI486266 EST244587 tomato ovary, TAMU Lycopersicon ... 41 4e-04
- 60 emb|AW677101|AW677101 DG1_4_D08.b1_A002 Dark Grown 1 (DG1) Sorgh... 47 5e-04
- emb|AB029099|AB029099 AB029099 Cucumis sativus library (Chono M)... 47 5e-04

- emb|AI897604|AI897604 EST267047 tomato ovary, TAMU Lycopersicon ... 47 6e-04
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 emb|AW101984|AW101984 sd81e10.y1 Gm-c1009 Glycine max cDNA clone... 46 9e-04
 5 emb|AW696975|AW696975 NF111A04ST1F1024 Developing stem Medicago ... 46 0.001
 emb|AL035475|PFMAL4P2 Plasmodium falciparum MAL4P2, complete seq... 46 0.001
 emb|AW396281|AW396281 sh26f02.y1 Gm-c1016 Glycine max cDNA clone... 38 0.002
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 10 emb|AI900423|AI900423 sc05e10.y1 Gm-c1012 Glycine max cDNA clone... 45 0.002
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 15 emb|AI461042|AI461042 sa73c01.y1 Gm-c1004 Glycine max cDNA clone... 44 0.006

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25 Database: plantfungal
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35	gb BE036593 BE036593 MP01G10 MP Mesembryanthemum crystallinum cD...	387	e-119	
	gb BE054676 BE054676 GA_Ea0032C08f Gossypium arboreum 7-10 dpa ...	405	e-113	
	emb AW728038 AW728038 GA_Ea0029I18 Gossypium arboreum 7-10 dpa ...	395	e-109	
	emb AW329378 AW329378 N200608e rootphos(-) Medicago truncatula c...	386	e-107	
	emb AW725467 AW725467 GA_Ea0018B18 Gossypium arboreum 7-10 dpa ...	275	e-105	
40	emb AI966343 AI966343 sc37e08.y1 Gm-c1014 Glycine max cDNA clone...	260	6e-97	
	emb AW442228 AW442228 EST311624 tomato fruit red ripe, TAMU Lyco...	308	5e-95	
	emb AW255529 AW255529 ML562 peppermint glandular trichome Menta...	319	3e-93	
	emb AW221896 AW221896 EST298707 tomato fruit red ripe, TAMU Lyco...	215	2e-78	
	emb AW678275 AW678275 WS1_14_A02.b1_A002 Water-stressed 1 (WS1) ...	157	1e-77	
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	emb AW219191 AW219191 EST301673 tomato root during/after fruit s...	211	5e-54	
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	emb AI759880 AI759880 sb65e12.y1 Gm-c1017 Glycine max cDNA clone...	152	3e-41	
	emb AW677045 AW677045 DG1_4_G06.b1_A002 Dark Grown 1 (DG1) Sorgh...	135	4e-31	
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55	emb AW684174 AW684174 NF013F01NR1F1000 Nodulated root Medicago t...	112	3e-24	
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	emb AW677709 AW677709 WS1_10_G12.g1_A002 Water-stressed 1 (WS1) ...	100	1e-20	
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60	emb AE001381 AE001381 Plasmodium falciparum chromosome 2, sectio...	57	2e-07	
	emb AW734973 AW734973 sk92g05.y1 Gm-c1035 Glycine max cDNA clone...	56	4e-07	

- emb|AI612519|AI612519 TENGO335 T. Cruzi epimastigote normalised ... 47 2e-04
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 emb|AW666632|AW666632 GA_Ea0005D10 Gossypium arboreum 7-10 dpa ... 37 0.25
 5 emb|AW695873|AW695873 NF100C01ST1F1004 Developing stem Medicago ... 36 0.48
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 emb|AW930970|AW930970 EST356813 tomato fruit mature green, TAMU ... 35 0.91
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 10 emb|AI211536|AI211536 p0h06a1.r1 Aspergillus nidulans 24hr asexu... 35 0.91
 emb|AQ640157|AQ640157 927P1-18A7.TP 927P1 Trypanosoma brucei gen... 35 1.2
 emb|AW349276|AW349276 GM21004B21H2R Gm-r1021 Glycine max cDNA 3... 34 2.4
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 15 gb|U19028|YSC18300 Saccharomyces cerevisiae chromosome XII cosmi... 34 2.4
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 25 gb|U32307|SCU32307 Saccharomyces cerevisiae oligosaccharyltransf... 32 6.1
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 emb|X94335|SC130KBXV S.cerevisiae 130kb DNA fragment from chromo... 32 6.1
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 30 emb|AI416552|AI416552 sa10f05.y1 Gm-c1003 Glycine max cDNA clone... 32 6.1
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 35 emb|AW671822|AW671822 LG1_351_G04.g1_A002 Light Grown 1 (LG1) So... 32 8.4
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- 50 Database: plantfungal
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 60 emb|AW678776|AW678776 WS1_1_A04.b2_A002 Water-stressed 1 (WS1) S... 224 1e-77
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15	emb AI731330 AI731330 BNLGHi9231 Six-day Cotton fiber Gossypium ...	236	4e-61
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	emb AW508088 AW508088 si50f10.y1 Gm-r1030 Glycine max cDNA clone...	156	4e-60
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30	emb AW203607 AW203607 sf36b08.y1 Gm-cl028 Glycine max cDNA clone...	174	2e-42
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	emb AW350463 AW350463 GM210008A20F3R Gm-r1021 Glycine max cDNA 3...	64	4e-09
60	emb AW563245 AW563245 LG1_204_C07.g1_A002 Light Grown 1 (LG1) So...	61	2e-08
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- emb|AW318040|AW318040 sg60d08.y1 Gm-c1007 Glycine max cDNA clone... 56 6e-07
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 5 emb|Z98547|PFMAL3P3 Plasmodium falciparum MAL3P3, complete seque... 38 2e-04
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 30 emb|AW200818|AW200818 se93h05.y1 Gm-c1027 Glycine max cDNA clone... 35 1.2
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 35 dbj|D86558|D86558 Glycyrrhiza glabra mRNA for polyketide reducta... 35 1.6

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Database: plantfungal
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55 emb AF212183 AF212183 Nicotiana tabacum harpin inducing protein ...	221	3e-62
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emb Y07563 NTHIN1 N.tabacum mRNA for hin1 gene.	212	2e-59
emb AW621495 AW621495 EST312293 tomato root during/after fruit s...	215	2e-59
emb AW032166 AW032166 EST275620 tomato callus, TAMU Lycopersicon...	212	1e-58
60 emb AJ484933 AJ484933 EST243196 tomato ovary, TAMU Lycopersicon ...	214	8e-55
emb AJ779911 AJ779911 EST260790 tomato susceptible, Cornell Lyco...	209	2e-53

	emb AW216459 AW216459 EST295089 tomato callus, TAMU Lycopersicon...	189	3e-53
	emb AW596126 AW596126 si98d02.y1 Gm-c1032 Glycine max cDNA clone...	126	1e-49
	emb AW034324 AW034324 EST277895 tomato callus, TAMU Lycopersicon...	182	2e-49
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35	emb AI896428 AI896428 EST265859 tomato callus, TAMU Lycopersicon...	132	2e-36
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40	emb AI780237 AI780237 EST261116 tomato susceptible, Cornell Lyco...	139	2e-32
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	emb AW033024 AW033024 EST276583 tomato callus, TAMU Lycopersicon...	111	3e-30
	emb AW216908 AW216908 EST295622 tomato callus, TAMU Lycopersicon...	108	4e-29
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- 10 emb|AW687417|AW687417 NF009D05RT1F1045 Developing root Medicago ... 93 2e-18
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- 15 emb|AT000898|AT000898 AT000898 Brassica rapa guard cell Brassica... 90 2e-17
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- 20 emb|AW738963|AW738963 gb16h01.y1 Moss EST library PPN Physcomitr... 85 3e-16
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- 30 emb|AI725475|AI725475 BNLGHi12255 Six-day Cotton fiber Gossypium... 54 4e-13
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Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

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- 55 emb|AW687497|AW687497 NF010C03RT1F1020 Developing root Medicago ... 53 6e-12
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- emb|AW040753|AW040753 EST283617 tomato mixed elicitor, BTI Lycop... 37 6e-07
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 gb|U22006|PGU22006 Phaenosperma globosa NADH dehydrogenase F (nd... 31 7.1
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emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 268 1e-91
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gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 221 5e-88
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35 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 275 2e-82
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50 emb|AI895838|AI895838 EST265281 tomato callus, TAMU Lycopersicon... 266 5e-70
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(1953 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	215	e-105		
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15	dbj D30049 BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti...	285	e-103		
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	287	e-103		
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	304	e-102		
	emb AB032474 AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc...	289	e-102		
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	292	e-102		
20	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	291	e-101		
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	303	e-101		
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	299	e-101		
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25	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	302	e-101		
	dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein...	287	e-100		
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	295	e-100		
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30	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	290	2e-99		
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 (1947 letters)

60

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	emb AF000521 AF000521 <i>Fragaria x ananassa</i> cell wall invertase pr...	413	0.0
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10	gb M58362 DARBFRUC <i>D.carota</i> cell wall beta-fructosidase mRNA, co...	239	0.0
	emb X81792 CRCIN1 <i>C.rubrum</i> CIN1 mRNA for extracellular invertase.	181	0.0
	emb X81834 NTMRNABDF <i>N.tabacum</i> mRNA for beta-fructosidase.	205	0.0
	emb AF030420 AF030420 <i>Triticum aestivum</i> cell wall invertase (IVR...	240	0.0
	emb Y11176 CIFRUCTOS <i>C.intybus</i> mRNA for fructosidase.	144	0.0
15	emb Z21486 STBETFRUA <i>S.tuberosum</i> mRNA for invertase gene encodin...	196	e-180
	emb AJ272305 LPE272305 <i>Lycopersicon pennellii</i> mRNA for beta-fruc...	190	e-170
	emb X85327 PSRNABFRU <i>P.sativum</i> mRNA for beta-fructofuranosidase.	398	e-169
	emb AF063246 AF063246 <i>Pisum sativum</i> cell wall invertase (bfructl...	398	e-169
	emb AJ272304 LES272304 <i>Lycopersicon esculentum</i> mRNA for beta-fru...	190	e-169
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	emb X75352 DCRNAABF <i>D.carota</i> (Nantaise) mRNA for soluble acid be...	203	e-119
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	emb AJ250634 TOF250634 <i>Taraxacum officinale</i> mRNA for sucrose:suc...	169	e-116
	emb Z49831 VFVCINVMR <i>V.faba</i> VFVCINVMR mRNA for invertase (beta-fru...	199	e-115
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	dbj D10265 VIRINVA <i>Vigna radiata</i> mRNA for invertase, complete cds.	194	e-114
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	emb A52468 A52468 Sequence 1 from Patent WO9621023.	171	e-113
	emb X70368 STPAIN1A <i>S.tuberosum</i> PAIN-1 mRNA for beta-fructofuran...	200	e-108
50	emb X67163 DCSBFRU <i>D.carota</i> mRNA for soluble beta-fructosidase.	140	e-107
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	dbj E07108 E07108 cDNA encoding acid invertase.	198	e-106
	dbj D11350 TOMBFSO <i>Tomato</i> mRNA for beta-fructosidase, complete cds.	198	e-106
	emb Z12026 LPBFRUCM <i>L.pimpinellifolium</i> beta-fructosidase mRNA fo...	198	e-106
55	emb Z12025 LEBFRUCM <i>L.esculentum</i> beta-fructosidase mRNA for vacu...	198	e-106
	gb M81081 TOMACIN <i>Tomato</i> acid invertase (TIV1) mRNA, complete cds.	198	e-106
	gb S70040 S70040 acid invertase [<i>Lycopersicon esculentum</i> =tomatoe...	198	e-106
	dbj E16293 E16293 cDNA encoding invertase.	198	e-106
	dbj E08976 E08976 cDNA encoding tomato invertase.	198	e-106
60	emb AF017082 AF017082 <i>Ipomoea batatas</i> beta-fructofuranosidase (S...	141	e-103
	emb Y11124 CIPINVERT <i>C.intybus</i> mRNA for putative invertase.	138	e-102

emb|X97642|TGINV5GEN T.gesneriana mRNA for invertase 5. 180 6e-97
 emb|X95651|TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96
 emb|X97643|TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
 emb|Y18706|DCA18706 Daucus carota Inv*Dc5 gene. 130 2e-93
 5 emb|Y18707|DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge... 161 2e-93
 emb|AF062735|AF062735 Saccharum officinarum soluble acid inverta... 129 1e-91
 emb|AF062734|AF062734 Saccharum robustum soluble acid invertase ... 129 1e-91
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 10 emb|AF091550|AF091550 Hamamelis virginiana clone C beta-fructofu... 330 3e-89
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 emb|AF091548|AF091548 Hamamelis virginiana clone 3 beta-fructofu... 327 1e-88
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 15 emb|Z12027|LEBFRUCG L.esculentum gene for vacuolar invertase. 157 6e-88
 emb|AJ009756|HTU9756 Helianthus tuberosus fft-1 gene. 161 2e-87
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 20 emb|X91392|LELIN8 L.esculentum mRNA for invertase (LIN8). 133 2e-82
 emb|AF091547|AF091547 Hamamelis virginiana clone 1 beta-fructofu... 295 3e-81
 emb|X81793|CRCIN2 C.rubrum CIN2 mRNA for intracellular invertase. 135 2e-80
 emb|X91389|LELIN5 L.esculentum mRNA for invertase (LIN5). 129 1e-78
 emb|X91391|LELIN7 L.esculentum mRNA for invertase (LIN7). 133 5e-78
 25 emb|Y07838|ACY07838 A.cepa mRNA for fructan:fructan 6G-fructosyl... 156 2e-77
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 30 emb|A48282|A48282 Sequence 3 from Patent WO9601904. 152 4e-75
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 emb|AV407850|AV407850 AV407850 Lotus japonicus young plants (two... 267 2e-70
 35 emb|A48284|A48284 Sequence 5 from Patent WO9601904. 130 1e-69
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 40 emb|AF069309|AF069309 Triticum aestivum vacuolar invertase (WIVR... 127 5e-67
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 45 emb|AI522941|AI522941 sa92d01.y1 Gm-c1004 Glycine max cDNA clone... 201 1e-63
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 (1947 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

55

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

60

emb|AF000521|AF000521 Fragaria x ananassa cell wall invertase pr... 413 0.0

- emb|Z35163|VFCWINV2 V.faba VFCWINV2 mRNA for cell wall invertase... 418 0.0
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5 emb|AF030420|AF030420 Triticum aestivum cell wall invertase (IVR... 240 0.0
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emb|AJ272305|LPE272305 Lycopersicon pennellii mRNA for beta-fruc... 190 e-170
emb|X85327|PSRNABFRU P.sativum mRNA for beta-fructofuranosidase. 398 e-169
10 emb|AF063246|AF063246 Pisum sativum cell wall invertase (bfruct1... 398 e-169
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emb|Z22645|STBETFRCA S.tuberosum invertase gene encoding beta-fr... 204 e-166
emb|AF000520|AF000520 Fragaria x ananassa cell wall invertase (I... 210 e-164
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15 emb|X69321|DCBFRUCT D.carota (Queen Anne's Lace) Inv*Dc1 gene. 178 e-145
emb|X78424|DCINCI D.carota (Queen Anne's Lace) Inv*Dc2 gene, 343... 161 e-136
emb|Z35162|VFCWINV1 V.faba VFCWINV1 mRNA for cell wall invertase I. 207 e-132
emb|AF030421|AF030421 Triticum aestivum cell wall invertase (IVR... 138 e-130
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20 gb|U87849|CAU87849 Capsicum annuum acid beta-fructosidase mRNA, ... 200 e-126
emb|AJ006067|ACE6067 Allium cepa mRNA for invertase. 210 e-126
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emb|X75352|DCRNAABF D.carota (Nantaise) mRNA for soluble acid be... 203 e-119
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30 emb|A94222|A94222 Sequence 5 from Patent EP0952222. 173 e-117
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35 emb|Z49831|VFVCINVMR V.faba VFVCINV mRNA for invertase (beta-fru... 199 e-115
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40 emb|A52468|A52468 Sequence 1 from Patent WO9621023. 171 e-113
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45 dbj|D11350|TOMBFSO Tomato mRNA for beta-fructosidase, complete cds. 198 e-106
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50 dbj|E16293|E16293 cDNA encoding invertase. 198 e-106
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55 emb|X95651|TGINV11GN T.gesneriana mRNA for invertase. 186 7e-96
emb|X97643|TGINV6GEN T.gesneriana mRNA for invertase 6. 186 2e-94
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emb|Y18707|DCA18707 Daucus carota Inv*Dc4, Inv*Dc4' (partial) ge... 161 2e-93
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60 emb|AF062734|AF062734 Saccharum robustum soluble acid invertase ... 129 1e-91
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 emb|X81793|CRCIN2 *C.rubrum* CIN2 mRNA for intracellular invertase. 135 2e-80
 15 emb|X91389|LELIN5 *L.esculentum* mRNA for invertase (LIN5). 129 1e-78
 emb|X91391|LELIN7 *L.esculentum* mRNA for invertase (LIN7). 133 5e-78
 emb|Y07838|ACY07838 *A.cepa* mRNA for fructan:fructan 6G-fructosyl... 156 2e-77
 emb|X81796|BVBIN44 *B.vulgaris* BIN44 mRNA for intracellular inver... 149 5e-77
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 20 emb|AJ006066|ACE6066 *Allium cepa* mRNA for sucrose sucrose 1-fruc... 132 2e-75
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 30 emb|A48280|A48280 Sequence 1 from Patent WO9601904. 82 2e-68
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 emb|AL356012|SPBC359 *Schizosaccharomyces pombe* cosmid c359. 291 e-112
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- emb|X97560|SC32KBF *S.cerevisiae* 32kb DNA fragment of chromosome ... 159 1e-94
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10 emb|AW476771|AW476771 ga37g03.y1 Moss EST library PPU Physcomitr... 275 1e-72
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emb|AL136538|SPAC30 *S.pombe* chromosome I cosmid c30. 144 1e-48
emb|AI974480|AI974480 T110430e KV0 *Medicago truncatula* cDNA clon... 196 1e-48
emb|AI495498|AI495498 sa98g09.y1 Gm-c1004 Glycine max cDNA clone... 194 4e-48
50 emb|AW736468|AW736468 EST332482 KV3 *Medicago truncatula* cDNA clo... 191 3e-47
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60 emb|AW155943|AW155943 ga22b09.y1 Moss EST library PPU Physcomitr... 167 7e-40
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 15 emb|AW781305|AW781305 sk68b06.y1 Gm-c1016 Glycine max cDNA clone... 152 2e-35
 emb|AW441948|AW441948 EST311344 tomato fruit red ripe, TAMU Lyco... 114 2e-35
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 20 emb|AB013851|AB013851 Aspergillus oryzae gene for beta-xylosidas... 122 5e-35
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 emb|AJ278038|BFU278038 Botryotinia fuckeliana BcatrG gene for MR... 148 4e-34
 gb|U62929|FNU62929 Filobasidiella neoformans multidrug resistanc... 93 1e-32
 emb|AQ946563|AQ946563 Sheared DNA-49C19.TR Sheared DNA Trypanoso... 142 2e-32
 25 emb|AQ646228|AQ646228 RPCI93-DpnII-30J14.TV RPCI93-DpnII Trypano... 141 5e-32
 gb|U62931|AFU62931 Aspergillus flavus multidrug resistance prote... 88 1e-31
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 emb|AI676508|AI676508 etmEST0269 EtH1 Eimeria tenella cDNA clone... 135 2e-30
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 30 emb|AI782195|AI782195 EST263074 tomato susceptible, Cornell Lyco... 134 4e-30
 emb|AW033521|AW033521 EST277092 tomato callus, TAMU Lycopersicon... 134 6e-30

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(2055 letters)

Database: plantfungal
 40 661,018 sequences; 426,114,510 total letters

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Score E
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- emb|AF078082|AF078082 Phaseolus vulgaris receptor-like protein k... 356 e-115
 emb|Y14285|BOY14285 Brassica oleracea mRNA for SFR1 protein. 318 e-100
 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 322 e-99
 50 gb|M97667|BNASTKR Brassica napus ssp. oleifera serine/threonine ... 312 9e-99
 emb|AB032473|AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc... 313 1e-97
 gb|U00443|BNU00443 Brassica napus cultivar T2 S-receptor kinase... 315 2e-97
 gb|M76647|BNASKR6A Brassica oleracea receptor protein kinase (SK... 323 3e-97
 emb|AB012106|AB012106 Brassica rapa mRNA for SRK45, complete cds. 307 4e-95
 55 gb|L08607|BNASRECKIN Brassica napus S-receptor kinase mRNA, comp... 308 1e-93
 emb|Y18260|BOY18260 Brassica oleracea mRNA for SRK15 protein, pa... 313 2e-93
 emb|AB008191|AB008191 Brassica rapa mRNA for SRK29, complete cds. 312 1e-92
 emb|AB024416|AB024416 Brassica oleracea SRK2-b mRNA, complete cds. 310 3e-92
 emb|Y18259|BOY18259 Brassica oleracea mRNA for SRK5 protein, par... 309 7e-92
 60 dbj|D30049|BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti... 266 1e-90
 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 182 6e-90

- dbj|D38564|BOLRPKB *Brassica campestris* mRNA for receptor protein... 260 1e-89
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emb|AB032474|AB032474 *Brassica oleracea* SRK60 mRNA for S60 S-loc... 262 4e-89
5 dbj|D38563|BOLRPKA *Brassica campestris* mRNA for receptor protein... 258 3e-87
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10 gb|U51741|ITU51741 *Ipomoea trifida* receptor protein kinase 2 (IR... 232 1e-80
emb|AI245479|BNA245479 *Brassica napus* SlI3, slk, srk, CePP, Fmt,... 105 3e-80
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15 emb|AJ245480|BNA245480 *Brassica napus* slg gene for S-locus glyco... 107 2e-68
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20 emb|AB024422|AB024422 S2 *Brassica oleracea* SRK13-b gene, exon 2, ... 105 5e-64
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25 emb|AW620957|AW620957 sj98a07.y1 Gm-c1023 *Glycine max* cDNA clone... 202 1e-62
emb|Z30211|BOSRK29G B.oleracea (*alboglabra*) srk29 gene. 109 2e-62
emb|AB013718|AB013718 S2 *Brassica rapa* gene for SRK46Bra, exon 2,... 104 2e-62
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30 emb|AB000971|AB000971 *Brassica campestris* pseudogene for recepto... 99 7e-61
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35 emb|AW033458|AW033458 EST277029 tomato callus, TAMU *Lycopersicon*... 215 7e-55
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emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 211 2e-53
40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 *Glycine max* cDNA clone... 166 5e-53
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50 emb|Y16999|TCA16999 *Theobroma cacao* microsatellite DNA, clone mT... 106 2e-49
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- emb|X81833|BOSLR31 *B.oleracea* mRNA for SLR3-1 protein. 85 5e-46
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5 emb|AI486331|AI486331 EST244652 tomato ovary, TAMU Lycopersicon ... 161 2e-45
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emb|AF220603|AF220603 *Lycopersicon esculentum* VFNT Cherry Pto lo... 96 2e-40
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(1533 letters)

Database: plantfungal
35 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E
40 Sequences producing significant alignments: (bits) Value

gb|U82977|CSU82977 *Citrus sinensis* pectinesterase mRNA, complete... 483 0.0
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gb|U49330|SLU49330 *Solanum lycopersicum* pectin methylesterase (P... 205 e-106
emb|Z71752|NPPME2MR *N.plumbaginifolia* mRNA for pectin methyleste... 177 e-104
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50 emb|X94443|VRPECMEST *V.radiata* mRNA for pectinmethylesterase. 175 e-100
gb|U82973|CSU82973 *Citrus sinensis* pectinesterase (PECS-1.1) gen... 218 8e-97
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emb|AF152171|AF152171 *Solanum tuberosum* cultivar Desiree pectin ... 190 2e-94
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60 gb|S66607|S66607 *Lycopersicon esculentum* pectinmethylesterase-li... 190 8e-93
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- emb|A15983|A15983 *L.esculentum* mRNA for pectin esterase. 190 1e-92
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10 emb|AB029461|AB029461 *Salix gilgiana* SgPME1 mRNA for pectin meth... 144 1e-82
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15 gb|U70677|LEU70677 *Lycopersicon esculentum* (LePME1) gene, partia... 188 4e-77
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20 emb|AW930691|AW930691 EST356534 tomato fruit mature green, TAMU ... 168 1e-70
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emb|AW220185|AW220185 EST302668 tomato root during/after fruit s... 172 2e-68
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emb|AW774605|AW774605 EST333756 KV3 Medicago truncatula cDNA clo... 141 4e-66
emb|AW299038|AW299038 EST305712 KV2 Medicago truncatula cDNA clo... 141 4e-66
35 emb|AW649176|AW649176 EST327630 tomato germinating seedlings, TA... 180 7e-65
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emb|X97762|STBPE1 *S.tuberosum* mRNA BPE1 for pectin methylesterase. 165 1e-63
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emb|AW257345|AW257345 EST305482 KV2 Medicago truncatula cDNA clo... 167 9e-63
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45 emb|AW758821|AW758821 NXNV_091_A04_F Nsf Xylem Normal wood Verti... 160 8e-62
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50 gb|U82974|CSU82974 *Citrus sinensis* pectinesterase (PECS-1.2) gen... 216 6e-60
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- emb|AW774676|AW774676 EST333827 KV3 Medicago truncatula cDNA clo... 113 1e-57
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 5 emb|AW458218|AW458218 sh79h10.y1 Gm-c1016 Glycine max cDNA clone... 120 1e-56
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 (825 letters)

30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| emb X57187 PVCHITIN P.vulgaris mRNA for chitinase. | 238 | e-123 |
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| dbj D45182 D45182 Chenopodium amaranticolor mRNA for chitinase, ... | 136 | 6e-95 |
| dbj D45181 D45181 Chenopodium amaranticolor mRNA for chitinase, ... | 136 | 4e-94 |
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| gb U52845 DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... | 143 | 5e-91 |
| emb AI897733 AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... | 164 | 1e-90 |
| gb U52848 DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... | 137 | 3e-90 |
| gb U52846 DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... | 142 | 4e-90 |
| 50 emb AI897843 AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... | 158 | 2e-89 |
| gb U52847 DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... | 133 | 4e-89 |
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| emb Z46948 SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re... | 166 | 2e-84 |
| emb AI897217 AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... | 164 | 2e-84 |
| 55 gb L25826 BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. | 185 | 9e-83 |
| emb X75945 BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. | 127 | 8e-80 |
| emb A23392 A23392 B.vulgaris mRNA for chitinase 4 (B15). | 127 | 8e-80 |
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- emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 126 2e-77
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 5 gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 156 7e-75
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 15 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68
 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68
 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67
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 30 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58
 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 224 6e-58
 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57
 gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57
 emb|AI488583|AI488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57
 35 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 118 4e-57
 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 221 4e-57
 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 111 1e-56
 emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 111 1e-56
 emb|AI897391|AI897391 EST266834 tomato ovary, TAMU Lycopersicon ... 126 1e-56
 40 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56
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 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54
 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54
 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54
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 50 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 110 7e-54
 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 105 1e-53
 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 105 1e-53
 emb|AF043247|AF043247 Solanum tuberosum class I chitinase (ChtC1... 105 1e-53
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 55 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 110 6e-53
 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 112 9e-53
 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 112 9e-53
 emb|AW029730|AW029730 EST272985 tomato callus, TAMU Lycopersicon... 125 1e-52
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 60 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 114 1e-51
 gb|BE034447|BE034447 MH05A08 MH Mesembryanthemum crystallinum cD... 83 1e-51

emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 108 2e-51
 emb|AF043248|AF043248 Solanum tuberosum class I chitinase (ChtC2... 100 3e-51
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 gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 112 4e-51
 5 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 102 7e-51
 gb|U02608|STU02608 Solanum tuberosum chitinase (chtB4) mRNA, par... 107 1e-50
 emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 107 2e-50
 emb|AF000964|AF000964 Poa pratensis chitinase (Chi1) gene, compl... 100 2e-50
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 103 4e-50
 10 emb|X63899|PSCHITIN P.sativum mRNA for chitinase. 94 1e-49
 emb|AB015655|AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49
 gb|BE034450|BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 84 1e-48
 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48
 15 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48

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(825 letters)

Database: plantfungal
 25 661,018 sequences; 426,114,510 total letters

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				(bits) Value
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	emb X57187 PVCHITIN P.vulgaris mRNA for chitinase.	238	e-123	
	gb U97522 VVU97522 Vitis vinifera class IV endochitinase (VvChi4...	248	e-112	
	emb X88803 VURNACHI4 V.unguiculata mRNA for chitinase clase 4 (p...	201	e-107	
35	gb U97521 VVU97521 Vitis vinifera class IV endochitinase (VvChi4...	247	1e-97	
	dbj D45183 D45183 Chenopodium amaranticolor mRNA for chitinase, ...	197	8e-96	
	dbj D45182 D45182 Chenopodium amaranticolor mRNA for chitinase, ...	136	6e-95	
	dbj D45181 D45181 Chenopodium amaranticolor mRNA for chitinase, ...	136	4e-94	
	emb AF112966 AF112966 Triticum aestivum chitinase IV precursor (...)	227	5e-91	
40	gb U52845 DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP...	143	5e-91	
	emb A1897733 A1897733 EST267176 tomato ovary, TAMU Lycopersicon ...	164	1e-90	
	gb U52848 DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3...	137	3e-90	
	gb U52846 DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP...	142	4e-90	
	emb A1897843 A1897843 EST267286 tomato ovary, TAMU Lycopersicon ...	158	2e-89	
45	gb U52847 DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP...	133	4e-89	
	emb X61488 BNCHITIN B.napus mRNA for chitinase.	181	5e-85	
	emb Z46948 SNCHJET15 S.nigra mRNA for chitinase, pathogenesis-re...	166	2e-84	
	emb A1897217 A1897217 EST266756 tomato ovary, TAMU Lycopersicon ...	164	2e-84	
	gb L25826 BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds.	185	9e-83	
50	emb X75945 BVCH4RNA B.vulgaris Ch4 mRNA for chitinase.	127	8e-80	
	emb A23392 A23392 B.vulgaris mRNA for chitinase 4 (B15).	127	8e-80	
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	gb BE034166 BE034166 MG05H02 MG Mesembryanthemum crystallinum cD...	167	4e-78	
	emb AW691007 AW691007 NF036E09ST1F1000 Developing stem Medicago ...	131	5e-78	
55	emb AW030814 AW030814 EST274069 tomato callus, TAMU Lycopersicon...	126	1e-77	
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60	gb BE034975 BE034975 ML07H10 ML Mesembryanthemum crystallinum cD...	156	7e-75	
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 emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 126 2e-74
 5 gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 104 3e-74
 emb|AJ897657|AJ897657 EST267100 tomato ovary, TAMU Lycopersicon ... 156 4e-72
 emb|X74919|PVGEC9 P.vulgaris gene for endochitinase. 238 6e-71
 emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 126 2e-70
 gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 132 2e-68
 10 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 126 3e-68
 gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 114 2e-67
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 emb|AW684552|AW684552 NF018C03NR1F1000 Nodulated root Medicago t... 122 5e-66
 emb|AW922776|AW922776 DG1_46_C01.g1_A002 Dark Grown 1 (DG1) Sorg... 215 5e-65
 15 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 79 2e-64
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 emb|AW680953|AW680953 WS1_9_A06.b1_A002 Water-stressed 1 (WS1) S... 224 7e-63
 emb|AJ729668|AJ729668 BNLGHI13889 Six-day Cotton fiber Gossypium... 121 1e-61
 emb|AJ055037|AJ055037 coau0002N18 Cotton Boll Abcission Zone cD... 111 3e-60
 20 gb|BE034616|BE034616 ML04B04 ML Mesembryanthemum crystallinum cD... 101 3e-60
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 emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed 1 (WS1) ... 171 4e-59
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 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 224 6e-58
 25 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 224 6e-58
 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 108 2e-57
 gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 208 2e-57
 emb|AJ488583|AJ488583 EST246922 tomato ovary, TAMU Lycopersicon ... 126 3e-57
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 30 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 221 4e-57
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 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 110 7e-56
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 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 214 7e-55
 40 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 108 2e-54
 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 110 2e-54
 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 107 5e-54
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 5 emb[AB015655]AB015655 Cucurbita sp. mRNA for chitinase, complete... 100 7e-49
 gb[BE034450]BE034450 MH05B01 MH Mesembryanthemum crystallinum cD... 84 1e-48
 gb[U02287]HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 111 3e-48
 emb[A16119]A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 108 6e-48
 gb[M15173]TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 108 6e-48
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 [arabidopsis thaliana] /blast_score 0 /ec_number /family /chip nova
 15 /gb_link /ncgi
 (1788 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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Searching.....done

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35 emb[AW460005]AW460005 si07d11.y1 Gm-c1029 Glycine max cDNA clone...	116	1e-57
gb[U18839]SCE9747 Saccharomyces cerevisiae chromosome V cosmids ...	123	4e-48
emb[X68327]SCTRP2 S.cerevisiae TRP2 gene for anthranilate syntha...	123	4e-48
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40 gb[K01388]YSCTRP2 Yeast (S.cerevisiae) TRP2 gene coding for anth...	122	4e-38
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45 emb[AF119554]AF119554 Plasmodium falciparum para-aminobenzoic ac...	67	6e-10
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	emb AL031746 PFMAL1P3 Plasmodium falciparum MAL1P3, complete seq...	35	1.9
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	gb BE021269 BE021269 sm56h04.y1 Gm-cl028 Glycine max cDNA clone ...	33	9.2
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	emb AB012116 AB012116 Vigna mungo UFGlyT mRNA for UDP-glucose:fl...	33	9.2
	emb AW725836 AW725836 GA_Ea0019N24 Gossypium arboreum 7-10 dpa ...	33	9.2
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 (1342 letters)

Database: plantfungal
 15 661,018 sequences; 426,114,510 total letters

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Score E
 20 Sequences producing significant alignments: (bits) Value

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 emb|AW737762|AW737762 EST339189 tomato flower buds, anthesis, Co... 169 1e-60
 30 emb|AW621695|AW621695 EST312493 tomato root during/after fruit s... 206 3e-52
 emb|AW350933|AW350933 GM210010B10D11R Gm-r1021 Glycine max cDNA ... 203 3e-51
 emb|AI166669|AI166669 xylem.est.479 Poplar xylem Lambda ZAPII li... 144 3e-50
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 35 emb|AI774565|AI774565 EST255665 tomato resistant, Cornell Lycopersicon... 192 7e-48
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10	emb AB015494 AB015494 Passiflora edulis PE-ACS1 mRNA for ACC syn...	36	5e-05
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	gb M34289 TOMACS Tomato 1-aminocyclopropane-1-carboxylate syntha...	36	1e-04
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	emb X62536 LEACC L.esculentum mRNA for ACC synthase.	36	1e-04
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	gb U73816 MDU73816 Malus domestica ACC synthase (MdACS-3) mRNA, ...	32	0.009
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30	emb Z11613 VRACCSYNM V.radiata mRNA for ACC synthase.	41	0.016
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(1752 letters)

Database: plantfungal
661,018 sequences; 426,114,510 total letters

10

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15	Sequences producing significant alignments:		
	emb A92838 A92838 Sequence 12 from Patent WO9804586.	258 e-123	
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	emb A92833 A92833 Sequence 7 from Patent WO9804586.	261 e-116	
	emb A92828 A92828 Sequence 2 from Patent WO9804586.	261 e-116	
20	emb AW216578 AW216578 EST295292 tomato callus, TAMU Lycopersicon...	165 6e-78	
	emb AJ005341 LUAJ5341 Linum usitatissimum mRNA for MLO-like prot...	287 2e-76	
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	emb AW132264 AW132264 sd98f11.y1 Gm-c1013 Glycine max cDNA clone...	128 2e-60	
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	emb AV426381 AV426381 AV426381 Lotus japonicus young plants (two...	145 3e-43	
30	emb AI729043 AI729043 BNLGHi12416 Six-day Cotton fiber Gossypium...	142 6e-42	
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	emb A92831 A92831 Sequence 5 from Patent WO9804586.	107 7e-41	
	emb AI731933 AI731933 BNLGHi11440 Six-day Cotton fiber Gossypium...	136 3e-40	
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 emb|AI563090|AI563090 EST00214 watermelon lambda zap library Cit... 37 0.010
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 10 gb|BE035329|BE035329 MM06C12 MM Mesembryanthemum crystallinum cD... 36 0.71
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 emb|X96770|SCLACHXVI S.cerevisiae chromosome XVI, left arm DNA. 35 1.8
 emb|X05498|SCSNR17B Yeast SNR17B gene for U3 small nuclear RNA. 35 1.8
 20 emb|Z73500|SCYPL144W S.cerevisiae chromosome XVI reading frame O... 35 1.8
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 emb|AJ242498|CCL242498 Candida cloacae mRNA for long chain fatty... 35 1.8
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 emb|AQ642037|AQ642037 RPCI93-DpnII-29K3.TJ RPCI93-DpnII Trypanos... 34 3.5
 30 emb|AQ445280|AQ445280 GSSTc01558 Trypanosoma cruzi random genom... 34 3.5
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 emb|AQ659145|AQ659145 Sheared DNA-16H2.TF Sheared DNA Trypanosom... 34 3.5
 gb|U88830|SCU88830 Saccharomyces cerevisiae Sgt1p (SGT1) gene, c... 34 3.5
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 40 emb|AW257222|AW257222 EST305359 KV2 Medicago truncatula cDNA clo... 34 4.7
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 emb|AQ655690|AQ655690 Sheared DNA-9G1.TR Sheared DNA Trypanosoma... 34 4.7
 45 emb|AZ212373|AZ212373 Sheared DNA-101E1.TF Sheared DNA Trypanoso... 34 4.7
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 gb|M17420|YSTHEP Saccharomyces cerevisiae heptapeptide repeat re... 33 6.5
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 emb|Z49511|SCYJR011C S.cerevisiae chromosome X reading frame ORF... 33 6.5
 50 gb|U59312|HVVU59312 Hordeum vulgare (1,4)-beta-xylan endohydrolas... 33 6.5
 emb|Z74188|SCYDL140C S.cerevisiae chromosome IV reading frame OR... 33 6.5
 emb|X87611|SCXCOSM83 S.cerevisiae chromosome X DNA (cosmid 83). 33 6.5
 emb|AA003500|AA003500 T3189 MVAT4 bloodstream form of serodeme W... 33 6.5
 emb|AQ951709|AQ951709 Sheared DNA-51E22.TF Sheared DNA Trypanoso... 33 6.5

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 60 [post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005314|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac005314|/ncgi)
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(1125 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	emb AJ245878 TAE245878 Triticum aestivum mRNA for serpin (WSZ1c ...	116	2e-65
	emb Y11485 TAESERPIN T.aestivum mRNA for serpin WZS2.	116	2e-62
15	emb Z49890 TAWZCISPIN T.aestivum WZCI mRNA for serpin.	109	3e-60
	emb X95277 HVSEH H.vulgare mRNA for serpin.	98	6e-58
	emb AW458573 AW458573 sh10b03.y1 Gm-c1016 Glycine max cDNA clone...	115	6e-55
	emb X97636 HVSERP H.vulgare mRNA for serpin.	96	2e-44
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20	gb BE058355 BE058355 sn15a03.y1 Gm-c1016 Glycine max cDNA clone ...	134	3e-40
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25	emb AI730301 AI730301 BNLGH16607 Six-day Cotton fiber Gossypium ...	77	8e-31
	emb AI725411 AI725411 BNLGH11751 Six-day Cotton fiber Gossypium...	55	9e-30
	emb AV420945 AV420945 AV420945 Lotus japonicus young plants (two...	126	4e-28
	emb AI772215 AI772215 EST253315 tomato resistant, Cornell Lycopers...	116	6e-27
	emb X51726 HVPZ1 Barley Paz1 gene for protein Z.	76	3e-26
30	emb AW219573 AW219573 EST302055 tomato root during/after fruit s...	83	4e-26
	emb AI726323 AI726323 BNLGH15614 Six-day Cotton fiber Gossypium ...	112	8e-26
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	emb AW983183 AW983183 HVSMEg0008J04f Hordeum vulgare pre-anthesi...	64	2e-21
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	emb AW099940 AW099940 sd18f07.y2 Gm-c1012 Glycine max cDNA clone...	57	5e-18
40	emb AW720162 AW720162 LjNEST16a4r Lotus japonicus nodule library...	84	1e-15
	emb AW598800 AW598800 ga88d04.y1 Moss EST library PPU Physcomitr...	84	3e-15
	gb BE058596 BE058596 sn18b11.y1 Gm-c1016 Glycine max cDNA clone ...	48	7e-14
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	emb AW560154 AW560154 EST315202 DSIR Medicago truncatula cDNA cl...	69	5e-11
	emb AQ917127 AQ917127 T233156b Medicago truncatula BAC library M...	47	3e-09
	emb AW306929 AW306929 sf50e08.y1 Gm-c1009 Glycine max cDNA clone...	56	4e-08
50	emb AW010023 AW010023 ST01E04 Pine Triplex shoot tip library Pin...	41	1e-07
	emb X51727 HVPZPSE Barley DNA for pseudogene PAZ.	51	3e-07
	gb BE022668 BE022668 sm75h09.y1 Gm-c1015 Glycine max cDNA clone ...	56	7e-07
	emb X05902 HVPROTZ Barley mRNA fragment for protein Z.	46	8e-07
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55	emb AI779352 AI779352 EST260231 tomato susceptible, Cornell Lyco...	51	1e-05
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	emb AV414917 AV414917 AV414917 Lotus japonicus young plants (two...	50	3e-05
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- emb|AW905918|AW905918 EST342091 potato stolon, Cornell Universit... 35 0.81
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 emb|AQ367717|AQ367717 tox0002L20r CUGI Tomato BAC Library Lycop... 34 2.1
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 10 emb|AL115273|CNS01CA9 *Botrytis cinerea* strain T4 cDNA library un... 34 2.1
 emb|AL113815|CNS01B5R *Botrytis cinerea* strain T4 cDNA library un... 34 2.1
 emb|AI490380|AI490380 EST248706 tomato ovary, TAMU Lycopersicon ... 34 2.9
 emb|AL116919|CNS01DJZ *Botrytis cinerea* strain T4 cDNA library un... 34 2.9
 gb|U68716|BFU68716 *Botryotinia fuckeliana* endopolygalacturonase ... 33 4.0
 15 gb|L25681|HYBRG18S *Hydnora africana* Thunb. 18S ribosomal RNA (18... 33 4.0
 emb|AI165169|AI165169 A077P18U Hybrid aspen plasmid library Popu... 33 4.0
 gb|BE020501|BE020501 sm44e08.y1 Gm-c1028 Glycine max cDNA clone ... 33 5.5
 gb|M55639|AURRR16S *Aureobasidium pullulans* 16S-like ribosomal RN... 33 5.5
 emb|AQ953266|AQ953266 Sheared DNA-39D4.TF Sheared DNA Trypanosom... 33 5.5
 20 emb|AI494738|AI494738 sb14f02.y1 Gm-c1004 Glycine max cDNA clone... 33 5.5
 gb|M35065|BLYPROZ Barley protein Z mRNA, partial cds. 33 5.5
 emb|AV409233|AV409233 Lotus japonicus young plants (two... 26 6.2
 emb|AJ273043|AJ273043 AJ273043 *Metarhizium anisopliae* ARSEF 2575... 32 7.5
 emb|AF106529|AF106529 *Monacrosporium leptosporum* 18S small subun... 32 7.5
 25 emb|AW569360|AW569360 si86a11.y1 Gm-c1031 Glycine max cDNA clone... 32 7.5
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 30 emb|AL356172|NCB23L21 *Neurospora crassa* DNA linkage group II BAC... 32 7.5
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 (1140 letters)

Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters

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| emb X78325 NTSNPNZ <i>N.tabacum</i> (Samsun NN) Pz mRNA. | 317 | e-139 | | |
| emb A72838 A72838 Sequence 1 from Patent WO9505467. | 314 | e-138 | | |
| emb X77110 NTCHIVR <i>N.tabacum</i> chi-V mRNA for chitinase class V. | 312 | e-137 | | |
| 55 emb AF088885 AF088885 <i>Nicotiana tabacum</i> receptor-like kinase CHR... | 189 | 3e-84 | | |
| emb X77111 NTCHIVD <i>N.tabacum</i> chi-V gene. | 204 | 1e-69 | | |
| emb A72844 A72844 Sequence 7 from Patent WO9505467. | 204 | 7e-69 | | |
| emb AW690230 AW690230 NF030F05ST1F1000 Developing stem <i>Medicago</i> ... | 139 | 4e-66 | | |
| emb AF108893 AF108893 <i>AF108893 Capsicum annuum</i> root 1st-branched... | 201 | 7e-51 | | |
| 60 emb AW032116 AW032116 EST275570 tomato callus, TAMU Lycopersicon... | 186 | 2e-46 | | |
| emb AW560415 AW560415 EST315463 DSIR <i>Medicago truncatula</i> cDNA cl... | 169 | 3e-41 | | |

- emb|AW351251|AW351251 GM210011A20A4R Gm-r1021 Glycine max cDNA 3... 145 6e-34
- emb|AV423067|AV423067 AV423067 Lotus japonicus young plants (two... 129 2e-32
- emb|AV412385|AV412385 AV412385 Lotus japonicus young plants (two... 129 4e-29
- 5 emb|AV411642|AV411642 AV411642 Lotus japonicus young plants (two... 84 3e-28
- emb|AI495953|AI495953 sb18c04.y1 Gm-cl004 Glycine max cDNA clone... 111 1e-23
- emb|AV422006|AV422006 AV422006 Lotus japonicus young plants (two... 75 3e-21
- emb|AF188932|AF188932 Hypocrea rufa strain Hy9 42 kDa endochitin... 68 1e-20
- emb|AF188921|AF188921 Trichoderma atroviride strain DAOM 165782 ... 70 3e-20
- 10 gb|U49455|THU49455 Trichoderma harzianum endochitinase (chi1) mR... 69 3e-20
- emb|AF188918|AF188918 Hypocrea koningii 42 kDa endochitinase gen... 71 3e-20
- emb|AF188930|AF188930 Trichoderma asperellum strain CBS 361.97, ... 68 6e-20
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- emb|AF188923|AF188923 Hypocrea rufa strain GJS 89-142 42 kDa end... 68 8e-20
- 15 emb|X79381|THECH42 T.harzianum (IMI 206040) ech-42 gene. 68 9e-20
- gb|L14614|TRRENDOCHI Trichoderma harzianum endochitinase mRNA, c... 68 9e-20
- emb|AF188920|AF188920 Trichoderma atroviride strain DAOM 165779 ... 68 9e-20
- emb|AF188929|AF188929 Trichoderma asperellum strain CBS 433.97, ... 68 9e-20
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- emb|AF188925|AF188925 Trichoderma viride strain Tr6 42 kDa endoc... 68 4e-19
- emb|AF188919|AF188919 Trichoderma viride strain ATCC 18652, syno... 66 2e-18
- 30 emb|AF188922|AF188922 Hypocrea rufa strain GJS 89-127 42 kDa end... 66 3e-18
- emb|AF050098|AF050098 Trichoderma virens chitinase gene, complet... 65 2e-17
- emb|X64104|AACHI1A A.album chi1 gene for chitinase. 65 3e-17
- emb|AJ243014|MFL243014 Metarhizium flavoviride mRNA for chitinas... 62 8e-17
- emb|AF027498|AF027498 Metarhizium anisopliae chitinase CHIT42 (C... 60 9e-16
- 35 emb|AF027497|AF027497 Metarhizium anisopliae chitinase CHIT42 (C... 60 9e-16
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- emb|AV421624|AV421624 AV421624 Lotus japonicus young plants (two... 63 2e-13
- emb|AI899627|AI899627 EST269070 tomato susceptible, Cornell Lyco... 75 1e-12
- dbj|D87894|D87894 Rhizopus oligosporus DNA for chitinase, comple... 59 2e-10
- 40 emb|AV407063|AV407063 AV407063 Lotus japonicus young plants (two... 68 2e-10
- emb|AF009354|AF009354 Leishmania donovani chitinase (Chi-1) gene... 57 4e-09
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- emb|AA966331|AA966331 w4a12a1.r1 Aspergillus nidulans 24hr asexu... 54 5e-09
- emb|AI212420|AI212420 x5f11a1.r1 Aspergillus nidulans 24hr asexu... 43 6e-08
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- emb|AA787768|AA787768 r1d06a1.r1 Aspergillus nidulans 24hr asexu... 46 2e-06
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- gb|L41663|COICTS1CHI Coccidioides immitis chitinase (cts1) gene,... 44 5e-06
- 50 gb|U51271|CIU51271 Coccidioides immitis complement-fixation anti... 44 5e-06
- gb|U60806|CIU60806 Coccidioides immitis complement-fixation chit... 44 5e-06
- emb|AI213337|AI213337 z1b11a1.r1 Aspergillus nidulans 24hr asexu... 50 7e-06
- emb|AI211269|AI211269 o0h07a1.r1 Aspergillus nidulans 24hr asexu... 43 1e-05
- emb|AW334147|AW334147 S31A10 AGS-1 Pneumocystis carinii f. sp. c... 51 1e-05
- 55 emb|Z71415|THENDOCHS T.hamatum endochitinase gene. 50 3e-05
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- emb|AI209456|AI209456 a0h06a1.r1 Aspergillus nidulans 24hr asexu... 43 6e-05
- gb|M11815|YSKGL1A Plasmid pGKL1 from killer yeast (K.lactis), c... 39 1e-04
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- 60 emb|X00762|KLKILL05 Kluyveromyces lactis (killer strain) plasmid... 39 1e-04
- emb|X07127|KLK1P Kluyveromyces lactis killer plasmid k1 DNA. 39 1e-04

- emb|X89212|MADNACHIA M.anisopliae DNA for ChiA gene. 48 1e-04
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 30 emb|AB027528|AB027528 Physcomitrella patens ppCRY1 mRNA for blue... 33 5.5

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 35 (2034 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Score E
 Sequences producing significant alignments: (bits) Value

- 45 emb|AI894928|AI894928 EST264371 tomato callus, TAMU Lycopersicon... 59 4e-11
 emb|AW621748|AW621748 EST312546 tomato root during/after fruit s... 62 1e-08
 emb|AW991081|AW991081 SsS0293 Suaeda salsa ZAP cDNA library Suae... 58 3e-07
 emb|AI896054|AI896054 EST265497 tomato callus, TAMU Lycopersicon... 55 2e-06
 emb|AW932874|AW932874 EST358717 tomato fruit mature green, TAMU ... 54 3e-06
 50 emb|AW035961|AW035961 EST282820 tomato callus, TAMU Lycopersicon... 53 5e-06
 emb|AW217271|AW217271 EST295985 tomato callus, TAMU Lycopersicon... 51 3e-05
 emb|AI736949|AI736949 sb35a01.y1 Gm-c1013 Glycine max cDNA clone... 45 6e-05
 emb|AI729969|AI729969 BNLGHi5823 Six-day Cotton fiber Gossypium ... 41 8e-05
 gb|BE033853|BE033853 MG01B02 MG Mesembryanthemum crystallinum cD... 49 1e-04
 55 emb|AZ124241|AZ124241 T223105b Medicago truncatula BAC library M... 47 4e-04
 emb|AI729861|AI729861 BNLGHi5428 Six-day Cotton fiber Gossypium ... 44 0.005
 emb|AW623353|AW623353 EST321298 tomato flower buds 3-8 mm, Come... 44 0.005
 emb|AZ124239|AZ124239 T223103b Medicago truncatula BAC library M... 44 0.005
 emb|AI166315|AI166315 xylem.est.16 Poplar xylem Lambda ZAPII lib... 42 0.013
 60 emb|AW219421|AW219421 EST301999 tomato root during/after fruit s... 42 0.013
 emb|AI974296|AI974296 T110298e KV0 Medicago truncatula cDNA clon... 42 0.013

	emb AI054990 AI054990 coau0002L09 Cotton Boll Abscission Zone cD...	40	0.037
	emb AW929405 AW929405 EST338193 tomato flower buds 8 mm to pre-a...	39	0.17
	emb AW649475 AW649475 EST327929 tomato germinating seedlings, TA...	39	0.17
	emb AW222512 AW222512 EST299323 tomato fruit red ripe, TAMU Lyco...	38	0.23
5	emb AW222518 AW222518 EST299329 tomato fruit red ripe, TAMU Lyco...	38	0.23
	emb AI781303 AI781303 EST262182 tomato susceptible, Cornell Lyco...	38	0.23
	emb AI779448 AI779448 EST260327 tomato susceptible, Cornell Lyco...	38	0.23
	emb AW053754 AW053754 L30-1647T3 Ice plant Lambda Uni-Zap XR exp...	38	0.23
	emb AF141013 AF141013 Vigna unguiculata clone KINE12 disease res...	32	0.32
10	emb AW164678 AW164678 se76b06.y1 Gm-cl023 Glycine max cDNA clone...	38	0.32
	emb AW736367 AW736367 EST332286 KV3 Medicago truncatula cDNA clo...	37	0.42
	emb Z67751 SC38KCXVI S.cerevisiae DNA (chromosome XVI; 38 kb).	34	0.77
	emb AV420300 AV420300 AV420300 Lotus japonicus young plants (two...	36	0.82
	emb AW424334 AW424334 sh64b12.y1 Gm-cl015 Glycine max cDNA clone...	36	0.82
15	emb Z73595 SCYPL239W S.cerevisiae chromosome XVI reading frame O...	34	0.94
	gb U34385 SCU34385 Saccharomyces cerevisiae ankyrin repeat prote...	34	0.98
	emb AQ522032 AQ522032 CpG0990A CpIOWAgDNA1 Cryptosporidium parvu...	36	1.1
	emb AQ083671 AQ083671 CpG0567A CpIOWAgDNA1 Cryptosporidium parvu...	36	1.1
	emb AF141012 AF141012 Vigna unguiculata clone KIND12 disease res...	30	1.4
20	emb AW283124 AW283124 LG1_224_H10.g1_A002 Light Grown 1 (LG1) So...	35	1.6
	emb AI054715 AI054715 coau0001M19 Cotton Boll Abscission Zone cD...	35	1.6
	emb Y10579 VFPOTCHAN V.faba mRNA for potassium channel.	29	1.7
	emb AQ935638 AQ935638 CpG2573A CpIOWAgDNA1 Cryptosporidium parvu...	35	2.1
	emb AW040703 AW040703 EST283567 tomato mixed elicitor, BTI Lycop...	35	2.1
25	emb X73850 BNPNL3 B.napus (pNL3) mRNA for acyl-ACP-thioesterase.	35	2.9
	emb AL096797 SPBC146 S.pombe chromosome II cosmid c146.	35	2.9
	emb X87842 BNDNAFATA B.napus FatA gene.	35	2.9
	emb AF073683 073693S155 Tinguarra sicala internal transcribed sp...	35	2.9
	dbj D30788 YSPCUT3B Schizosaccharomyces pombe gene for cut3 prot...	35	2.9
30	gb BE035556 BE035556 MO09B06 MO Mesembryanthemum crystallinum cD...	35	2.9
	gb M21813 YSCSELF2B S.cerevisiae SUI3 gene encoding translation i...	35	2.9
	gb BE036920 BE036920 MP09B06 MP Mesembryanthemum crystallinum cD...	35	2.9
	gb BE035567 BE035567 MO09C08 MO Mesembryanthemum crystallinum cD...	27	3.2
	emb AW923857 AW923857 DG1_60_G12.g1_A002 Dark Grown 1 (DG1) Sorg...	30	3.4
35	emb AA680502 AA680502 T3691 Bloodstream form of serodeme ILTat1....	34	4.0
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	emb AI055156 AI055156 coau0003D05 Cotton Boll Abscission Zone cD...	34	4.0
	emb AL356815 NCB24H17 Neurospora crassa DNA linkage group II BAC...	30	4.2
	emb AF181702 AF181702 Leptosphaeria contecta 18S ribosomal RNA g...	34	5.5
40	emb AW145916 AW145916 ga35g12.y1 Moss EST library PPN Physcomitr...	34	5.5
	emb AW617253 AW617253 EST323664 L. hirsutum trichome, Cornell Un...	34	5.5
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	emb AW691785 AW691785 NF044B05ST1F1000 Developing stem Medicago ...	34	5.5
	dbj D38256 YSCSCT1 Yeast gene for suppressor of ctr mutation.	34	5.5
45	gb U26175 LDU26175 Leishmania donovani lipophosphoglycan biosynt...	34	5.5
	emb AB029613 AB029613 Aspergillus terreus TOP2 gene for type II ...	34	5.5
	emb AW696259 AW696259 NF104F08ST1F1074 Developing stem Medicago ...	34	5.5
	emb AC004710 AC004710 Plasmodium falciparum chromosome 12, *** S...	33	7.6
	emb AV421315 AV421315 AV421315 Lotus japonicus young plants (two...	33	7.6
50	emb AW599293 AW599293 gb13a06.y1 Moss EST library PPN Physcomitr...	33	7.6
	emb AC005507 AC005507 Plasmodium falciparum chromosome 12 clone ...	33	7.6
	gb U16862 PFU16862 Plasmodium falciparum HSP70-like protein gene...	33	7.6
	emb AI213448 AI213448 z2a11a1.fl Aspergillus nidulans 24hr asexu...	33	7.6
	emb X73849 BNPNL2 B.napus (pNL2) mRNA for acyl-ACP-thioesterase.	33	7.6
55	emb AW694856 AW694856 NF080G09ST1F1071 Developing stem Medicago ...	33	7.6
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	emb AV412721 AV412721 AV412721 Lotus japonicus young plants (two...	33	7.6
	emb AI759851 AI759851 sb65b08.y1 Gm-cl017 Glycine max cDNA clone...	33	7.6
	emb AZ124240 AZ124240 T223104b Medicago truncatula BAC library M...	33	7.6
60	emb Y08926 PFAARPIPR P.falciparum mRNA for AARPI protein, partial.	33	7.6
	emb AV410224 AV410224 AV410224 Lotus japonicus young plants (two...	33	7.6

emb|AQ849926|AQ849926 LMAJFV1_lm51f05.x1 Leishmania major FV1 ra... 33 7.6
 emb|AL034557|PFMAL4P1 Plasmodium falciparum chromosome 4 strain ... 27 8.3
 emb|AQ944606|AQ944606 Sheared DNA-48P15.TR Sheared DNA Trypanoso... 28 8.4
 emb|AF099095|AF099095 Samanea saman pulvinus inward-rectifying c... 26 9.8

5

Query= AC005896.161_g_at 20620_g_at /id_source genbank /description
 gb|aac98070.1|(ac005896) putative c2h2-type zinc finger protein
 [arabidopsis thaliana] /blast_score 8.00e-92 /ec_number /family
 /chip nova /gb_link /ncgi
 (864 letters)

10

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

15 Searching.....done

		Score	E
	Sequences producing significant alignments:	(bits)	Value
20	emb AB006600 AB006600 Petunia x hybrida mRNA for ZPT2-13, comple...	86	1e-30
	emb AB000451 AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com...	74	5e-29
	emb AW685937 AW685937 NF031H10NR1F1000 Nodulated root Medicago t...	76	9e-29
	emb AB006599 AB006599 Petunia x hybrida mRNA for ZPT2-12, comple...	77	1e-28
	emb AB006601 AB006601 Petunia x hybrida mRNA for ZPT2-14, comple...	72	2e-26
25	emb AI898309 AI898309 EST267752 tomato ovary, TAMU Lycopersicon ...	68	3e-26
	emb AI485362 AI485362 EST243683 tomato ovary, TAMU Lycopersicon ...	67	1e-25
	emb AI483886 AI483886 EST249757 tomato ovary, TAMU Lycopersicon ...	68	1e-25
	emb AW030869 AW030869 EST274159 tomato callus, TAMU Lycopersicon...	68	5e-24
	emb AI966235 AI966235 sc35g05.y1 Gm-c1014 Glycine max cDNA clone...	72	3e-23
30	emb AB006603 AB006603 Petunia x hybrida mRNA for ZPT2-8, complet...	65	1e-22
	emb AI486627 AI486627 EST244948 tomato ovary, TAMU Lycopersicon ...	61	1e-22
	emb AI485555 AI485555 EST243876 tomato ovary, TAMU Lycopersicon ...	61	1e-22
	emb AI488341 AI488341 EST246663 tomato ovary, TAMU Lycopersicon ...	61	1e-22
	emb AI486228 AI486228 EST244549 tomato ovary, TAMU Lycopersicon ...	61	1e-22
35	emb AI959966 AI959966 sc35g05.x1 Gm-c1014 Glycine max cDNA clone...	69	2e-22
	emb AI771123 AI771123 EST252223 tomato ovary, TAMU Lycopersicon ...	61	3e-22
	emb AI897376 AI897376 EST266819 tomato ovary, TAMU Lycopersicon ...	68	5e-22
	emb AI894711 AI894711 EST264154 tomato callus, TAMU Lycopersicon...	68	6e-22
40	emb AV422177 AV422177 AV422177 Lotus japonicus young plants (two...	103	2e-21
	emb AB006602 AB006602 Petunia x hybrida mRNA for ZPT2-7, complet...	66	6e-21
	emb AI485123 AI485123 EST243427 tomato ovary, TAMU Lycopersicon ...	68	6e-21
	emb AW216442 AW216442 EST295072 tomato callus, TAMU Lycopersicon...	68	8e-21
	emb AW687462 AW687462 NF009H03RT1F1031 Developing root Medicago ...	70	2e-20
	emb AI771824 AI771824 EST252924 tomato ovary, TAMU Lycopersicon ...	68	2e-20
45	emb AW034640 AW034640 EST278324 tomato callus, TAMU Lycopersicon...	68	7e-20
	emb AW033868 AW033868 EST277439 tomato callus, TAMU Lycopersicon...	72	1e-19
	emb AI487993 AI487993 EST246315 tomato ovary, TAMU Lycopersicon ...	68	1e-18
	emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root Medicago t...	68	2e-18
	emb X60700 PHEPF1 P.hybrida EPF1 gene for DNA-binding protein.	61	2e-18
50	emb AB006604 AB006604 Petunia x hybrida mRNA for ZPT2-9, complet...	59	5e-18
	emb AI489727 AI489727 EST248066 tomato ovary, TAMU Lycopersicon ...	50	1e-16
	emb AW034622 AW034622 EST278306 tomato callus, TAMU Lycopersicon...	87	2e-16
	emb AB035132 AB035132 Petunia x hybrida gene for C2H2 zinc-finge...	57	1e-15
	emb AB006597 AB006597 Petunia x hybrida mRNA for ZPT2-10, comple...	57	1e-15
55	emb AB035133 AB035133 Petunia x hybrida gene for C2H2 zinc-finge...	56	2e-15
	emb AB006605 AB006605 Petunia x hybrida mRNA for ZPT3-3, complet...	56	2e-15
	emb AW777036 AW777036 M111167e DSIR Medicago truncatula cDNA clo...	74	2e-15
	emb AI488445 AI488445 EST246784 tomato ovary, TAMU Lycopersicon ...	50	4e-15
	emb AF119050 AF119050 Datisca glomerata zinc-finger protein 1 (z...	53	7e-15
60	emb AB000455 AB000455 Petunia hybrida mRNA for PETHy;ZPT4-1, com...	55	9e-15
	emb AI988657 AI988657 sd06b03.y1 Gm-c1020 Glycine max cDNA clone...	51	1e-14

- emb|AW781249|AW781249 sk67b08.y1 Gm-c1016 Glycine max cDNA clone... 51 1e-14
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emb|Y16131|Y16131 Y16131 young root nodules Medicago sativa subs... 51 2e-14
dbj|D26085|PETZFDB3 Petunia zinc-finger DNA binding protein gene. 50 2e-14
5 dbj|D16415|WHTWZF1A Wheat gene for WZF1, complete cds. 53 2e-14
emb|AB000453|AB000453 Petunia hybrida mRNA for PETHy;ZPT3-1, com... 55 2e-14
dbj|D16416|WHTWZF1B Wheat mRNA for WZF1, complete cds. 53 2e-14
dbj|D26084|PETZFDB2 Petunia mRNA for zinc-finger DNA binding pro... 52 3e-14
emb|Y18788|MSY18788 Medicago sativa mRNA for putative TFIIIA (or... 51 3e-14
10 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 51 3e-14
emb|AI988290|AI988290 sc98f10.y1 Gm-c1020 Glycine max cDNA clone... 52 3e-14
emb|AW706944|AW706944 sk08e10.y1 Gm-c1023 Glycine max cDNA clone... 50 5e-14
dbj|D26083|PETZFDB1 Petunia hybrida gene for zinc-finger DNA bin... 52 6e-14
emb|AF053077|AF053077 Nicotiana tabacum osmotic stress-induced z... 51 6e-14
15 emb|AW729218|AW729218 GA_Ea0024G18 Gossypium arboreum 7-10 dpa ... 51 1e-13
emb|AW102472|AW102472 sd88f02.y1 Gm-c1009 Glycine max cDNA clone... 52 1e-13
emb|AW680050|AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S... 50 2e-13
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20 gb|U76555|BRU76555 Brassica rapa zinc-finger protein BcZFP1 (BcA... 52 2e-13
gb|U76554|BRU76554 Brassica rapa zinc-finger protein-1 (BR42) mR... 52 2e-13
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25 gb|BE059872|BE059872 sn38c04.y1 Gm-c1016 Glycine max cDNA clone ... 48 3e-13
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emb|AW030876|AW030876 EST274166 tomato callus, TAMU Lycopersicon... 48 4e-13
emb|AW033257|AW033257 EST276828 tomato callus, TAMU Lycopersicon... 48 4e-13
30 emb|AI771191|AI771191 EST252387 tomato ovary, TAMU Lycopersicon ... 48 4e-13
emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 48 4e-13
emb|AW279005|AW279005 sg04d04.y1 Gm-c1019 Glycine max cDNA clone... 48 6e-13
emb|AW164639|AW164639 se74f02.y1 Gm-c1023 Glycine max cDNA clone... 48 6e-13
emb|AW030858|AW030858 EST274148 tomato callus, TAMU Lycopersicon... 48 1e-12
35 emb|AW278572|AW278572 sf46c03.y1 Gm-c1009 Glycine max cDNA clone... 48 1e-12
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40 emb|AI487287|AI487287 EST245609 tomato ovary, TAMU Lycopersicon ... 46 1e-11
emb|AW037956|AW037956 EST279600 tomato mixed elicitor, BTI Lycop... 46 1e-11
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emb|AB006606|AB006606 Petunia x hybrida mRNA for ZPT4-4, complet... 53 2e-11
emb|AW035987|AW035987 EST282846 tomato callus, TAMU Lycopersicon... 48 2e-11
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emb|AW625323|AW625323 EST319146 tomato radicle, 5 d post-imbibit... 46 6e-11
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50 gb|BE058334|BE058334 sn14g01.y1 Gm-c1016 Glycine max cDNA clone ... 48 3e-10
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emb|AW032112|AW032112 EST275566 tomato callus, TAMU Lycopersicon... 45 5e-10
55 emb|AB006598|AB006598 Petunia x hybrida mRNA for ZPT2-11, comple... 64 7e-10
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emb|AW924443|AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) ... 48 9e-10
emb|AB000452|AB000452 Petunia hybrida mRNA for PETHy;ZPT2-6, com... 64 1e-09
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emb|cab41131.1| (al049658) hypothetical protein [arabidopsis thaliana]

/blast_score 0 /ec_number /family /chip nova /gb_link
<http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al049658|/ncgi>
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 5 (1890 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

10 Searching.....done

	Score	E	(bits)	Value
Sequences producing significant alignments:				
15	emb AW559251 AW559251	EST306087	DSIR Medicago truncatula cDNA cl...	169 3e-49
	emb AW032676 AW032676	EST276235	tomato callus, TAMU Lycopersicon...	181 1e-44
	emb AI778594 AI778594	EST259473	tomato susceptible, Cornell Lyco...	181 1e-44
	emb AW774727 AW774727	EST333878	KV3 Medicago truncatula cDNA clo...	169 6e-41
	emb AV423915 AV423915	AV423915	Lotus japonicus young plants (two...	163 3e-39
20	emb AW559836 AW559836	EST314884	DSIR Medicago truncatula cDNA cl...	131 6e-37
	emb AW349142 AW349142	GM210003B22H5R	Gm-r1021 Glycine max cDNA 3...	107 3e-23
	emb AW560074 AW560074	EST315122	DSIR Medicago truncatula cDNA cl...	84 6e-23
	emb AI855891 AI855891	sc30h08.y1	Gm-cl014 Glycine max cDNA clone...	100 4e-21
25	emb AW560073 AW560073	EST315121	DSIR Medicago truncatula cDNA cl...	77 5e-21
	emb AW225676 AW225676	ST70B12	Pine Triplex shoot tip library Pin...	91 3e-17
	emb AW870069 AW870069	NXNV_123_G03_F	Nsf Xylem Normal wood Verti...	68 3e-17
	emb AW587665 AW587665	ST63B10	Pine Triplex shoot tip library Pin...	87 4e-17
	emb AW011208 AW011208	ST18A05	Pine Triplex shoot tip library Pin...	89 1e-16
30	emb AW438038 AW438038	ST83G07	Pine Triplex shoot tip library Pin...	84 5e-15
	emb AV417662 AV417662	AV417662	Lotus japonicus young plants (two...	54 7e-15
	emb AI920196 AI920196	1726	Pine Lambda Zap Xylem library Pinus t...	54 2e-14
	emb AW981483 AW981483	EST392636	DSIL Medicago truncatula cDNA cl...	70 5e-13
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	emb AW933515 AW933515	EST359274	tomato fruit mature green, TAMU ...	48 3e-12
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	emb AW290408 AW290408	NXNV019H08F	Nsf Xylem Normal wood Vertical...	67 4e-11
	emb AW065112 AW065112	ST39G09	Pine Triplex shoot tip library Pin...	51 5e-11
	emb AW560897 AW560897	EST315945	DSIR Medicago truncatula cDNA cl...	55 7e-11
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50	emb AW888098 AW888098	NXNV_108_F09_F	Nsf Xylem Normal wood Verti...	56 1e-06
	emb AW032082 AW032082	EST275536	tomato callus, TAMU Lycopersicon...	51 2e-06
	emb AW032864 AW032864	EST276423	tomato callus, TAMU Lycopersicon...	46 2e-06
	emb AW736866 AW736866	NXNV_083_H05_F	Nsf Xylem Normal wood Verti...	52 2e-05
	emb AW775153 AW775153	EST334304	KV3 Medicago truncatula cDNA clo...	51 4e-05
55	emb AV411498 AV411498	AV411498	Lotus japonicus young plants (two...	47 5e-04
	emb AW934555 AW934555	EST353447	tomato flower buds 0-3 mm, Corne...	36 9e-04
	emb AW010126 AW010126	ST02C06	Pine Triplex shoot tip library Pin...	46 0.001
	emb AW031593 AW031593	EST275047	tomato callus, TAMU Lycopersicon...	31 0.001
	emb AW746715 AW746715	WS1_55_B02.b1_A002	Water-stressed 1 (WS1) ...	39 0.001
60	emb AW720513 AW720513	LjNEST18e1r	Lotus japonicus nodule library...	46 0.001
	emb AW773847 AW773847	EST332833	KV3 Medicago truncatula cDNA clo...	35 0.004

	emb AZ051219 AZ051219 Gm_UMB001_062_F16R UMN Soybean BAC Library...	38	0.006
	emb AW684275 AW684275 NF014H05NR1F1000 Nodulated root Medicago t...	43	0.007
	emb AW043221 AW043221 ST30G04 Pine TriplEx shoot tip library Pin...	43	0.007
	emb AW687647 AW687647 NF011F10RT1F1090 Developing root Medicago ...	35	0.019
5	emb AW560122 AW560122 EST315170 DSIR Medicago truncatula cDNA cl...	35	0.019
	emb AW687408 AW687408 NF009C08RT1F1065 Developing root Medicago ...	35	0.019
	emb AW980840 AW980840 EST391993 GVN Medicago truncatula cDNA clo...	35	0.019
	emb AW560121 AW560121 EST315169 DSIR Medicago truncatula cDNA cl...	35	0.019
	gb BE123705 BE123705 NXNV_151_H02_F Nsf Xylem Normal wood Vertic...	41	0.032
10	emb AI781175 AI781175 EST262054 tomato susceptible, Cornell Lyco...	40	0.060
	emb AW616497 AW616497 EST322908 L. hirsutum trichome, Cornell Un...	31	0.063
	emb AZ214029 AZ214029 Sheared DNA-77H12.TF Sheared DNA Trypanoso...	40	0.083
	emb AW693887 AW693887 NF070B08ST1F1064 Developing stem Medicago ...	40	0.083
	emb AZ214023 AZ214023 Sheared DNA-77H11.TF Sheared DNA Trypanoso...	38	0.22
15	emb AI487450 AI487450 EST245772 tomato ovary, TAMU Lycopersicon ...	37	0.41
	emb AI780239 AI780239 EST261118 tomato susceptible, Cornell Lyco...	37	0.41
	emb AI485040 AI485040 EST243320 tomato ovary, TAMU Lycopersicon ...	37	0.41
	emb AW618666 AW618666 EST320652 L. pennellii trichome, Cornell U...	28	0.52
	emb AZ213147 AZ213147 Sheared DNA-96E11.TR Sheared DNA Trypanoso...	35	0.53
20	emb AW698283 AW698283 NXNV_071_C12_F Nsf Xylem Normal wood Verti...	33	0.53
	emb AW690496 AW690496 NF035B12ST1F1000 Developing stem Medicago ...	37	0.56
	emb AW693913 AW693913 NF070E02ST1F1017 Developing stem Medicago ...	37	0.56
	emb AW686233 AW686233 NF035E09NR1F1000 Nodulated root Medicago t...	37	0.56
	emb AW257090 AW257090 EST305227 KV2 Medicago truncatula cDNA clo...	37	0.56
25	emb AW573732 AW573732 EST316323 GVN Medicago truncatula cDNA clo...	37	0.56
	emb AW559393 AW559393 EST314441 DSIR Medicago truncatula cDNA cl...	37	0.56
	emb AW329638 AW329638 N200899e rootphos(-) Medicago truncatula c...	36	0.77
	gb BE123796 BE123796 NXNV_156_E06_F Nsf Xylem Normal wood Vertic...	27	0.96
	emb AW257266 AW257266 EST305403 KV2 Medicago truncatula cDNA clo...	36	1.1
30	emb AW317531 AW317531 sg51e11.y1 Gm-c1025 Glycine max cDNA clone...	33	1.3
	emb AC009259 AC009259 Trypanosoma brucei chromosome VI clone RPC...	35	1.4
	emb AW702888 AW702888 TgESTzz91a12.y1 TgRH*-Tachyzoite cDNA Toxo...	35	1.4
	emb AF013339 AF013339 Cucurbita moschata clone 3 internal transc...	35	1.4
	emb AW704685 AW704685 sk39c02.y1 Gm-c1028 Glycine max cDNA clone...	35	1.4
35	emb AQ650196 AQ650196 Sheared DNA-18B3.TF Sheared DNA Trypanosom...	35	1.4
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	emb AW773999 AW773999 EST332985 KV3 Medicago truncatula cDNA clo...	35	2.0
	emb Z38060 SC5610 S.cerevisiae chromosome IX sequence derived fr...	35	2.0
	emb AW033298 AW033298 EST276869 tomato callus, TAMU Lycopersicon...	35	2.0
40	gb L36822 SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas...	35	2.0
	emb AQ952285 AQ952285 Sheared DNA-39M20.TF Sheared DNA Trypanoso...	35	2.0
	emb AI812757 AI812757 18G10 Pine Lambda Zap Xylem library Pinus ...	30	2.3
	emb AI441832 AI441832 sa47h09.y1 Gm-c1004 Glycine max cDNA clone...	35	2.7
	emb AW694970 AW694970 NF082B02ST1F1015 Developing stem Medicago ...	31	3.1
45	emb AW685287 AW685287 NF027B11NR1F1000 Nodulated root Medicago t...	31	3.1
	emb AW932856 AW932856 EST358699 tomato fruit mature green, TAMU ...	34	3.8
	emb AF013320 AF013320 Cucurbita fraterna clone 2 internal transc...	34	3.8
	emb AW719424 AW719424 LjNEST4d11r Lotus japonicus nodule library...	29	4.2
	emb X90770 LEMSREPRG L.esculentum microsatellite repeat DNA region.	34	5.2
50	emb AW133354 AW133354 se17h02.y1 Gm-c1013 Glycine max cDNA clone...	34	5.2
	emb AI967637 AI967637 Ljimpest08-639-b9 Ljirnp Lambda HybriZap ...	34	5.2
	emb AW156054 AW156054 ga24c05.y1 Moss EST library PPU Physcomitr...	34	5.2
	emb AF053127 AF053127 Malus domestica leucine-rich receptor-like...	34	5.2
	emb AB000394 AB000394 Ipomoea purpurea DNA, LTR retrotransposon ...	34	5.2
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	"emb caa63012.1 (x91919) lea76 homologue type1 [arabidopsis thaliana]		
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	from this gene." /blast_score 9.00e-78 /ec_number /family /chip nova		
60	/gb_link http://www3.ncbi.nlm.nih.gov/htbin-		
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<http://www.ncgr.org/cgi-bin/ff?x91919>
(762 letters)

Database: plantfungal
5 661,018 sequences; 426,114,510 total letters

Searching.....done

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10	Sequences producing significant alignments:	(bits)	Value
	emb AJ224519 CAR224519 Cicer arietinum mRNA for LEA protein (clo...	148	6e-35
	emb X15348 BNLEA76 Brassica napus LEA76 mRNA for late embryogene...	135	4e-31
	emb AF117884 AF117884 Glycine max seed maturation protein PM30 (...	88	1e-30
15	emb AJ224518 CAR224518 Cicer arietinum mRNA for LEA protein (clo...	126	2e-28
	emb AW472097 AW472097 si20a05.y1 Gm-c1029 Glycine max cDNA clone...	86	9e-27
	emb AW395529 AW395529 sg72c09.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24
	emb AW507599 AW507599 si53h08.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24
	emb AW318205 AW318205 sg62d04.y1 Gm-c1007 Glycine max cDNA clone...	88	7e-24
20	emb AW568476 AW568476 si59c06.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24
	emb AW567816 AW567816 si66b10.y1 Gm-r1030 Glycine max cDNA clone...	88	7e-24
	emb AW706800 AW706800 sk03e03.y1 Gm-c1023 Glycine max cDNA clone...	88	1e-23
	emb AW509384 AW509384 si22d10.y1 Gm-c1029 Glycine max cDNA clone...	86	2e-23
	emb AW746690 AW746690 WS1_54_F07.g1_A002 Water-stressed 1 (WS1) ...	106	2e-22
25	emb AW096396 AW096396 EST289576 tomato mixed elicitor, BTI Lycop...	103	1e-21
	emb X78205 HVVHVA1 H.vulgare (Himalaya) HVA1 gene.	77	1e-20
	emb X13498 HVABAIP Barley pHVA1 mRNA for an ABA-inducible protein.	77	1e-20
	gb M36000 BLYABA Barley abscisic acid (ABA) mRNA, complete cds.	77	1e-20
	emb AW680076 AW680076 WS1_3_C03.g1_A002 Water-stressed 1 (WS1) S...	100	2e-20
30	emb AW397921 AW397921 sg69h06.y1 Gm-c1007 Glycine max cDNA clone...	57	3e-20
	emb AW747095 AW747095 WS1_65_C09.g1_A002 Water-stressed 1 (WS1) ...	95	4e-19
	gb BE034388 BE034388 MH04B06 MH Mesembryanthemum crystallinum cD...	73	1e-18
	emb X13201 GHLEA7 Cotton set 5A Lea gene for seed protein D-7.	61	1e-18
	emb X15086 GHLEA29R Cotton set 5A Lea mRNA for seed protein D-29.	61	1e-18
35	emb X56882 TA3LEA Wheat mRNA for a group 3 late embryogenesis ab...	75	1e-18
	emb AW746385 AW746385 WS1_49_G03.g1_A002 Water-stressed 1 (WS1) ...	93	2e-18
	emb AW680063 AW680063 WS1_3_B02.g1_A002 Water-stressed 1 (WS1) S...	91	1e-17
	emb AF255052 AF255052 Triticum aestivum cold-responsive LEA/RAB-...	85	6e-17
	emb AF139915 AF139915 Triticum aestivum ABA-inducible protein WR...	85	6e-17
40	emb AW164114 AW164114 Ljirmp20-575-b9 Ljirmp Lambda HybriZap ...	88	7e-17
	emb Y10779 SSY10779 S.stapfianus pSD.42 mRNA.	86	3e-16
	emb AW569002 AW569002 si62c03.y1 Gm-r1030 Glycine max cDNA clone...	62	4e-16
	emb AW508284 AW508284 si52b01.y1 Gm-r1030 Glycine max cDNA clone...	62	4e-16
	gb BE034389 BE034389 MH04B07 MH Mesembryanthemum crystallinum cD...	72	7e-16
45	emb AW681055 AW681055 WS1_8_F06.b1_A002 Water-stressed 1 (WS1) S...	75	7e-13
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	emb AW678335 AW678335 WS1_14_F02.g1_A002 Water-stressed 1 (WS1) ...	75	7e-13
	emb AW678291 AW678291 WS1_14_D10.g1_A002 Water-stressed 1 (WS1) ...	74	1e-12
	emb AW679525 AW679525 WS1_29_F04.g1_A002 Water-stressed 1 (WS1) ...	74	1e-12
50	emb Z18891 BPBP8GEN Betula pendula BP8 gene.	74	1e-12
	emb AW432699 AW432699 sh85b12.y1 Gm-c1016 Glycine max cDNA clone...	74	1e-12
	emb AW678194 AW678194 WS1_13_E06.g1_A002 Water-stressed 1 (WS1) ...	72	5e-12
	emb AW459847 AW459847 sh96a04.y1 Gm-c1016 Glycine max cDNA clone...	70	2e-11
	emb X13203 GHLEA29 Cotton set 5A Lea gene for seed protein D-29.	62	5e-09
55	emb Z49713 PMDORORF6 P.menziesii mRNA (open reading frame) (DF77B).	59	3e-08
	emb Z49712 PMDORORF5 P.menziesii mRNA (open reading frame) (DF77A).	59	3e-08
	emb AJ225460 AJ225460 AJ225460 Abscisic acid-treated protonemata...	59	5e-08
	emb X89041 RFLASPPRO R.fluitans mRNA for landform specific protein.	58	6e-08
	gb M80664 SOYLEAB Soybean late embryogenesis abundant (LEA) prot...	58	9e-08
60	emb AF166485 AF166485 Glycine max maturation protein pPM32 (PM32...	57	2e-07
	gb M19388 COTSPG G.hirsutum (cotton) storage protein (late embry...	57	2e-07

- gb|U47096|DCU47096 *Daucus carota* LEA protein mRNA, somatic embryo... 57 2e-07
 gb|U02966|GMU02966 *Glycine max* Shi-shi 51 kDa seed maturation pr... 56 3e-07
 emb|Z49715|PMDORORF8 *P.menziesii* mRNA (open reading frame) (DF77D). 56 4e-07
 gb|L47932|L47932 BNAF1873 Mustard flower buds *Brassica rapa* cDNA... 56 4e-07
 5 emb|Z49714|PMDORORF7 *P.menziesii* mRNA (open reading frame) (DF77C). 55 8e-07
 emb|AW746616|AW746616 WS1_54_F07.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
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 emb|AW924712|AW924712 WS1_71_A12.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 10 emb|AW679366|AW679366 WS1_24_E04.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW746766|AW746766 WS1_55_D06.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AW678206|AW678206 WS1_14_D10.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
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 15 emb|AW679354|AW679354 WS1_24_G08.b1_A002 Water-stressed 1 (WS1) ... 52 4e-06
 emb|AJ305014|AJ305014 EST00119 mRNP Lambda ZapII Express Library... 51 8e-06
 emb|AF009953|AF009953 *Glycine max* 35 kDa seed maturation protein... 51 8e-06
 emb|Z22872|GMLEAPROA *G.max* Lea protein mRNA, complete CDS. 51 1e-05
 emb|X92955|BOPC15 *B.oleracea* mRNA for pollen coat protein. 51 1e-05
 20 emb|AW680922|AW680922 WS1_8_F06.g1_A002 Water-stressed 1 (WS1) S... 51 1e-05
 emb|AW678045|AW678045 WS1_13_A03.b1_A002 Water-stressed 1 (WS1) ... 50 2e-05
 gb|L33614|L33614 BNAESTF503 Mustard flower buds *Brassica rapa* cD... 50 2e-05
 emb|X79466|HVES2A *H.vulgare* (Dbg 567) ES2A mRNA. 39 4e-05
 emb|AJ000100|HVAJ100 *Hordeum vulgare* mRNA for cold-regulated pro... 39 4e-05
 25 emb|AJ130888|FSY130888 *Fagus sylvatica* mRNA for ABA-inducible pr... 49 4e-05
 emb|AW703962|AW703962 sk14e10.y1 *Gm-c1023* *Glycine max* cDNA clone... 49 5e-05
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 emb|AW679440|AW679440 WS1_24_C05.g1_A002 Water-stressed 1 (WS1) ... 48 1e-04
 gb|L46517|L46517 BNAF1718 Mustard flower buds *Brassica rapa* cDNA... 47 1e-04
 30 emb|AW185164|AW185164 se87g01.y1 *Gm-c1023* *Glycine max* cDNA clone... 38 2e-04
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 35 emb|AW679463|AW679463 WS1_24_E04.g1_A002 Water-stressed 1 (WS1) ... 44 0.002
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 emb|AF255053|AF255053 *Triticum aestivum* cold-responsive LEA/RAB-... 39 0.004
 emb|AW680686|AW680686 WS1_6_H05.g1_A002 Water-stressed 1 (WS1) S... 42 0.004
 emb|AW747334|AW747334 WS1_67_C01.g1_A002 Water-stressed 1 (WS1) ... 42 0.004
 40 emb|AW747282|AW747282 WS1_67_C01.b1_A002 Water-stressed 1 (WS1) ... 42 0.004
 emb|AW983308|AW983308 HVSMEg0010C18f *Hordeum vulgare* pre-anthesi... 35 0.005
 emb|AW679087|AW679087 WS1_22_A07.b1_A002 Water-stressed 1 (WS1) ... 42 0.006
 emb|AW981621|AW981621 PC14G04 *Pine* TriplEx pollen cone library P... 42 0.006
 emb|AJ225515|AJ225515 AJ225515 Absciscic acid-treated protonemata... 37 0.017
 45 emb|AW754577|AW754577 PC03H06 *Pine* TriplEx pollen cone library P... 40 0.021
 emb|AW458460|AW458460 sh09e04.y1 *Gm-c1016* *Glycine max* cDNA clone... 39 0.040
 emb|AW981729|AW981729 PC18A04 *Pine* TriplEx pollen cone library P... 39 0.055
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 50 emb|AW679089|AW679089 WS1_22_A07.g1_A002 Water-stressed 1 (WS1) ... 38 0.10

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 55 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|z99708|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|z99708|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|z99708|/ncgi)
<http://www.ncgr.org/cgi-bin/ff/z99708>
 (885 letters)

60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	emb AI486681 AI486681 EST245003 tomato ovary, TAMU Lycopersicon ...	414	e-115
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10	emb AW776370 AW776370 EST335435 DSIL Medicago truncatula cDNA cl...	316	1e-85
	emb AW441466 AW441466 EST310862 tomato fruit red ripe, TAMU Lyco...	311	4e-84
	emb AW775237 AW775237 EST331959 GVN Medicago truncatula cDNA clo...	278	4e-74
	emb AW564397 AW564397 LG1_292_F08.b1_A002 Light Grown 1 (LG1) So...	275	2e-73
	emb AW648604 AW648604 EST327154 tomato germinating seedlings, TA...	275	3e-73
15	emb AW309188 AW309188 sg05d07.y1 Gm-c1019 Glycine max cDNA clone...	274	8e-73
	emb AW329561 AW329561 N200812e rootphos(-) Medicago truncatula c...	204	3e-69
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	emb AI775112 AI775112 EST256212 tomato resistant, Cornell Lycope...	248	4e-65
	emb AI898201 AI898201 EST267644 tomato ovary, TAMU Lycopersicon ...	118	1e-51
20	emb AW011189 AW011189 ST17G07 Pine TriplEx shoot tip library Pin...	172	4e-48
	emb AW622515 AW622515 EST313315 tomato root during/after fruit s...	189	3e-47
	emb AW933718 AW933718 EST359561 tomato fruit mature green, TAMU ...	188	7e-47
	emb AI897919 AI897919 EST267362 tomato ovary, TAMU Lycopersicon ...	102	6e-45
	emb AW623431 AW623431 EST321376 tomato flower buds 3-8 mm, Corne...	179	2e-44
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	emb AW616498 AW616498 EST322909 L. hirsutum trichome, Cornell Un...	174	1e-42
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30	emb AW257178 AW257178 EST305315 KV2 Medicago truncatula cDNA clo...	144	7e-34
	emb AW699388 AW699388 gb07g07.y1 Moss EST library PPN Physcomitr...	139	2e-32
	emb AV421449 AV421449 AV421449 Lotus japonicus young plants (two...	132	4e-30
	emb AW626193 AW626193 EST320100 tomato radicle, 5 d post-imbibit...	132	5e-30
	emb AL109608 SPCC23B6 S.pombe chromosome III cosmid c23B6.	99	3e-28
35	emb AV426790 AV426790 AV426790 Lotus japonicus young plants (two...	123	2e-27
	emb AI778049 AI778049 EST258928 tomato susceptible, Cornell Lyco...	116	2e-25
	emb AW626687 AW626687 NXNV068E07 Nsf Xylem Normal wood Vertical ...	114	1e-24
	emb AW929355 AW929355 EST338143 tomato flower buds 8 mm to pre-a...	106	2e-22
	emb AW719259 AW719259 LjNEST1h10r Lotus japonicus nodule library...	105	4e-22
40	emb Z69381 SCCXIV39K S.cerevisiae 38,855 bp segment of chromosom...	60	1e-17
	emb Z71507 SCYNL231C S.cerevisiae chromosome XIV reading frame O...	60	1e-17
	emb AB001995 AB001995 Schizosaccharomyces pombe gene for Tellp, ...	82	6e-17
	emb AI442227 AI442227 sa49c11.y1 Gm-c1004 Glycine max cDNA clone...	85	8e-16
	emb AI725484 AI725484 BNLGHi12268 Six-day Cotton fiber Gossypium...	54	2e-15
45	emb X92494 SCBNI1 S.cerevisiae BNI1, N0647, APL1, N0665, N0670, ...	46	5e-13
	emb Z71540 SCYNL264C S.cerevisiae chromosome XIV reading frame O...	46	5e-13
	emb AI731920 AI731920 BNLGHi11386 Six-day Cotton fiber Gossypium...	44	2e-12
	emb AI729569 AI729569 BNLGHi13678 Six-day Cotton fiber Gossypium...	44	6e-11
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50	emb AI725979 AI725979 BNLGHi13788 Six-day Cotton fiber Gossypium...	45	6e-10
	emb AJ273110 AJ273110 AJ273110 Metarhizium anisopliae ARSEF 2575...	52	6e-09
	emb AQ655616 AQ655616 Sheared DNA-2J3.TR Sheared DNA Trypanosoma...	61	1e-08
	emb AQ501933 AQ501933 V11E10 mTn-3xHA/lacZ Insertion Library Sac...	60	2e-08
	emb X97320 CGSEC14GN C.glabrata SEC14 gene.	55	7e-08
55	emb Z49259 SC9582X S.cerevisiae chromosome XIII cosmid 9582.	55	9e-08
	emb X15483 SCSEC14G Yeast SEC14 gene for cytosolic factor.	55	9e-08
	gb BE053932 BE053932 GA_Ea0031D10f Gossypium arboreum 7-10 dpa ...	46	6e-07
	emb AQ023632 AQ023632 CpGR0082A Cryptosporidium parvum genomic r...	55	7e-07
	emb AQ449556 AQ449556 500001H03.x1 CplOWAM13mp18gDNA1 Cryptospor...	55	7e-07
60	emb Z28091 SCYKL091C S.cerevisiae chromosome XI reading frame OR...	50	8e-07
	emb A86344 A86344 Sequence 1003 from Patent EP0866129.	54	1e-06

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 emb|AL114465|CNS01BNT Botrytis cinerea strain T4 cDNA library un... 51 2e-06
 gb|C96579|C96579 C96579 Marchantia polymorpha immature sex organ... 42 4e-06
 emb|AQ855615|AQ855615 CpG1709A CpIOWAgDNA1 Cryptosporidium parvu... 52 5e-06
 5 gb|L20972|YSJSEC14A Yarrowia lipolytica phosphatidylinositol-pho... 51 9e-06
 emb|X81937|CASEC14 C.albicans SEC14 gene. 49 3e-05
 gb|U61975|CAU61975 Candida albicans phosphatidylinositol/phospha... 49 3e-05
 gb|BE123583|BE123583 NXNV_145_C08_F Nsf Xylem Normal wood Vertic... 49 4e-05
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 10 emb|AW738979|AW738979 gb23b03.y1 Moss EST library PPN Physcomitr... 49 6e-05
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 emb|AI727743|AI727743 BNLGHi8966 Six-day Cotton fiber Gossypium ... 45 8e-04
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 15 emb|AI729716|AI729716 BNLGHi14012 Six-day Cotton fiber Gossypium... 45 0.001
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 emb|AI731713|AI731713 BNLGHi10565 Six-day Cotton fiber Gossypium... 44 0.001
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 45 emb|AW925728|AW925728 HVSMEg0005F19 Hordeum vulgare pre-anthesis... 40 0.026

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- 55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- 60 Score E
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 5 emb|AW203623|AW203623 sf36d02.y1 Gm-c1028 Glycine max cDNA clone... 205 2e-60
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 emb|AW720506|AW720506 LjNEST18d11r Lotus japonicus nodule librar... 142 3e-41
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 10 emb|AI165948|AI165948 B004p66u Hybrid aspen plasmid library Popu... 62 2e-29
 emb|AW508607|AW508607 si34b12.y1 Gm-r1030 Glycine max cDNA clone... 78 3e-27
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 emb|AL353821|NC68B2 Neurospora crassa DNA linkage group V Cosmid... 34 7.3
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Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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15	gb BE020862 BE020862 sm53c05.y1 Gm-c1028 Glycine max cDNA clone ...	50	2e-07
	emb AI777049 AI777049 EST252016 tomato callus, TAMU Lycopersicon...	51	2e-07
	emb AW032807 AW032807 EST276366 tomato callus, TAMU Lycopersicon...	51	2e-07
	emb AI776903 AI776903 EST258003 tomato resistant, Cornell Lycop...	47	3e-07
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 (1899 letters)

- 60 Database: plantfungal
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30	gb L38454 PFAORFAE	Plasmodium falciparum	(clone pS31H) ORF mRNA,...	27	1.8
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	emb AQ906953 AQ906953	GSSTc02997	Trypanosome cruzi random genomi...	35	2.5
	emb AL116053 CNS01CVX	Botrytis cinerea	strain T4 cDNA library un...	34	2.6
40	gb BE052627 BE052627	GA_Ea0032J13f	Gossypium arboreum 7-10 dpa ...	34	2.6
	emb AI668074 AI668074	TENG0996	T. Cruzi epimastigote normalised ...	34	3.5
	emb AF242312 AF242312	Euphorbia esula	cyclophilin mRNA, partial ...	34	3.5
	emb AC004157 AC004157	Plasmodium falciparum	chromosome 12 clone ...	34	3.6
	emb AA550286 AA550286	1415m3 gmbPpHB3.1	G. Roman Reddy Plasmodi...	34	3.6
45	emb Z49390 SCYJL115W	S.cerevisiae	chromosome X reading frame ORF...	34	3.6
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	emb AQ902283 AQ902283	LMAJFV1_lm47f04.x1	Leishmania major FV1 ra...	34	3.6
	emb AQ845786 AQ845786	LMAJFV1_lm25h11.x1	Leishmania major FV1 ra...	34	3.6
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	emb AW703668 AW703668	sk11h05.y1	Gm-c1023 Glycine max cDNA clone...	34	4.8
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 5 gb|L06323|THEGLUMEMP Theileria parva glutamine rich membrane pro... 33 6.5
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 10 gb|U75347|ENU75347 Emericella nidulans fatty acid synthase, alph... 33 6.9
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 15 emb|AA519692|AA519692 TgESTzz27f06.r1 TgME49 invivo Bradyzoite c... 33 8.9
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 20 emb|Z29537|NTPROTINH N.tabacum (Samsun NN) gene for proteinase i... 32 9.4
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 25 emb|AF102653|AF102653 Podranea ricasoliana ribulose 1,5-bisphosp... 32 9.4
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 35 (2196 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments:				
45	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	375	e-120	
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	332	e-105	
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	339	e-105	
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	330	e-105	
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	333	e-104	
50	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	332	e-104	
	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	328	e-103	
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	329	e-100	
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	321	1e-99	
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	316	2e-98	
55	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	323	2e-98	
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	324	4e-98	
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	195	4e-97	
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	312	4e-95	
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23BoI, parti...	314	4e-95	
60	emb AW620957 AW620957 sj98a07.y1 Gm-c1023 Glycine max cDNA clone...	285	3e-94	
	emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR...	306	6e-94	

- gb|U20948|ITU20948 Ipomoea trifida receptor protein kinase (IRK1... 221 1e-93
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 gb|BE034855|BE034855 ML05C11 ML Mesembryanthemum crystallinum cD... 289 2e-90
 5 emb|AB032474|AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc... 275 7e-90
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 dbj|D38563|BOLRPKA Brassica campestris mRNA for receptor protein... 272 6e-88
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 10 emb|AJ245480|BNA245480 Brassica napus slg gene for S-locus glyco... 122 2e-82
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 15 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 127 6e-73
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 20 emb|AI486193|AI486193 EST244514 tomato ovary, TAMU Lycopersicon ... 182 4e-68
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 30 emb|AW203661|AW203661 sf36g06.y1 Gm-c1028 Glycine max cDNA clone... 208 2e-63
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 emb|AW220676|AW220676 EST297145 tomato fruit mature green, TAMU ... 231 2e-59
 35 emb|AW220675|AW220675 EST297144 tomato fruit mature green, TAMU ... 231 2e-59
 emb|AI486584|AI486584 EST244905 tomato ovary, TAMU Lycopersicon ... 171 3e-59
 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 136 1e-58
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 40 emb|AW666141|AW666141 sk32f11.y1 Gm-c1028 Glycine max cDNA clone... 176 7e-56
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 45 emb|AI822355|AI822355 L0-804T3 Ice plant Lambda Uni-Zap XR expre... 116 4e-53
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- emb|AI822347|AI822347 L0-796T3 Ice plant Lambda Uni-Zap XR expre... 116 5e-47
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 20 emb|AW687052|AW687052 NF005E02RT1F1017 Developing root Medicago ... 177 2e-43
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 30 http://www.ncgr.org/cgi-bin/ff?ac002392
 (2631 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| | emb AW774582 AW774582 EST333733 KV3 Medicago truncatula cDNA clo... | 204 | 5e-74 |
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| | emb Z73295 CRPK1 C.roseus mRNA for receptor-like protein kinase. | 146 | 5e-56 |
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| | gb U59317 LPU59317 Lycopersicon pimpinellifolium serine/threonin... | 108 | 7e-54 |
| | gb U13923 LEU13923 Lycopersicon pimpinellifolium serine/threonin... | 108 | 7e-54 |
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| | gb BE053916 BE053916 GA_Ea0031D03f Gossypium arboreum 7-10 dpa ... | 209 | 8e-53 |
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 5 emb|AF053127|AF053127 *Malus domestica* leucine-rich receptor-like... 130 4e-46
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 25 emb|AF121449|AF121449 *Capsicum annuum* protein kinase homolog C15... 99 1e-42
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 emb|AB032473|AB032473 *Brassica oleracea* SRK18 mRNA for S18 S-loc... 115 6e-42
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 emb|AB013720|AB013720 *Brassica oleracea* mRNA for SRK23Bol, parti... 111 3e-40
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 45 emb|AW615998|AW615998 EST325448 tomato flower buds 0-3 mm, Corne... 117 3e-40
 emb|AW218745|AW218745 EST301225 tomato root during/after fruit s... 120 5e-40
 emb|AI731501|AI731501 BNLGHi9983 Six-day Cotton fiber *Gossypium* ... 98 6e-40
 gb|M76647|BNASKR6A *Brassica oleracea* receptor protein kinase (SK... 108 9e-40
 emb|AF121448|AF121448 *Capsicum annuum* protein kinase homolog C11... 95 2e-39
 50 emb|AI771280|AI771280 EST252296 tomato ovary, TAMU Lycopersicon ... 165 2e-39
 emb|AI486547|AI486547 EST244868 tomato ovary, TAMU Lycopersicon ... 123 2e-39
 emb|AW094468|AW094468 EST287648 tomato mixed elicitor, BTI Lycop... 156 2e-39
 emb|AB008191|AB008191 *Brassica rapa* mRNA for SRK29, complete cds. 108 3e-39
 emb|AI771841|AI771841 EST252941 tomato ovary, TAMU Lycopersicon ... 164 4e-39
 55 emb|AI485090|AI485090 EST243394 tomato ovary, TAMU Lycopersicon ... 164 4e-39
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 emb|AF078082|AF078082 *Phaseolus vulgaris* receptor-like protein k... 111 4e-39
 emb|Y18260|BOY18260 *Brassica oleracea* mRNA for SRK15 protein, pa... 107 6e-39
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 60 emb|AW267961|AW267961 EST306183 DSIR *Medicago truncatula* cDNA cl... 94 7e-39
 emb|Y18259|BOY18259 *Brassica oleracea* mRNA for SRK5 protein, par... 107 1e-38

- emb|AI486766|AI486766 EST245088 tomato ovary, TAMU Lycopersicon ... 89 1e-38
 emb|AI485862|AI485862 EST244183 tomato ovary, TAMU Lycopersicon ... 162 1e-38
 emb|AI487456|AI487456 EST245778 tomato ovary, TAMU Lycopersicon ... 123 2e-38
 gb|BE060160|BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis... 75 2e-38
 5 emb|X98520|BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2. 107 3e-38
 emb|AF142596|AF142596 Nicotiana tabacum LRR receptor-like protei... 78 3e-38
 emb|AW617255|AW617255 EST323666 L. hirsutum trichome, Cornell Un... 148 4e-38
 gb|U51741|ITU51741 Ipomoea trifida receptor protein kinase 2 (IR... 71 4e-38
 emb|AW774790|AW774790 EST333941 KV3 Medicago truncatula cDNA clo... 95 5e-38
 10 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 105 5e-38
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 gb|BE020963|BE020963 sm54a06.y1 Gm-c1028 Glycine max cDNA clone ... 125 3e-37
 emb|AI730535|AI730535 BNLGHI7007 Six-day Cotton fiber Gossypium ... 73 5e-37
 15 emb|AF085167|AF085167 Hordeum vulgare receptor-like kinase ARK1A... 81 7e-37
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 emb|AW650851|AW650851 EST329305 tomato germinating seedlings, TA... 126 2e-36

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25 Database: plantfungal
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 Sequences producing significant alignments: (bits) Value
- emb|AF135130|AF135130 Arabis holboellii from Denmark class I chi... 438 0.0
 emb|X16939|NTECHITR Nicotiana tabacum mRNA for endochitinase (EC... 491 e-158
 35 gb|M15173|TOBECH Tobacco (N.tabacum) endochitinase mRNA, partial... 494 e-158
 gb|S44869|S44869 basic chitinase [Nicotiana tabacum=tobacco, cv ... 490 e-158
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 493 e-158
 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 541 e-153
 emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 541 e-153
 40 emb|Y10373|MTCHITIN1 M.truncatula mRNA for chitinase. 482 e-151
 gb|U02606|STU02606 Solanum tuberosum chitinase (chtB2) mRNA, par... 442 e-150
 gb|U02605|STU02605 Solanum tuberosum chitinase (chtB1) mRNA, par... 443 e-150
 emb|Z15140|LECHI9 L.esculentum mRNA for chitinase. 442 e-149
 gb|U02607|STU02607 Solanum tuberosum chitinase (chtB3) mRNA, par... 440 e-148
 45 emb|Z78202|PACHI1 Persea americana mRNA for endochitinase. 467 e-148
 gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 310 e-146
 gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 310 e-146
 gb|L37876|PEACHI2I Pisum sativum chitinase class I (chi2) gene, ... 309 e-146
 emb|AF000966|AF000966 Poa pratensis chitinase (Chi2) gene, compl... 472 e-146
 50 emb|Z54234|VVCHIT1MR V.vinifera mRNA for chitinase. 463 e-146
 gb|M13968|PHVCHM P.vulgaris chitinase mRNA, complete cds. 286 e-145
 emb|AJ012821|CAR012821 Cicer arietinum mRNA for class I chitinase. 305 e-144
 emb|X76041|TACHIG T.aestivum (Chinese spring) chi gene for endoc... 466 e-144
 gb|U78888|GHU78888 Gossypium hirsutum class I endochitinase mRNA... 332 e-144
 55 emb|AF034566|AF034566 Gossypium hirsutum class I chitinase mRNA,... 333 e-144
 emb|AF000965|AF000965 Poa pratensis chitinase (Chi3) pseudogene ... 469 e-144
 emb|X14133|STENCHIT Potato mRNA fragment for endochitinase (EC 3... 435 e-143
 gb|S43926|S43926 CH5B=chitinase [Phaseolus vulgaris=beans, cv Sa... 284 e-143
 emb|X88800|VURNACHI1 V.unguiculata mRNA for chitinase clase 1 (p... 296 e-143
 60 gb|U02287|HVU02287 Hordeum vulgare cultivar NK1558 chitinase gen... 459 e-141
 gb|M94106|ALCCHINTIA Allium sativum chitinase mRNA, 3' end. 455 e-140

- gb|M94105|ALCCHITIN *Allium sativum* chitinase mRNA, 3' end. 448 e-140
 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 286 e-139
 emb|AF000964|AF000964 *Poa pratensis* chitinase (Chi1) gene, compl... 408 e-139
 gb|L34211|BLYCHI33A *Hordeum vulgare* chitinase (CHI33) gene, comp... 448 e-138
 5 gb|U02608|STU02608 *Solanum tuberosum* chitinase (chtB4) mRNA, par... 408 e-137
 emb|X63899|PSCHITIN *P. sativum* mRNA for chitinase. 270 e-135
 emb|AF061805|AF061805 *Elaeagnus umbellata* acidic chitinase mRNA,... 430 e-134
 emb|AF202731|AF202731 *Glycine max* endochitinase homolog (Chn1) m... 273 e-134
 gb|L34210|BLYCHI26A *Hordeum vulgare* chitinase (CHI26) gene, comp... 475 e-133
 10 emb|A37990|A37990 Sequence 9 from Patent EP0616035. 475 e-133
 gb|M62904|BLYCHI H. vulgare L. 26kD chitinase mRNA, complete cds. 475 e-133
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 gb|U30324|TCU30324 *Theobroma cacao* class I chitinase gene, compl... 238 e-131
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 15 gb|U48687|CSU48687 *Castanea sativa* endochitinase mRNA, complete ... 259 e-130
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 20 emb|AF135152|AF135152 *Arabis parishii* country USA class I chitin... 455 e-127
 emb|AF135141|AF135141 *Arabis gunnisoniana* class I chitinase gene... 455 e-127
 emb|AF135135|AF135135 *Arabis drummondii* class I chitinase gene, ... 455 e-127
 emb|AF135143|AF135143 *Arabis lemmonii* country USA class I chitin... 452 e-126
 emb|X67693|STMREN *S. tuberosum* mRNA for endochitinase. 452 e-126
 25 emb|AF135132|AF135132 *Arabis gunnisoniana* from USA class I chiti... 452 e-126
 emb|AF135144|AF135144 *Arabis lemmonii* country USA class I chitin... 451 e-126
 emb|AF135140|AF135140 *Arabis glabra* country USA class I chitinas... 449 e-125
 gb|U30465|LEU30465 *Lycopersicon esculentum* class II chitinase (C... 447 e-125
 emb|AF135153|AF135153 *Arabis parishii* country USA class I chitin... 445 e-124
 30 gb|L22032|ULMCHITIN *Ulmus americana* chitinase (pHS2) mRNA, compl... 295 e-124
 emb|AF135148|AF135148 *Arabis lyallii* class I chitinase gene, par... 444 e-124
 emb|AF135151|AF135151 *Arabis microphylla* country USA class I chi... 444 e-124
 emb|AF135150|AF135150 *Arabis microphylla* country USA class I chi... 443 e-124
 emb|AF135147|AF135147 *Arabis lignifera* country USA class I chiti... 443 e-124
 35 emb|AF135136|AF135136 *Arabis fecunda* country USA class I chitina... 443 e-124
 emb|AF135145|AF135145 *Arabis lignifera* country USA class I chiti... 443 e-123
 emb|AF135146|AF135146 *Arabis lignifera* country USA class I chiti... 441 e-123
 emb|AF135149|AF135149 *Arabis microphylla* class I chitinase gene,... 441 e-123
 emb|AF043247|AF043247 *Solanum tuberosum* class I chitinase (ChtC1... 431 e-122
 40 emb|AF043248|AF043248 *Solanum tuberosum* class I chitinase (ChtC2... 431 e-122
 emb|Z15138|LECHI14 *L. esculentum* mRNA for chitinase (partial). 439 e-122
 emb|AF135142|AF135142 *Halimolobos perplexa* var. *perplexa* class I... 435 e-121
 emb|AF135134|AF135134 *Arabis blepharophylla* class I chitinase ge... 434 e-121
 gb|U01660|U01660 *Populus trichocarpa* x *Populus deltoides* acidic ... 207 e-121
 45 emb|AF135138|AF135138 *Arabis glabra* country USA class I chitinas... 431 e-120
 emb|AF135133|AF135133 *Arabis blepharophylla* country USA class I ... 423 e-118
 gb|M95835|BNACH25A *Brassica napus* (clone BnCh25) endochitinase g... 422 e-117
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 emb|AF082713|AF082713 AF082713 *Capsicum annuum* leaf mRNA Capsicu... 364 e-106
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 55 emb|AF141373|AF141373 *Petroselinum crispum* chitinase precursor (... 237 e-104
 emb|Z70032|CSACHIT2 *C. sinensis* mRNA for class II acidic chitinase. 197 e-104
 emb|AW030745|AW030745 EST274000 tomato callus, TAMU *Lycopersicon*... 360 e-104
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 60 emb|AW216454|AW216454 EST295084 tomato callus, TAMU *Lycopersicon*... 373 e-102
 emb|AW267781|AW267781 EST305909 DSIR *Medicago truncatula* cDNA cl... 316 e-102

emb|AW033757|AW033757 EST277328 tomato callus, TAMU Lycopersicon... 285 e-101
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 5 emb|AW031102|AW031102 EST274409 tomato callus, TAMU Lycopersicon... 275 1e-98
 emb|X15349|HVENDCHT Barley (H.vulgare) mRNA for endochitinase. 359 2e-98
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 emb|Z15139|LECHI17 L.esculentum mRNA for chitinase. 242 2e-96
 10 emb|AW032161|AW032161 EST275615 tomato callus, TAMU Lycopersicon... 334 2e-96
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 (1881 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters
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	gb U79958 PSU79958	Pisum sativum BP-80 vacuolar sorting receptor...	810 0.0
	emb AB006809 AB006809	Cucurbita sp. mRNA for PV72, complete cds. .	780 0.0
	emb AW267745 AW267745	EST305873 DSIR Medicago truncatula cDNA cl...	453 e-126
	emb AW931583 AW931583	EST357426 tomato fruit mature green, TAMU ...	308 e-112
30	emb AW309187 AW309187	sg05d06.y1 Gm-cl019 Glycine max cDNA clone...	405 e-112
	gb BE054150 BE054150	GA_Ea0034H17f Gossypium arboreum 7-10 dpa ...	398 e-110
	emb AW622833 AW622833	EST306903 tomato flower buds 3-8 mm, Corne...	387 e-106
	emb AW689392 AW689392	NF018F12ST1F1000 Developing stem Medicago ...	371 e-102
	emb AW737948 AW737948	EST339375 tomato flower buds, anthesis, Co...	342 3e-94
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	emb AW932529 AW932529	EST358372 tomato fruit mature green, TAMU ...	326 3e-88
	emb AW615949 AW615949	EST325315 tomato flower buds 0-3 mm, Corne...	216 1e-87
	emb AI728635 AI728635	BNLGH11276 Six-day Cotton fiber Gossypium...	281 8e-84
	emb AI782787 AI782787	EST263666 tomato susceptible, Cornell Lyco...	307 2e-82
40	emb AI443067 AI443067	sa47a01.y1 Gm-cl004 Glycine max cDNA clone...	305 6e-82
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	emb AI727826 AI727826	BNLGH1915 Six-day Cotton fiber Gossypium ...	280 1e-77
	emb AI484571 AI484571	EST242801 tomato ovary, TAMU Lycopersicon ...	284 1e-75
	emb AW685785 AW685785	NF030C07NR1F1000 Nodulated root Medicago t...	166 1e-71
45	emb AV406766 AV406766	AV406766 Lotus japonicus young plants (two...	260 2e-68
	emb AW509740 AW509740	ga63h11.y1 Moss EST library PPU Physcomitr...	232 1e-65
	emb AV428420 AV428420	AV428420 Lotus japonicus young plants (two...	249 4e-65
	emb AW695542 AW695542	NF096C05ST1F1037 Developing stem Medicago ...	124 1e-58
	emb AW289687 AW289687	NXNV004E04F Nsf Xylem Normal wood Vertical...	226 4e-58
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	emb AW309191 AW309191	sg05d10.y1 Gm-cl019 Glycine max cDNA clone...	171 3e-52
	emb AW096632 AW096632	EST289812 tomato mixed elicitor, BTI Lycop...	165 7e-52
	emb AW568619 AW568619	si60a11.y1 Gm-r1030 Glycine max cDNA clone...	205 1e-51
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	emb AI162330 AI162330 A016P01U Hybrid aspen plasmid library Popu...	131	2e-39
	emb AI161766 AI161766 A006P54U Hybrid aspen plasmid library Popu...	93	3e-38
5	emb AW737369 AW737369 EST338892 tomato flower buds, anthesis, Co...	149	5e-35
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	emb AW398931 AW398931 EST309431 L. pennellii trichome, Cornell U...	95	2e-34
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	gb L38113 L38113 BNAF0628E Mustard flower buds Brassica rapa cDN...	117	4e-26
	emb AW317388 AW317388 sg48g10.y1 Gm-c1025 Glycine max cDNA clone...	80	1e-25
	emb AW706755 AW706755 sk02f10.y1 Gm-c1023 Glycine max cDNA clone...	118	2e-25
15	emb AA660955 AA660955 00852 MtrHE Medicago truncatula cDNA 5' si...	74	7e-25
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	emb AW348825 AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3...	68	8e-24
	emb AW932524 AW932524 EST358367 tomato fruit mature green, TAMU ...	80	1e-23
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	emb AW037563 AW037563 EST278890 tomato mixed elicitor, BTI Lycop...	79	8e-14
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	emb AW685952 AW685952 NF036G09NR1F1000 Nodulated root Medicago t...	46	2e-11
30	emb AW760128 AW760128 sl58d09.y1 Gm-c1027 Glycine max cDNA clone...	58	1e-10
	emb AW119909 AW119909 sd54d08.y1 Gm-c1016 Glycine max cDNA clone...	66	8e-10
	emb AI794754 AI794754 sb68f11.y1 Gm-c1019 Glycine max cDNA clone...	64	4e-09
	emb AW774852 AW774852 EST334003 KV3 Medicago truncatula cDNA clo...	64	4e-09
	emb AW127457 AW127457 M110648 DSIL Medicago truncatula cDNA clon...	58	3e-07
35	emb AW443352 AW443352 EST308282 tomato mixed elicitor, BTI Lycop...	56	1e-06
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60	emb AQ639257 AQ639257 927P1-10E12.TV 927P1 Trypanosoma brucei ge...	35	1.4
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 emb|AF001525|AF001525 Musa acuminata ripening-associated protein... 35 2.0

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 subterraneum] /blast_score 0 /ec_number /family /chip nova /gb_link
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 (1962 letters)

10

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

15

Score E
 Sequences producing significant alignments: (bits) Value

gb|L11747|POPPALGA Populus tricarpa X Populus deltoides (hybri... 354 0.0
 20 emb|X99997|BFPAL B. finlaysoniana mRNA for phenylalanine ammonia-... 352 0.0
 emb|X58180|MSPAL M. sativa PAL mRNA for phenylalanine ammonia-lyase. 351 0.0
 gb|U43338|CLU43338 Citrus limon phenylalanine ammonia-lyase (pal... 350 0.0
 gb|L36822|SSNPAL Stylosanthes humilis phenylalanine ammonia-lyas... 350 0.0
 emb|AF036948|AF036948 Prunus avium phenylalanine ammonia-lyase (... 349 0.0
 25 emb|AJ250836|CAR250836 Cicer arietinum mRNA for phenylalanine am... 349 0.0
 emb|X17462|PCPAL4 P. crispum RNA for PAL4, phenylalanine ammonia-... 349 0.0
 emb|X81158|PCPAL2 P. crispum mRNA for phenylalanine ammonia-lyase 2. 349 0.0
 emb|X81159|PCPAL3 P. crispum mRNA for phenylalanine ammonia-lyase 3. 348 0.0
 dbj|D83075|D83075 Lithospermum erythrorhizon mRNA for phenylalan... 348 0.0
 30 emb|AF237955|AF237955 Rubus idaeus phenylalanine ammonia-lyase 2... 348 0.0
 emb|AJ002221|DLJ002221 Digitalis lanata mRNA for phenylalanine a... 347 0.0
 gb|M29232|IPBPAL Sweet potato phenylalanine ammonia-lyase mRNA (... 345 0.0
 dbj|D26596|CMEPAL Camellia sinensis mRNA for phenylalanine ammon... 344 0.0
 dbj|D17467|TOBPAL1 Tobacco mRNA for phenylalanine ammonia-lyase,... 344 0.0
 35 emb|X78269|NTPHEAL N. tabacum (Samsun NN) mRNA for phenylalanine ... 343 0.0
 dbj|D83076|D83076 Lithospermum erythrorhizon mRNA for phenylalan... 343 0.0
 dbj|D78640|IPBPALA Ipomoea batatas mRNA for phenylalanine ammoni... 342 0.0
 emb|Y12461|HAPHAMLY Helianthus annuus mRNA for phenylalanine amm... 341 0.0
 emb|AB042520|AB042520 Catharanthus roseus mRNA for phenylalanine... 339 0.0
 40 emb|AF237954|AF237954 Rubus idaeus phenylalanine ammonia-lyase 1... 330 0.0
 dbj|D10001|PEAPAL P. sativum mRNA for phenylalanine ammonia-lyase... 349 0.0
 emb|X63103|STPAL1 S. tuberosum PAL-1 gene for phenylalanine ammon... 353 0.0
 emb|AJ238754|CCL238754 Citrus clementina X Citrus reticulata mRN... 350 0.0
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 45 dbj|D10003|PEAPAL2 P. sativum gene for phenylalanine ammonia-lyas... 349 0.0
 dbj|E04042|E04042 cDNA sequence coding for pea phenylalanine amm... 349 0.0
 emb|AF165998|AF165998 Vigna unguiculata phenylalanine ammonia-ly... 355 0.0
 gb|U16130|PAU16130 Persea americana phenylalanine ammonia lyase ... 331 0.0
 dbj|D30656|POPPALA Populus kitakamiensis gene for phenylalanine ... 356 0.0
 50 gb|M84466|TOBTPA1A Tobacco phenylalanine ammonia-lyase (tpa1) gen... 352 0.0
 emb|AB008200|AB008200 Nicotiana tabacum palB gene for phenylalan... 352 0.0
 dbj|D85850|D85850 Daucus carota gDcPAL1 gene for phenylalanine a... 347 0.0
 emb|X52953|DMPAL1 Glycine max PAL1 gene for phenylalanine ammoni... 355 0.0
 emb|X99705|TAPALGEN1 T. aestivum PAL gene. 342 0.0
 55 gb|M91192|TFRPAL1X Trifolium subterraneum phenylalanine ammonia-... 345 0.0
 gb|M90692|TOMPAL5A Lycopersicon esculentum phenylalanine ammonia... 347 0.0
 emb|AB008199|AB008199 Nicotiana tabacum palA gene for phenylalan... 344 0.0
 emb|Y07654|PCPAL1 P. crispum pal1 gene. 350 0.0
 emb|X16772|PCPAL1EX2 P. crispum PAL-1 gene for phenylalanine ammo... 350 0.0
 60 dbj|D43803|POPPALG4B Populus kitakamiensis gene for phenylalanin... 336 0.0
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- emb|X76130|CMPAL C.melo (cantaloupe) pal mRNA. 318 0.0
 dbj|D30657|POPPALB Populus kitakamiensis gene for phenylalanine ... 333 0.0
 dbj|D43802|POPPALG2BA Populus kitakamiensis gene for phenylalanine... 336 0.0
 emb|AF081215|AF081215 Capsicum chinense phenylalanine ammonia-lyase... 346 0.0
 5 dbj|D10002|PEAPAL1 P.sativum gene for phenylalanine ammonia-lyase... 349 0.0
 emb|Z49147|HVPAL7RM H.vulgare partial PAL mRNA for phenylalanine... 342 0.0
 emb|X63104|STPAL2 S.tuberosum PAL-2 gene for phenylalanine ammon... 353 0.0
 gb|U39792|PTU39792 Pinus taeda phenylalanine ammonia-lyase (lpPA... 311 0.0
 gb|M11939|PHVPAL Phaseolus vulgaris L. phenylalanine ammonia-lyase... 354 0.0
 10 dbj|E04043|E04043 cDNA sequence coding for kidney bean phenylala... 354 0.0
 emb|AB015871|AB015871 Vitis vinifera gene for phenylalanine ammo... 350 0.0
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 emb|Z49146|HVPAL3MR H.vulgare partial PAL mRNA for phenylalanine... 311 0.0
 emb|X75967|VVPAL V.vinifera PAL mRNA for phenylalanine ammonia l... 350 0.0
 15 gb|S46988|S46988 phenylalanine ammonia-lyase [soybeans, mRNA, 14... 344 0.0
 emb|AF206634|AF206634 Prunus persica cultivar Loring phenylalanine... 336 0.0
 emb|AF167487|AF167487 Eucalyptus globulus phenylalanine ammonia ... 334 e-178
 emb|X99725|TAPALGEN2 T.aestivum PAL gene, coding region. 300 e-137
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 20 emb|AW031612|AW031612 EST275066 tomato callus, TAMU Lycopersicon... 327 e-132
 emb|AJ289609|BPE289609 Betula pendula partial pal gene for pheny... 205 e-128
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 emb|AW219303|AW219303 EST301785 tomato root during/after fruit s... 339 e-126
 emb|AW726548|AW726548 GA_Ea0022A01 Gossypium arboreum 7-10 dpa ... 323 e-124
 25 emb|AI166817|AI166817 xylem.est.611 Poplar xylem Lambda ZAPII li... 251 e-117
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 30 emb|AF218453|AF218453 Coffea arabica clone 369.1.6r phenylalanine... 247 e-105
 emb|AW216505|AW216505 EST295219 tomato callus, TAMU Lycopersicon... 209 e-104
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 emb|AW220322|AW220322 EST302805 tomato root during/after fruit s... 255 2e-98
 35 emb|AW734312|AW734312 sk81e07.y1 Gm-c1016 Glycine max cDNA clone... 324 6e-98
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 emb|AI777483|AI777483 EST258362 tomato susceptible, Cornell Lyco... 294 3e-90
 emb|AW621418|AW621418 EST312216 tomato root during/after fruit s... 330 2e-89
 40 emb|AW443181|AW443181 EST308111 tomato mixed elicitor, BTI Lycop... 329 6e-89
 emb|AW781748|AW781748 sl90e11.y1 Gm-c1037 Glycine max cDNA clone... 326 3e-88
 emb|X68126|MSPALMR Malus sp. PAL mRNA for phenylalanine ammonia-... 324 1e-87
 emb|AW760268|AW760268 sl48b08.y1 Gm-c1027 Glycine max cDNA clone... 323 3e-87
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 45 emb|AF218454|AF218454 Coffea arabica clone 430.4 phenylalanine a... 243 6e-85
 emb|AI899698|AI899698 EST269141 tomato susceptible, Cornell Lyco... 314 2e-84
 emb|AW455294|AW455294 EST311832 tomato root during/after fruit s... 313 3e-84
 emb|AW685111|AW685111 NF026A05NR1F1000 Nodulated root Medicago t... 236 6e-84
 50 emb|AW667320|AW667320 GA_Ea0008P06 Gossypium arboreum 7-10 dpa ... 189 2e-83
 gb|BE021354|BE021354 sm57e05.y1 Gm-c1028 Glycine max cDNA clone ... 308 9e-83
 emb|AI772657|AI772657 EST253757 tomato resistant, Cornell Lyco... 299 2e-80
 emb|AI894514|AI894514 EST263957 tomato callus, TAMU Lycopersicon... 294 1e-78
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 60 http://www.ncgr.org/cgi-bin/ff?al022347
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

5 Searching.....done

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Sequences producing significant alignments:				
10	emb AF078082 AF078082 Phaseolus vulgaris receptor-like protein k...	251	1e-65	
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	emb AW031255 AW031255 EST274630 tomato callus, TAMU Lycopersicon...	231	1e-59	
	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	230	2e-59	
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	227	1e-58	
15	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	226	4e-58	
	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	225	7e-58	
	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	225	7e-58	
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	224	1e-57	
	gb BE034855 BE034855 ML05C11 ML Mesembryanthemum crystallinum cD...	186	1e-57	
20	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	222	6e-57	
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	221	8e-57	
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	221	2e-56	
	gb BE057261 BE057261 sm99f12.y1 Gm-c1015 Glycine max cDNA clone ...	220	3e-56	
	emb Y14285 BOY14285 Brassica oleracea mRNA for SFR1 protein.	219	6e-56	
25	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	218	8e-56	
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	216	3e-55	
	gb L08607 BNASRECKIN Brassica napus S-receptor kinase mRNA, comp...	215	5e-55	
	emb AF088885 AF088885 Nicotiana tabacum receptor-like kinase CHR...	213	3e-54	
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23BoI, parti...	211	1e-53	
30	emb Y12531 BOBRLKGEN B.oleraceae gene encoding serine/threonine ...	116	6e-53	
	emb AB032474 AB032474 Brassica oleracea SRK60 mRNA for S60 S-loc...	207	2e-52	
	emb Y14286 BOY14286 Brassica oleracea SFR3 gene, partial.	117	1e-51	
	dbj D38564 BOLRPKB Brassica campestris mRNA for receptor protein...	204	1e-51	
	emb AW736407 AW736407 EST332421 KV3 Medicago truncatula cDNA clo...	198	4e-51	
35	dbj D38563 BOLRPKA Brassica campestris mRNA for receptor protein...	202	7e-51	
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	dbj D30049 BOLSRKA Turnip mRNA for S-receptor kinase SRK9, parti...	196	2e-49	
	emb AW760240 AW760240 sl59g07.y1 Gm-c1027 Glycine max cDNA clone...	196	4e-49	
40	emb AW033458 AW033458 EST277029 tomato callus, TAMU Lycopersicon...	196	4e-49	
	emb AB024420 AB024419S2 Brassica oleracea SRK13 gene, exon 2, 3,...	114	4e-48	
	emb AJ245480 BNA245480 Brassica napus slg gene for S-locus glyco...	113	7e-48	
	emb Y12530 BOARLKGEN B.oleraceae gene encoding serine/threonine ...	115	1e-47	
	emb Z18921 BOSRKL B.oleracea gene for S-receptor kinase-like pro...	111	2e-47	
45	emb AB024422 AB024421S2 Brassica oleracea SRK13-b gene, exon 2, ...	112	3e-47	
	emb AB000970 AB000970 Brassica campestris gene for receptor kina...	111	3e-47	
	emb X79432 BOSRK3 B.oleracea SRK3 gene.	107	6e-47	
	emb Z30211 BOSRK29G B.oleracea (alboglabra) srk29 gene.	108	6e-47	
	emb AB013718 AB013717S2 Brassica rapa gene for SRK46Bra, exon 2,...	111	2e-46	
50	emb AW684339 AW684339 NF015G04NR1F1000 Nodulated root Medicago t...	120	3e-46	
	emb AB000971 AB000971 Brassica campestris pseudogene for recepto...	105	8e-46	
	emb AI895838 AI895838 EST265281 tomato callus, TAMU Lycopersicon...	184	2e-45	
	emb AW039406 AW039406 EST281663 tomato mixed elicitor, BTI Lycop...	107	3e-45	
	emb AJ245479 BNA245479 Brassica napus Sll3, slk, srk, CePP, Fmt,...	106	4e-45	
55	emb AW034624 AW034624 EST278308 tomato callus, TAMU Lycopersicon...	182	6e-45	
	dbj D88193 D88193 Brassica rapa DNA for S-receptor kinase, compl...	109	9e-45	
	emb Z18884 BOSRKRPC B.oleracea encoding S-receptor kinase relate...	116	1e-43	
	emb AI775997 AI775997 EST257097 tomato resistant, Cornell Lycope...	177	2e-43	
	emb AI895623 AI895623 EST265066 tomato callus, TAMU Lycopersicon...	177	3e-43	
60	emb AI901283 AI901283 sc31d08.y1 Gm-c1014 Glycine max cDNA clone...	171	9e-42	
	emb AW706972 AW706972 sk20a03.y1 Gm-c1028 Glycine max cDNA clone...	171	9e-42	

emb|Z18861|BOSRKRPA B.oleracea encoding S-receptor kinase relate... 111 4e-41
emb|AW216673|AW216673 EST295387 tomato callus, TAMU Lycopersicon... 169 6e-41
emb|AW154835|AW154835 EST290228 tomato root deficiency, Cornell ... 169 6e-41
5 emb|AW031816|AW031816 EST275270 tomato callus, TAMU Lycopersicon... 97 3e-40
emb|AI898854|AI898854 EST268297 tomato ovary, TAMU Lycopersicon ... 163 4e-39
emb|AW620957|AW620957 sj98a07.y1 Gm-cl023 Glycine max cDNA clone... 162 7e-39
emb|AW776492|AW776492 EST335557 DSIL Medicago truncatula cDNA cl... 160 4e-38
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10 emb|Z18883|BOSRKRPA B.oleracea encoding S-receptor kinase relate... 156 3e-37
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emb|AW455306|AW455306 EST311844 tomato root during/after fruit s... 124 9e-37
emb|AI730535|AI730535 BNLGHi7007 Six-day Cotton fiber Gossypium ... 80 1e-36
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15 emb|AW223870|AW223870 EST300681 tomato fruit red ripe, TAMU Lyco... 96 6e-36
emb|AW224241|AW224241 EST300968 tomato fruit red ripe, TAMU Lyco... 96 6e-36
emb|AI486766|AI486766 EST245088 tomato ovary, TAMU Lycopersicon ... 110 8e-36
emb|AW934655|AW934655 EST353547 tomato flower buds 0-3 mm, Corne... 87 1e-34
emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 87 1e-34
20 dbj|D31737|TOBPSTK Tobacco mRNA for protein-serine/threonine kin... 100 2e-34
dbj|E05046|E05046 DNA encoding ZmPK1 homologue protein in tobacco. 100 2e-34
emb|AW687233|AW687233 NF007D09RT1F1077 Developing root Medicago ... 88 3e-34
emb|Z18862|BOSRKRPA B.oleracea encoding S-receptor kinase protein. 80 5e-34
emb|AI896183|AI896183 EST265626 tomato callus, TAMU Lycopersicon... 96 5e-34
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25 emb|AI055189|AI055189 coau0003E19 Cotton Boll Abscission Zone cD... 91 1e-33
emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 144 2e-33
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emb|AI937984|AI937984 sc06e07.y1 Gm-cl012 Glycine max cDNA clone... 144 2e-33
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30 emb|AW290044|AW290044 NXNV009D10F Nsf Xylem Normal wood Vertical... 91 4e-33
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emb|AI772117|AI772117 EST253217 tomato resistant, Cornell Lycopersicon... 142 6e-33
emb|AA738544|AA738544 SbRLK2 Sorghum bicolor cv. TX430 leaf Sorg... 117 8e-33
emb|A67797|A67797 Sequence 2 from Patent WO9743427. 76 2e-32
35 gb|U93048|DCU93048 Daucus carota somatic embryogenesis receptor... 76 2e-32
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45 emb|AW220677|AW220677 EST297146 tomato fruit mature green, TAMU ... 136 5e-31
emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 88 7e-31
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(1323 letters)

55 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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60 Score E
Sequences producing significant alignments: (bits) Value

- emb|AW031251|AW031251 EST274626 tomato callus, TAMU Lycopersicon... 372 e-102
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5 emb|AW930806|AW930806 EST356649 tomato fruit mature green, TAMU ... 346 2e-94
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10 emb|AI965412|AI965412 sc71d05.y1 Gm-c1016 Glycine max cDNA clone... 322 3e-87
emb|AW185064|AW185064 se86c08.y1 Gm-c1023 Glycine max cDNA clone... 321 6e-87
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emb|AI895246|AI895246 EST264689 tomato callus, TAMU Lycopersicon... 317 1e-85
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30 emb|AW686159|AW686159 NF034F08NR1F1000 Nodulated root Medicago t... 231 7e-60
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35 emb|AI728658|AI728658 BNLGHi11350 Six-day Cotton fiber Gossypium... 222 5e-57
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55 emb|AW096584|AW096584 EST289764 tomato mixed elicitor, BTI Lycop... 181 1e-44
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emb|AW220837|AW220837 EST297306 tomato fruit mature green, TAMU ... 180 2e-44
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60 emb|AW559359|AW559359 EST314407 DSIR Medicago truncatula cDNA cl... 178 9e-44
emb|AW616711|AW616711 EST323122 L. hirsutum trichome, Cornell Un... 177 1e-43

- emb|AW310207|AW310207 sf32g10.x1 Gm-c1028 Glycine max cDNA clone... 176 4e-43
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 15 emb|AI778980|AI778980 EST259859 tomato susceptible, Cornell Lyco... 138 1e-31
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 gb|BE054249|BE054249 GA_Ea0033L21f Gossypium arboreum 7-10 dpa ... 120 3e-30
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 20 emb|AI725556|AI725556 BNLGHI12118 Six-day Cotton fiber Gossypium... 125 7e-28
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 25 emb|AW091914|AW091914 EST285094 tomato mixed elicitor, BTI Lycopersicon... 112 5e-24
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 30 emb|AT000037|AT000037 AT000037 Apple young fruit cDNA library Ma... 101 1e-20
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 emb|AW423725|AW423725 sh50h06.y1 Gm-c1017 Glycine max cDNA clone... 98 1e-19
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 35 emb|AW495793|AW495793 NXNV_065_E02_FF Nsf Xylem Normal wood Vert... 94 2e-18
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 emb|AW255631|AW255631 ML690 peppermint glandular trichome Mentha... 86 7e-16
 40 emb|AW102109|AW102109 sd83c02.y1 Gm-c1009 Glycine max cDNA clone... 83 6e-15
 emb|X68950|TRUROCAN T.repens gene for urocanase. 58 5e-14

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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emb|AB012932|AB012932 Vigna radiata mRNA for Ca²⁺/H⁺ exchanger, ... 324 e-141
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 emb|AW395054|AW395054 sh38h04.y1 Gm-c1017 Glycine max cDNA clone... 323 2e-87
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 60 emb|AB018526|AB018526 Ipomoea nil mRNA for H⁺/Ca²⁺ exchanger 2, ... 262 4e-86
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- gb|BE059799|BE059799 sn37c09.y1 Gm-c1016 Glycine max cDNA clone ... 270 1e-71
emb|AW424368|AW424368 sh64g04.y1 Gm-c1015 Glycine max cDNA clone... 221 6e-70
emb|AW283631|AW283631 LG1_242_D12.g1_A002 Light Grown 1 (LG1) So... 243 2e-63
emb|AW668567|AW668567 GA_Ea0014K15 Gossypium arboreum 7-10 dpa ... 141 1e-61
5 emb|AW648038|AW648038 EST326492 tomato germinating seedlings, TA... 230 2e-59
emb|AW132572|AW132572 se05h06.y1 Gm-c1013 Glycine max cDNA clone... 151 3e-52
emb|AW399625|AW399625 EST310125 L. pennellii trichome, Cornell U... 154 4e-49
gb|U18944|SCU18944 Saccharomyces cerevisiae putative transmembra... 195 5e-49
gb|U36603|SCU36603 Saccharomyces cerevisiae vacuolar H⁺/Ca²⁺ exc... 195 5e-49
10 emb|Z74176|SCYDL128W S.cerevisiae chromosome IV reading frame OR... 195 5e-49
emb|AJ001273|SCMNR1W30 Saccharomyces cerevisiae MNR1 gene, strai... 194 1e-48
emb|AW737408|AW737408 EST338751 tomato flower buds, anthesis, Co... 149 5e-48
emb|AJ001272|SCMNR1MNR Saccharomyces cerevisiae mnr1 gene, strai... 191 1e-47
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15 emb|AF053229|AF053229 Neurospora crassa calcium/proton exchanger... 167 3e-46
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20 emb|AL022598|SPCC1795 S.pombe chromosome III cosmid c1795. 150 1e-39
emb|AL035247|SPCC895 S.pombe chromosome III cosmid c895. 150 1e-39
emb|AW934664|AW934664 EST353556 tomato flower buds 0-3 mm, Corne... 120 1e-39
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25 emb|AI484823|AI484823 EST243084 tomato ovary, TAMU Lycopersicon ... 106 2e-35
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emb|AW289857|AW289857 NXNV007A07F Nsf Xylem Normal wood Vertical... 145 8e-34
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emb|AW691013|AW691013 NF036F12ST1F1000 Developing stem Medicago ... 105 9e-33
30 emb|AW737653|AW737653 EST339080 tomato flower buds, anthesis, Co... 140 3e-32
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emb|AW329767|AW329767 N201036e rootphos(-) Medicago truncatula c... 136 3e-31
emb|AW695100|AW695100 NF091E10ST1F1082 Developing stem Medicago ... 98 1e-30
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35 emb|AI899610|AI899610 EST269053 tomato susceptible, Cornell Lyco... 121 7e-30
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emb|AI780101|AI780101 EST260980 tomato susceptible, Cornell Lyco... 88 8e-28
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40 emb|AW691346|AW691346 NF043G04ST1F1000 Developing stem Medicago ... 85 4e-27
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emb|AI771453|AI771453 EST252553 tomato ovary, TAMU Lycopersicon ... 84 3e-24
emb|AW695020|AW695020 NF082E03ST1F1021 Developing stem Medicago ... 76 7e-24
50 emb|AI211368|AI211368 o6g04a1.fl Aspergillus nidulans 24hr asexu... 111 9e-24
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emb|AW690067|AW690067 NF027E05ST1F1000 Developing stem Medicago ... 58 8e-22
55 emb|AW218225|AW218225 EST303406 tomato radicle, 5 d post-imbibit... 105 1e-21
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60 emb|AW432234|AW432234 sh70h05.y1 Gm-c1015 Glycine max cDNA clone... 93 6e-18
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- emb|AW310634|AW310634 sg22e01.x1 Gm-c1024 Glycine max cDNA clone... 82 1e-14
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 5 emb|AW923051|AW923051 DG1_48_G08.g1_A002 Dark Grown 1 (DG1) Sorg... 74 2e-12
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 emb|AW704472|AW704472 sk53e05.y1 Gm-c1019 Glycine max cDNA clone... 74 3e-12
 emb|AA901983|AA901983 NCM5F6T7 Mycelial Neurospora crassa cDNA c... 72 9e-12
 gb|BE022406|BE022406 sm85d09.y1 Gm-c1015 Glycine max cDNA clone ... 72 9e-12
 10 emb|AW694605|AW694605 NF078B03ST1F1027 Developing stem Medicago ... 58 4e-11
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 40 [post/entrez/query?db=n&form=6&dopt=g&cuid=gb|af033205|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&cuid=gb|af033205|/ncgi)
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 60 emb|AW220185|AW220185 EST302668 tomato root during/after fruit s... 134 1e-31
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- emb|X94443|VRPECMEST V.radiata mRNA for pectinmethylesterase. 133 2e-31
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 10 emb|X97762|STBPE1 S.tuberosum mRNA BPE1 for pectin methylesterase. 131 7e-31
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 20 emb|AW784073|AW784073 NXNV_117_D06_F Nsf Xylem Normal wood Verti... 126 2e-29
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 emb|AW888107|AW888107 NXNV_129_C06_F Nsf Xylem Normal wood Verti... 125 5e-29
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 25 emb|A17010|A17010 tomato fruit pectin esterase seq ID no1. 121 1e-27
 emb|AW930691|AW930691 EST356534 tomato fruit mature green, TAMU ... 121 1e-27
 emb|AW934244|AW934244 EST360087 tomato fruit mature green, TAMU ... 121 1e-27
 emb|AW930330|AW930330 EST340883 tomato fruit mature green, TAMU ... 121 1e-27
 gb|S66607|S66607 Lycopersicon esculentum pectinmethylesterase-li... 121 1e-27
 30 emb|AW221911|AW221911 EST298722 tomato fruit red ripe, TAMU Lyco... 121 1e-27
 emb|AW221863|AW221863 EST298674 tomato fruit red ripe, TAMU Lyco... 121 1e-27
 emb|X74638|LEPEC1 L.esculentum mRNA for pectin esterase. 121 1e-27
 emb|AW696177|AW696177 NF103C11ST1F1085 Developing stem Medicago ... 121 1e-27
 emb|AW760550|AW760550 sl51g07.yl Gm-cl027 Glycine max cDNA clone... 120 2e-27
 35 emb|AW289642|AW289642 NXNV003F09F Nsf Xylem Normal wood Vertical... 119 3e-27
 gb|U50986|SLU50986 Solanum lycopersicum pectin methylesterase PM... 119 4e-27
 gb|U70675|LEU70675 Lycopersicon esculentum fruit-specific pectin... 118 6e-27
 gb|U70676|LEU70676 Lycopersicon esculentum pectin methylesteras... 118 6e-27
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 40 emb|AW932254|AW932254 EST358097 tomato fruit mature green, TAMU ... 118 8e-27
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 gb|U82974|CSU82974 Citrus sinensis pectinesterase (PECS-1.2) gen... 117 1e-26
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 45 gb|U50985|SLU50985 Solanum lycopersicum pectin methylesterase PM... 116 3e-26
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 emb|X07910|LEPECES Tomato mRNA for pectin esterase. 116 3e-26
 50 emb|A15983|A15983 L.esculentum mRNA for pectin esterase. 116 3e-26
 emb|AW623570|AW623570 EST321515 tomato flower buds 3-8 mm, Corne... 116 3e-26
 emb|AW221834|AW221834 EST298645 tomato fruit red ripe, TAMU Lyco... 115 5e-26
 emb|X97763|STBPE2 S.tuberosum mRNA BPE2 for pectin methylesterase. 115 5e-26
 emb|A24196|A24196 L.esculentum pectin esterase clone pPE1. 113 2e-25
 55 emb|AW687047|AW687047 NF005D06RT1F1057 Developing root Medicago ... 113 2e-25
 emb|AW424141|AW424141 sh61d11.yl Gm-cl015 Glycine max cDNA clone... 112 6e-25
 emb|AW398532|AW398532 EST309032 L. pennellii trichome, Cornell U... 111 8e-25
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 60 emb|AW620942|AW620942 sj95g05.yl Gm-cl023 Glycine max cDNA clone... 108 5e-24
 emb|AI440753|AI440753 sa53f07.yl Gm-cl004 Glycine max cDNA clone... 108 7e-24

- gb|U82977|CSU82977 Citrus sinensis pectinesterase mRNA, complete... 84 2e-23
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 emb|AW666437|AW666437 sk36e11.y1 Gm-c1028 Glycine max cDNA clone... 95 7e-20
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 661,018 sequences; 426,114,510 total letters
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Database: plantfungal
661,018 sequences; 426,114,510 total letters

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emb AI729894 AI729894 BNLGHi5504 Six-day Cotton fiber Gossypium ...	93	8e-20	
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Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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 emb|AI896076|AI896076 EST265519 tomato callus, TAMU Lycopersicon... 102 1e-23
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 45 emb|AW398760|AW398760 EST309260 L. pennellii trichome, Cornell U... 54 2e-12
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 5 emb|AW154916|AW154916 EST290281 tomato root deficiency, Cornell ... 40 6e-05
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 45 emb|AI965348|AI965348 sc70c09.y1 Gm-c1016 Glycine max cDNA clone... 39 0.11
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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- emb|AA660464|AA660464 00349 MtRHE Medicago truncatula cDNA 5', m... 128 6e-38
- emb|AW693268|AW693268 NF064A03ST1F1000 Developing stem Medicago ... 109 5e-32
- emb|AW508697|AW508697 si35c12.y1 Gm-r1030 Glycine max cDNA clone... 77 6e-31
- emb|AW689377|AW689377 NF018E07ST1F1000 Developing stem Medicago ... 78 2e-30
- 15 gb|BE058474|BE058474 sn16f08.y1 Gm-c1016 Glycine max cDNA clone ... 102 6e-21
- emb|AW704030|AW704030 sk27a04.y1 Gm-c1028 Glycine max cDNA clone... 64 5e-20
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- emb|AW720399|AW720399 LjNEST22c8r Lotus japonicus nodule library... 83 1e-18
- emb|AU089968|AU089968 AU089968 Hordeum vulgare subsp. vulgare Up... 45 5e-17
- 20 emb|AV417193|AV417193 AV417193 Lotus japonicus young plants (two... 88 2e-16
- emb|AQ855554|AQ855554 CpG1646A CpIOWAgDNA1 Cryptosporidium parvu... 35 1.1
- emb|Z37536|LTND9 L.tarentolae ND9 mRNA encoding putative NADH de... 35 2.1
- emb|AW934637|AW934637 EST353529 tomato flower buds 0-3 mm, Corne... 35 2.1
- emb|AF050740|AF050740 Plasmodium falciparum variant-specific sur... 35 2.1
- 25 emb|AI329848|AI329848 b8h09ne.r1 Neurospora crassa evening cDNA ... 35 2.1
- emb|AW035275|AW035275 EST280638 tomato callus, TAMU Lycopersicon... 35 2.1
- emb|AW933190|AW933190 EST359033 tomato fruit mature green, TAMU ... 35 2.1
- emb|AL109832|SPAC630 S.pombe chromosome I cosmid c630. 34 2.9
- emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 34 4.0
- 30 emb|A85491|A85491 Sequence 150 from Patent EP0866129. 34 4.0
- emb|AC004688|AC004688 Plasmodium falciparum chromosome 12 clone ... 34 4.0
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- emb|AL356172|NCB23L21 Neurospora crassa DNA linkage group II BAC... 33 5.5
- 35 emb|AW617216|AW617216 EST323627 L. hirsutum trichome, Cornell Un... 33 5.5
- emb|AL160493|LMFLCHR26 Leishmania major Friedlin assembled chrom... 33 7.6
- emb|AF056622|AF056622 Vitis vinifera putative Cu/Zn superoxide d... 33 7.6
- gb|BE053037|BE053037 GA_Ea0031O23f Gossypium arboreum 7-10 dpa ... 33 7.6
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- thaliana] /blast_score 0 /cc_number /family /chip nova /gb_link
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

Searching.....done

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Score E

Sequences producing significant alignments: (bits) Value

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- 55 emb|AW268012|AW268012 EST306234 DSIR Medicago truncatula cDNA cl... 246 2e-83
- emb|AW041000|AW041000 EST283864 tomato mixed elicitor, BTI Lycop... 307 1e-82
- emb|AW472433|AW472433 si25b07.y1 Gm-c1029 Glycine max cDNA clone... 306 3e-82
- emb|AW560118|AW560118 EST315166 DSIR Medicago truncatula cDNA cl... 166 3e-64
- emb|AW394771|AW394771 sh35b02.y1 Gm-c1017 Glycine max cDNA clone... 213 3e-54
- 60 emb|AW622568|AW622568 EST313368 tomato root during/after fruit s... 181 5e-51
- emb|AW737712|AW737712 EST339139 tomato flower buds, anthesis, Co... 162 1e-45

- emb|AW694002|AW694002 NF071F03ST1F1029 Developing stem Medicago ... 135 2e-45
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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	emb AI728590 AI728590 BNLGHi11133 Six-day Cotton fiber Gossypium...	60	7e-13
	emb AI731959 AI731959 BNLGHi11511 Six-day Cotton fiber Gossypium...	60	7e-13
	emb AI775217 AI775217 EST256317 tomato resistant, Cornell Lycope...	59	7e-13
55	emb AW458973 AW458973 sh17e01.y1 Gm-c1016 Glycine max cDNA clone...	61	3e-12
	emb AW132527 AW132527 se05c02.y1 Gm-c1013 Glycine max cDNA clone...	61	3e-12
	emb AW102493 AW102493 sd88h04.y1 Gm-c1009 Glycine max cDNA clone...	61	4e-12
	emb AV421249 AV421249 AV421249 Lotus japonicus young plants (two...	62	2e-09
	emb AW691065 AW691065 NF040H08ST1F1000 Developing stem Medicago ...	61	3e-09
60	emb AW349295 AW349295 GM210004B12D12R Gm-r1021 Glycine max cDNA ...	46	8e-08
	emb AW101242 AW101242 sd97a09.y1 Gm-c1013 Glycine max cDNA clone...	56	2e-07

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5	emb AI771636 AI771636 EST252736 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AW219417 AW219417 EST301995 tomato root during/after fruit s...	45	3e-04
	emb AI898830 AI898830 EST268273 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AI489478 AI489478 EST247817 tomato ovary, TAMU Lycopersicon ...	45	3e-04
	emb AI489770 AI489770 EST248109 tomato ovary, TAMU Lycopersicon ...	45	3e-04
10	emb AW672287 AW672287 LG1_358_A02.b1_A002 Light Grown 1 (LG1) So...	44	5e-04
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	emb AI488844 AI488844 EST247183 tomato ovary, TAMU Lycopersicon ...	44	7e-04
	emb AJ238740 CRO238740 Catharanthus roseus mRNA for AP2-domain D...	43	0.001
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20	emb AW727628 AW727628 GA_Ea0015E08 Gossypium arboreum 7-10 dpa ...	42	0.003
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25	emb AI731460 AI731460 BNLGHi9812 Six-day Cotton fiber Gossypium ...	42	0.003
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30	emb AI795106 AI795106 sb76f04.y1 Gm-c1010 Glycine max cDNA clone...	41	0.004
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	emb AW278066 AW278066 sf39c09.y1 Gm-c1009 Glycine max cDNA clone...	40	0.007
40	emb AW318239 AW318239 sg62g03.y1 Gm-c1007 Glycine max cDNA clone...	40	0.007
	emb AW706818 AW706818 sk03g11.y1 Gm-c1023 Glycine max cDNA clone...	40	0.009
	emb AI166481 AI166481 xylem.est.309 Poplar xylem Lambda ZAPII li...	40	0.013
	emb AW759250 AW759250 sl38g10.y1 Gm-c1027 Glycine max cDNA clone...	39	0.018
	emb AW981151 AW981151 EST392345 DSIL Medicago truncatula cDNA cl...	39	0.018
45	emb AW981228 AW981228 EST392318 DSIL Medicago truncatula cDNA cl...	39	0.018
	emb AI896723 AI896723 EST266166 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AW216598 AW216598 EST295312 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AW034686 AW034686 EST278417 tomato callus, TAMU Lycopersicon...	39	0.018
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50	emb AW031292 AW031292 EST274667 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AI487841 AI487841 EST246163 tomato ovary, TAMU Lycopersicon ...	39	0.018
	emb AW032262 AW032262 EST275716 tomato callus, TAMU Lycopersicon...	39	0.018
	emb AI486694 AI486694 EST245016 tomato ovary, TAMU Lycopersicon ...	39	0.018
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55	emb AI988644 AI988644 sd05h06.y1 Gm-c1020 Glycine max cDNA clone...	39	0.024
	emb AW278190 AW278190 sf40g11.y1 Gm-c1009 Glycine max cDNA clone...	39	0.024
	emb AW030009 AW030009 EST273264 tomato callus, TAMU Lycopersicon...	39	0.024
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60	emb AW030386 AW030386 EST273641 tomato callus, TAMU Lycopersicon...	39	0.024
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 5 emb|AW774176|AW774176 EST333259 KV3 Medicago truncatula cDNA clo... 38 0.033
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 10 emb|AW308784|AW308784 sf71h01.y1 Gm-c1013 Glycine max cDNA clone... 38 0.033
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 emb|AW394770|AW394770 sh35b01.y1 Gm-c1017 Glycine max cDNA clone... 38 0.046
 emb|AW164648|AW164648 se75g05.y1 Gm-c1023 Glycine max cDNA clone... 38 0.046
 15 emb|AI966402|AI966402 sc38e09.y1 Gm-c1014 Glycine max cDNA clone... 38 0.046
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 emb|AI442716|AI442716 sa85d10.y1 Gm-c1004 Glycine max cDNA clone... 38 0.046
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 20 emb|AW930485|AW930485 EST340858 tomato fruit mature green, TAMU ... 38 0.046
 emb|AI899237|AI899237 EST268680 tomato ovary, TAMU Lycopersicon ... 38 0.046
 emb|AW034216|AW034216 EST277787 tomato callus, TAMU Lycopersicon... 38 0.046
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 25 emb|AI895984|AI895984 EST265427 tomato callus, TAMU Lycopersicon... 38 0.046
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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022023|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022023|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al022023|/ncgi)
 35 <http://www.ncgr.org/cgi-bin/ff?al022023>
 (1161 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

		Score	E
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45	emb AW185155 AW185155 se87e11.y1 Gm-c1023 Glycine max cDNA clone...	134	2e-30
	emb AW278569 AW278569 sf46b12.y1 Gm-c1009 Glycine max cDNA clone...	131	1e-29
	emb AW683973 AW683973 NF004E08NR1F1000 Nodulated root Medicago t...	97	2e-19
	emb AI055338 AI055338 coau0003L11 Cotton Boll Abscission Zone cD...	56	2e-07
	emb AW693058 AW693058 NF059E03ST1F1021 Developing stem Medicago ...	49	9e-05
50	emb AW686062 AW686062 NF033A11NR1F1000 Nodulated root Medicago t...	49	9e-05
	gb BE060490 BE060490 HVSMeg0012H04f Hordeum vulgare pre-anthesis...	37	0.22
	emb AW979446 AW979446 EST310344 tomato root deficiency, Cornell ...	35	1.0
	emb AI726520 AI726520 BNLGHi6046 Six-day Cotton fiber Gossypium ...	34	1.0
	gb M86518 PFAHMGLP Plasmodium falciparum high mobility group-lik...	35	1.1
55	emb AQ952389 AQ952389 Sheared DNA-32H3.TF Sheared DNA Trypanosom...	35	1.1
	emb AW775865 AW775865 EST334930 DSIL Medicago truncatula cDNA cl...	35	1.1
	emb AQ988902 AQ988902 04D1B01NE.R1 C. parvum Lambda Zap Express ...	35	1.1
	emb AV425088 AV425088 AV425088 Lotus japonicus young plants (two...	34	1.5
	emb AA676132 AA676132 TENF0683 T.cruzi epimastigote normalized c...	34	2.1
60	emb AL049183 PFMAL13P6 Plasmodium falciparum chromosome 13 strai...	33	2.8
	emb AF108883 AF108883 Capsicum annuum small GTP-binding protein ...	28	3.6

- emb|X75082|STCITS *S.tuberosum* mRNA for mitochondrial citrate-syn... 33 3.9
 emb|A46545|A46545 Sequence 1 from Patent WO9524487. 33 3.9
 emb|X07693|SPNUC2 Fission yeast nuc2 gene encoding nuclear scaff... 33 3.9
 emb|X83997|CPEAPC *C.parasitica* eapC gene. 33 3.9
 5 emb|AF143971|AF143971 *Pinus taeda* microsatellite PtTX3026 sequence. 33 3.9
 emb|AW667663|AW667663 GA_Ea0010C16 *Gossypium arboreum* 7-10 dpa ... 33 5.0
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 10 emb|AB012123|AB012123 *Candida albicans* CHS5 gene, complete cds. 32 5.3
 emb|AI055163|AI055163 coau0003D12 Cotton Boll Abcission Zone cD... 32 6.9
 emb|AW761626|AW761626 gb27h09.y1 Moss EST library PPN Physcomitr... 32 6.9
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 emb|AW761333|AW761333 sl66b07.y1 *Gm-c1027* Glycine max cDNA clone... 32 6.9
 emb|AI822729|AI822729 L0-1261T3 Ice plant Lambda Uni-Zap XR expr... 32 6.9
 emb|AW931465|AW931465 EST357308 tomato fruit mature green, TAMU ... 32 7.3
 15 emb|AA555413|AA555413 CpEST.644 uniZAPCpIOWAsporoLib3 Cryptospor... 32 7.3
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 emb|AQ640247|AQ640247 927P1-18B12.TV 927P1 *Trypanosoma brucei* ge... 32 7.3
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 20 emb|AF143965|AF143965 *Pinus taeda* microsatellite PtTX3011 sequence. 32 7.3
 gb|U51031|YSCD9819 *Saccharomyces cerevisiae* chromosome IV cosmid... 32 7.3
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 emb|AQ850277|AQ850277 LMAJFV1_lm28b03.x1 *Leishmania major* FV1 ra... 32 9.4
 emb|AJ225402|AJ225402 AJ225402 Absciscic acid-treated protonemata... 32 9.4
 25 emb|AW735860|AW735860 EST336628 tomato flower buds 0-3 mm, Corne... 32 9.4
 emb|AW756470|AW756470 sl21g05.y1 *Gm-c1036* Glycine max cDNA clone... 32 9.4

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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002521|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002521|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac002521|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?ac002521>
 (999 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

	Score	E	
	Sequences producing significant alignments:		(bits) Value
45	emb AI727718 AI727718 BNLGHi8830 Six-day Cotton fiber <i>Gossypium</i> ...	405	e-112
	emb AI894939 AI894939 EST264382 tomato callus, TAMU <i>Lycopersicon</i> ...	405	e-112
	emb AI727173 AI727173 BNLGHi7479 Six-day Cotton fiber <i>Gossypium</i> ...	404	e-112
	emb AW091566 AW091566 EST284842 tomato mixed elicitor, BTI <i>Lycop</i> ...	364	e-100
	emb AW201381 AW201381 sf02d09.y1 <i>Gm-c1027</i> Glycine max cDNA clone...	301	1e-98
	emb AW397167 AW397167 sg67f10.y1 <i>Gm-c1007</i> Glycine max cDNA clone...	287	1e-94
50	emb AW038822 AW038822 EST280778 tomato mixed elicitor, BTI <i>Lycop</i> ...	282	3e-75
	emb AI488594 AI488594 EST246933 tomato ovary, TAMU <i>Lycopersicon</i> ...	280	2e-74
	emb AW926055 AW926055 HVSMEg0006C20 <i>Hordeum vulgare</i> pre-anthesis...	160	2e-71
	gb T14872 T14872 crs323 lambdaZAPST <i>Ricinus communis</i> cDNA clone ...	187	4e-68
	emb AW329252 AW329252 N200470e rootphos(-) <i>Medicago truncatula</i> c...	246	2e-64
55	emb AW932653 AW932653 EST358496 tomato fruit mature green, TAMU...	246	2e-64
	emb AW508528 AW508528 si33a06.y1 <i>Gm-r1030</i> Glycine max cDNA clone...	177	8e-60
	emb AW201152 AW201152 se98d11.y1 <i>Gm-c1027</i> Glycine max cDNA clone...	137	1e-49
	emb AW011518 AW011518 ST21G07 Pine TriplEx shoot tip library Pin...	178	5e-44
	emb AW568929 AW568929 si74c04.y1 <i>Gm-c1031</i> Glycine max cDNA clone...	169	3e-41
60	emb AW459302 AW459302 sh23c04.y1 <i>Gm-c1016</i> Glycine max cDNA clone...	166	3e-40
	emb AV392100 AV392100 AV392100 <i>Chlamydomonas reinhardtii</i> C9 Chla...	114	1e-36

- emb|Z67751|SC38KCXVI *S.cerevisiae* DNA (chromosome XVI; 38 kb). 87 8e-28
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emb|AL096796|SPBC839 *S.pombe* chromosome II cosmid c839. 65 2e-25
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5 emb|AW395997|AW395997 sh08a03.y1 Gm-c1016 Glycine max cDNA clone... 114 1e-24
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emb|AC007862|AC007862 *Trypanosoma brucei* chromosome II clone RPC... 35 0.97
emb|AQ872760|AQ872760 V21H1 mTn-3xHA/lacZ Insertion Library, str... 35 1.3
25 emb|Z38062|SC9687 *S.cerevisiae* chromosome IX cosmid 9687. 35 1.3
emb|AW428965|AW428965 EST306505 tomato flower buds 0-3 mm, Corne... 35 1.3
emb|X79743|SCBPPS *S.cerevisiae* BET1, PAN1, PRI1 and STS1 genes. 35 1.3
emb|AZ221045|AZ221045 Sheared DNA-64E9.TF Sheared DNA Trypanosom... 35 1.3
emb|AF014809|AF014809 *Lycopersicon esculentum* proline transporte... 35 1.3
30 emb|AF106079|AF106079 *Chlamydomonas reinhardtii* dynein heavy cha... 34 1.8
gb|M80437|YSCSEQ *Saccharomyces cerevisiae* gene, complete cds. 34 2.5
gb|J05603|YSCCTR *Saccharocyces cerevisiae* choline transport prot... 34 2.5
emb|Z72599|SCYGL077C *S.cerevisiae* chromosome VII reading frame O... 34 2.5
gb|T36987|T36987 EST102029 *S. cerevisiae* strain X2180-1A Sacchar... 34 2.5
35 emb|Z71519|SCYNL243W *S.cerevisiae* chromosome XIV reading frame O... 33 3.4
emb|AW649403|AW649403 EST327857 tomato germinating seedlings, TA... 33 3.4
emb|Z22811|SCSLA2PA *S.cerevisiae* of Sla2p gene. 33 3.4
emb|Z69381|SCCXIV39K *S.cerevisiae* 38,855 bp segment of chromosom... 33 3.4
emb|AI898010|AI898010 EST267453 tomato ovary, TAMU *Lycopersicon* ... 33 3.4
40 gb|L12352|YSCMOP2G *Saccharomyces cerevisiae* transmembrane protei... 33 3.4
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emb|AQ841780|AQ841780 T134030 Soybean RFLP probe Glycine max gen... 33 4.7
45 dbj|D90206|CRECAH1G *C. reinhardtii* CAH1 gene for carbonic anhydr... 33 4.7
emb|X54487|CRCAH1 *Chlamydomonas reinhardtii* CAH1 gene for carbo... 33 4.7
emb|AW596179|AW596179 si99a03.y1 Gm-c1032 Glycine max cDNA clone... 33 4.7
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55 emb|AL031324|SPCC1672 *S.pombe* chromosome III cosmid c1672. 32 6.5
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emb|AW255452|AW255452 ML474 peppermint glandular trichome *Mentha*... 26 7.0
emb|AI490316|AI490316 EST248642 tomato ovary, TAMU *Lycopersicon* ... 28 7.2
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emb|AJ133001|CPL133001 *Craterostigma plantagineum* mRNA for phosp... 32 8.9

- emb|AW348239|AW348239 GM210001B12D9R Gm-r1021 Glycine max cDNA 3... 32 8.9
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 emb|AF016328|AF016328 Hordeum vulgare Barperm2 (perm2) mRNA, par... 32 8.9
 5 emb|AW696053|AW696053 NF102A09ST1F1068 Developing stem Medicago ... 32 8.9
 emb|AW691566|AW691566 NF046E03ST1F1000 Developing stem Medicago ... 32 8.9
 emb|AW309484|AW309484 sf20a10.x1 Gm-c1028 Glycine max cDNA clone... 32 8.9
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 10 emb|X54488|CRAH2 Chlamydomonas reinhardtii CAH2 gene for carbon... 32 8.9
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 emb|AF020814|AF020814 Pisum sativum glucose-6-phosphate/phosphat... 32 8.9
 emb|AW184970|AW184970 se84g02.y1 Gm-c1023 Glycine max cDNA clone... 32 8.9
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 15 emb|AI163250|AI163250 A038p15u Hybrid aspen plasmid library Popu... 32 8.9
 emb|AL023592|SPCC550 S.pombe chromosome III cosmid c550. 32 8.9
 emb|AW668371|AW668371 GA_Ea0013L20 Gossypium arboreum 7-10 dpa ... 26 9.3
 emb|AW255363|AW255363 ML376 peppermint glandular trichome Menth... 26 9.5
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 20 emb|AW255126|AW255126 ML1418 peppermint glandular trichome Menth... 26 9.8

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 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac000348|/ncgi)
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 (1869 letters)

30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- emb|AW622865|AW622865 EST306935 tomato flower buds 3-8 mm, Corne... 246 3e-64
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 40 emb|AW596038|AW596038 si97b04.y1 Gm-c1032 Glycine max cDNA clone... 98 4e-28
 emb|AW774367|AW774367 EST333518 KV3 Medicago truncatula cDNA clo... 101 1e-25
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 emb|AW777159|AW777159 Str2-E4 Sugar Beet germination cDNA librar... 82 1e-20
 emb|AW694460|AW694460 NF076E10ST1F1082 Developing stem Medicago ... 95 1e-18
 45 emb|AW651335|AW651335 EST329789 tomato germinating seedlings, TA... 82 8e-15
 gb|BE052602|BE052602 GA_Ea0032J02f Gossypium arboreum 7-10 dpa ... 50 2e-13
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 emb|AW226419|AW226419 ST82B05 Pine TriplEx shoot tip library Pin... 62 2e-08
 emb|AW398212|AW398212 EST298059 L. pennellii trichome, Cornell U... 60 4e-08
 50 emb|AT002124|AT002124 AT002124 Flower bud cDNA Brassica rapa sub... 44 0.004
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 55 emb|Z48618|SCCHVII35 S.cerevisiae genes for RAD54, ACE1(CUP2), P... 36 0.68
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- emb|AB025421|AB025421 *Pyrus pyrifolia* gene for S3-RNase, complet... 35 1.3
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 emb|AW180136|AW180136 MgA0212f MgA Library *Mycosphaerella gramin...* 35 1.8
 5 emb|AW677734|AW677734 WS1_10_E07.g1_A002 Water-stressed 1 (WS1) ... 35 1.8
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 emb|AL355928|NCB1D4 *Neurospora crassa* DNA linkage group II BAC c... 34 2.4
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 10 gb|M23080|BLYHORA *Hordeum vulgare* alpha-hordothionin (Hth-1) gen... 26 3.3
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 emb|X55685|LEEXTEN5 Tomato extensin mRNA (clone uG-18). 34 3.3
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 15 emb|AL035064|SPAC1687 *S.pombe* chromosome I cosmid c1687. 34 3.3
 emb|AJ223010|SCP223010 *Schizosaccharomyces pombe* pmt2 gene. 34 3.3
 emb|AL356456|LMFLUNK01 *Leishmania major* Friedlin cosmid clones L... 34 3.3
 emb|AW683291|AW683291 NF010B07LF1F1060 Developing leaf *Medicago* ... 34 3.3
 emb|X63357|HVNREHTh *H.vulgare* Hth-1 gene (promoter region). 26 3.3
 20 emb|AW710511|AW710511 e4c05ne.fl *Neurospora crassa* evening cDNA ... 34 4.4
 emb|AQ411888|AQ411888 CpG0892A CpIOWAgDNA1 *Cryptosporidium parvu...* 34 4.4
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 emb|AA901701|AA901701 NCP2A2T7 Perithecial *Neurospora crassa* cDN... 33 4.6
 emb|AF128526|AF128526 *Theileria lestoquardi* sporozoite antigen S... 33 4.6
 25 gb|M76671|TOMEXTENB *L.esculentum* extensin (class II) gene, compl... 33 4.6
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 emb|AW690872|AW690872 NF039H07ST1F1000 Developing stem *Medicago* ... 33 6.3
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 gb|L38908|TOBEXTE *Nicotiana tabacum* extensin gene, complete cds. 33 6.3
 40 dbj|D13951|TOBEXTS Tobacco gene for extensin, complete cds. 33 6.3
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 emb|AA901958|AA901958 NCC2C12T7 Conidial *Neurospora crassa* cDNA ... 33 8.3
 emb|AW704352|AW704352 sk18c03.y1 *Gm-c1028* Glycine max cDNA clone... 33 8.3
 emb|AF085735|AF085735 *Trypanosoma triglae* kinetoplast minicircle... 33 8.3
 45 emb|AW457944|AW457944 sh97h02.y1 *Gm-c1016* Glycine max cDNA clone... 33 8.3
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 emb|AQ941354|AQ941354 Sheared DNA-19O3.TR Sheared DNA *Trypanosom...* 32 8.6
 emb|AF046120|AF046120 *Candida glabrata* ATP-binding cassette tran... 32 8.6
 50 emb|AW725268|AW725268 GA_Ea0015L23 *Gossypium arboreum* 7-10 dpa ... 32 8.6
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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10 emb AW222063 AW222063 EST298874 tomato fruit red ripe, TAMU Lyco...	103	4e-40
emb AW218145 AW218145 EST303326 tomato radicle, 5 d post-imbibit...	103	1e-39
emb AW398260 AW398260 EST298107 L. pennellii trichome, Cornell U...	101	3e-39
emb AW477271 AW477271 ga44c12.y1 Moss EST library PPU Physcomitr...	94	1e-38
emb AW568049 AW568049 si56g06.y1 Gm-r1030 Glycine max cDNA clone...	102	1e-36
15 emb AW565775 AW565775 LG1_349_D04.g1_A002 Light Grown 1 (LG1) So...	108	5e-35
emb AW218146 AW218146 EST303327 tomato radicle, 5 d post-imbibit...	108	5e-26
emb AI488047 AI488047 EST246369 tomato ovary, TAMU Lycopersicon ...	78	3e-24
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emb AI495965 AI495965 sb18d07.y1 Gm-c1004 Glycine max cDNA clone...	102	3e-21
20 emb AT002115 AT002115 AT002115 Flower bud cDNA Brassica rapa sub...	52	1e-09
emb AT001714 AT001714 AT001714 Flower bud cDNA Brassica rapa sub...	52	3e-09
emb AW621058 AW621058 sj95d05.y1 Gm-c1023 Glycine max cDNA clone...	52	3e-08
emb AW099304 AW099304 sd38a08.y1 Gm-c1016 Glycine max cDNA clone...	33	0.092
emb AI774719 AI774719 EST255819 tomato resistant, Cornell Lycope...	35	0.12
25 emb AW040524 AW040524 EST283484 tomato mixed elicitor, BTI Lycop...	35	0.12
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emb AB003073 AB003073 Trypanosoma cruzi clone CE5-9-5 mRNA, part...	34	1.5
emb AI899521 AI899521 EST268964 tomato susceptible, Cornell Lyco...	30	1.8
35 emb AI055583 AI055583 coau0004G11 Cotton Boll Abscission Zone cD...	33	2.0
emb AI776180 AI776180 EST257280 tomato resistant, Cornell Lycope...	30	2.4
emb AL110509 SPAC1250 S.pombe chromosome I cosmid c1250.	33	2.8
emb Z74775 SCYOL033W S.cerevisiae chromosome XV reading frame OR...	33	2.8
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gb L39015 YSCMSE1G Saccharomyces cerevisiae nuclear-encoded mito...	33	2.8
emb AI398391 AI398391 NCSM1H10T7 Subtracted Mycelial Neurospora ...	33	2.8
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emb AI487645 AI487645 EST245967 tomato ovary, TAMU Lycopersicon ...	32	3.8
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55 emb AQ952955 AQ952955 Sheared DNA-52J12.TR Sheared DNA Trypanoso...	32	5.3
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 5 emb|X64601|ANNIMTMR A.nidulans nimT mRNA for tyrosine phosphatase. 31 9.9

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 (1761 letters)

- 15 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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| | emb AW906097 AW906097 EST342218 potato stolon, Cornell Universit... | 162 | 8e-39 | |
| | emb AV413830 AV413830 AV413830 Lotus japonicus young plants (two... | 161 | 1e-38 | |
| | emb AV419573 AV419573 AV419573 Lotus japonicus young plants (two... | 82 | 5e-36 | |
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| 30 | emb AI507855 AI507855 sa88a07.y1 Gm-c1004 Glycine max cDNA clone... | 91 | 2e-35 | |
| | emb AW160273 AW160273 EST290131 L. pennellii trichome, Cornell U... | 146 | 4e-34 | |
| | emb AV428532 AV428532 AV428532 Lotus japonicus young plants (two... | 80 | 3e-30 | |
| | emb AV424557 AV424557 AV424557 Lotus japonicus young plants (two... | 128 | 1e-28 | |
| | emb AW668007 AW668007 GA_Ea0012E04 Gossypium arboreum 7-10 dpa ... | 117 | 2e-25 | |
| 35 | emb AW922981 AW922981 DG1_48_B03.b1_A002 Dark Grown 1 (DG1) Sorg... | 105 | 8e-22 | |
| | emb AW432282 AW432282 sh71f09.y1 Gm-c1015 Glycine max cDNA clone... | 100 | 3e-20 | |
| | emb AW621610 AW621610 EST312408 tomato root during/after fruit s... | 100 | 5e-20 | |
| | emb AV419981 AV419981 AV419981 Lotus japonicus young plants (two... | 95 | 2e-18 | |
| | emb AI937949 AI937949 sc06a10.y1 Gm-c1012 Glycine max cDNA clone... | 88 | 3e-16 | |
| 40 | emb AV406642 AV406642 AV406642 Lotus japonicus young plants (two... | 67 | 6e-10 | |
| | emb AW497095 AW497095 ga53g06.y1 Moss EST library PPU Physcomitr... | 42 | 3e-06 | |
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| | emb AI001408 AI001408 L0-330M13R Ice plant Lambda Uni-Zap XR exp... | 38 | 0.20 | |
| | emb AI731457 AI731457 BNLGHi9807 Six-day Cotton fiber Gossypium ... | 38 | 0.27 | |
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| 55 | gb BE124825 BE124825 EST393860 GVN Medicago truncatula cDNA clon... | 35 | 1.8 | |
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| 60 | emb AW926002 AW926002 HVSMEg0006A15 Hordeum vulgare pre-anthesis... | 35 | 2.5 | |
| | emb AA660722 AA660722 00613 MtRHE Medicago truncatula cDNA 5', m... | 34 | 3.5 | |

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 5 emb|AQ654502|AQ654502 Sheared DNA-25C14.TR Sheared DNA Trypanoso... 33 6.6
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 gb|U05612|CSU05612 Colysis sintenensis chloroplast large subunit... 28 6.8
 10 emb|X02433|MIPSCOX2 Pea mitochondrial gene for cytochrome oxidas... 24 6.9
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 25 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&cuid=gb|af000657|/ncgi)
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[http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&cuid=gb|af000657|/ncgi)
 (564 letters)

- 30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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- 35 Score E
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- emb|AW622665|AW622665 EST313465 tomato root during/after fruit s... 166 8e-42
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 40 emb|AI776839|AI776839 EST257939 tomato resistant, Cornell Lycopersicon... 166 2e-40
 emb|AI898331|AI898331 EST267774 tomato ovary, TAMU Lycopersicon ... 166 2e-40
 emb|AI772887|AI772887 EST253987 tomato resistant, Cornell Lycopersicon... 166 2e-40
 emb|AI782639|AI782639 EST263518 tomato susceptible, Cornell Lycopersicon... 161 2e-40
 emb|AW035141|AW035141 EST280403 tomato callus, TAMU Lycopersicon... 162 3e-40
 45 emb|AW559773|AW559773 EST314821 DSIR Medicago truncatula cDNA cl... 136 4e-40
 emb|AI488935|AI488935 EST247274 tomato ovary, TAMU Lycopersicon ... 162 1e-39
 emb|AW626015|AW626015 EST319922 tomato radicle, 5 d post-imbibit... 161 4e-39
 emb|AW035118|AW035118 EST280380 tomato callus, TAMU Lycopersicon... 159 1e-38
 emb|AI442841|AI442841 sa27e02.x1 Gm-c1004 Glycine max cDNA clone... 131 2e-38
 50 gb|BE057238|BE057238 sm99d06.y1 Gm-c1015 Glycine max cDNA clone ... 133 4e-37
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 55 emb|AW348098|AW348098 GM210001A11F3R Gm-r1021 Glycine max cDNA 3... 121 1e-35
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- emb|AW306271|AW306271 se48e06.y1 Gm-c1017 Glycine max cDNA clone... 125 6e-35
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25 emb|AI494896|AI494896 sb06g10.y1 Gm-c1004 Glycine max cDNA clone... 140 9e-33
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30 emb|AW234737|AW234737 sf18f10.y1 Gm-c1028 Glycine max cDNA clone... 136 2e-31
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40 emb|AW460064|AW460064 si08g11.y1 Gm-c1029 Glycine max cDNA clone... 105 4e-29
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emb|AI900284|AI900284 sc03d11.y1 Gm-c1012 Glycine max cDNA clone... 111 4e-25
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- emb|AW310235|AW310235 sF33b10.x1 Gm-c1028 Glycine max cDNA clone... 110 1e-23
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 (393 letters)

30 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

35 Score E
 Sequences producing significant alignments: (bits) Value

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 40 emb|AI894486|AI894486 EST263929 tomato callus, TAMU Lycopersicon... 100 3e-29
 emb|AW255546|AW255546 ML580 peppermint glandular trichome Mentha... 96 4e-25
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 emb|AW980335|AW980335 EST391488 GVN Medicago truncatula cDNA clo... 94 1e-24
 emb|AW982334|AW982334 HVSMEg0002O20f Hordeum vulgare pre-anthesi... 86 1e-24
 45 gb|H74448|H74448 150 Standard Brassica napus cDNA clone R29F, mR... 92 4e-24
 emb|AI960943|AI960943 sc93a04.y1 Gm-c1019 Glycine max cDNA clone... 92 5e-24
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 emb|AW598247|AW598247 sj42f01.y1 Gm-c1008 Glycine max cDNA clone... 80 3e-23
 emb|AW100651|AW100651 sd58b12.y1 Gm-c1008 Glycine max cDNA clone... 89 4e-23
 50 emb|AW208200|AW208200 M110845e GVSN Medicago truncatula cDNA clo... 88 5e-23
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 emb|AW690635|AW690635 NF031H11ST1F1000 Developing stem Medicago ... 75 6e-20
 emb|AW126039|AW126039 N100235e rootphos(-) Medicago truncatula c... 75 6e-20
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 60 emb|AI043565|AI043565 L30-578T3 Ice plant Lambda Uni-Zap XR expr... 75 3e-19
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gb|BE125244|BE125244 DG1_18_B07.b1_A002 Dark Grown 1 (DG1) Sorgh... 127 1e-28
emb|AW922420|AW922420 DG1_18_B07.g1_A002 Dark Grown 1 (DG1) Sorg... 123 2e-27
55 gb|BE024006|BE024006 sm95c09.y1 Gm-c1015 Glycine max cDNA clone ... 122 2e-27
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emb|AI898070|AI898070 EST267513 tomato ovary, TAMU Lycopersicon ... 119 2e-26
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- emb|AI776842|AI776842 EST257942 tomato resistant, Cornell Lycopersicon... 110 2e-23
emb|AA556663|AA556663 518 Loblolly pine CA Pinus taeda cDNA clone... 61 2e-20
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emb|AA519752|AA519752 TgESTzz28f05.r1 TgME49 invivo Bradyzoite c... 34 1.4
emb|AA785314|AA785314 g6d11a1.fl Aspergillus nidulans 24hr asexu... 34 1.9
emb|AQ367507|AQ367507 tox0002H01r CUGI Tomato BAC Library Lycop... 34 1.9
emb|AW348996|AW348996 GM210003B22A1R Gm-r1021 Glycine max cDNA 3... 33 2.6
25 emb|AW348959|AW348959 GM210004A12C6R Gm-r1021 Glycine max cDNA 3... 33 2.6
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emb|AW348503|AW348503 GM210002B12C1R Gm-r1021 Glycine max cDNA 3... 33 2.6
emb|AW398499|AW398499 EST308999 L. pennellii trichome, Cornell U... 33 2.6
emb|AW349705|AW349705 GM210005B21C6R Gm-r1021 Glycine max cDNA 3... 33 2.6
30 emb|AW596289|AW596289 sj01e09.y1 Gm-c1032 Glycine max cDNA clone... 33 3.5
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emb|AI441442|AI441442 sa86a02.y1 Gm-c1004 Glycine max cDNA clone... 33 3.5
emb|X78037|MIOB250 O. berteriana mitochondrial DNA for orf250. 33 3.5
35 emb|AC004688|AC004688 Plasmodium falciparum chromosome 12 clone ... 32 4.8
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emb|AC004709|AC004709 Plasmodium falciparum chromosome 12, *** S... 32 4.8
emb|AF119172|AF119172 Cyanophora paradoxa alpha-tubulin (atub) g... 32 4.8
emb|AW101722|AW101722 sd69d02.y1 Gm-c1008 Glycine max cDNA clone... 32 4.8
40 gb|U56098|AOU56098 Aspergillus oryzae putative DNA binding prote... 32 4.8
emb|AI507866|AI507866 sa88b06.y1 Gm-c1004 Glycine max cDNA clone... 32 4.8
gb|BE125213|BE125213 DG1_16_E11.b1_A002 Dark Grown 1 (DG1) Sorgh... 32 4.8
emb|AA785315|AA785315 g6d11a1.r1 Aspergillus nidulans 24hr asexu... 32 4.8
gb|BE059192|BE059192 sn27d12.y1 Gm-c1016 Glycine max cDNA clone ... 32 4.8
45 emb|Z71334|SCYNL058C S.cerevisiae chromosome XIV reading frame O... 32 6.6
emb|AW219947|AW219947 EST302430 tomato root during/after fruit s... 32 6.6
emb|X56235|SCHYP1 Yeast (S.cerevisiae) HYP1 gene for hypusine co... 32 6.6
emb|AL121851|LMFL2581 Leishmania major Friedlin chromosome 23 co... 32 6.6
emb|AW686452|AW686452 NF041F08NR1F1000 Nodulated root Medicago t... 32 6.6
50 emb|Z67961|SPAC30D11 S.pombe chromosome I cosmid c30D11. 32 6.6
emb|AW395281|AW395281 sh46b07.y1 Gm-c1017 Glycine max cDNA clone... 32 6.6
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emb|AW667846|AW667846 GA_Ea0010022 Gossypium arboreum 7-10 dpa ... 32 6.6
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55 emb|AI043452|AI043452 TENU1011 T. cruzi epimastigote normalized ... 32 6.6
emb|AW773882|AW773882 EST332868 KV3 Medicago truncatula cDNA clo... 32 6.6
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gb|UI2141|SCU12141 Saccharomyces cerevisiae chromosome XIV left ... 32 6.6
emb|AQ653810|AQ653810 Sheared DNA-8B13.TF Sheared DNA Trypanosom... 32 6.6
60 emb|AW219759|AW219759 EST302241 tomato root during/after fruit s... 32 6.6
emb|AI069155|AI069155 mgae0005dA02f Magnaporthe grisea Appressor... 27 7.0

- emb|AC023488|AC023488 Trypanosoma brucei chromosome IV clone RPC... 31 9.1
 emb|AW509230|AW509230 sh92h07.y1 Gm-c1016 Glycine max cDNA clone... 31 9.1
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 emb|AF206700|AF206700 Neurospora crassa heterokaryon incompatibi... 31 9.1
 5 emb|AW621293|AW621293 EST312091 tomato root during/after fruit s... 31 9.1
 dbj|D15051|BLYIDS2NK Hordeum vulgare gene for ids2, complete cds. 31 9.1
 gb|BE021558|BE021558 sm49e02.y1 Gm-c1028 Glycine max cDNA clone ... 31 9.1
 emb|AW442607|AW442607 EST307537 tomato mixed elicitor, BTI Lycop... 31 9.1
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 10 emb|AI780125|AI780125 EST261004 tomato susceptible, Cornell Lyco... 31 9.1

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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- emb|AI938176|AI938176 sc40e07.y1 Gm-c1014 Glycine max cDNA clone... 226 1e-58
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 30 gb|BE057559|BE057559 sn04a01.y1 Gm-c1015 Glycine max cDNA clone ... 210 1e-53
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 emb|AW219398|AW219398 EST301976 tomato root during/after fruit s... 190 9e-48
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 emb|AW399412|AW399412 EST309912 L. pennellii trichome, Cornell U... 189 2e-47
 35 emb|AW399345|AW399345 EST309845 L. pennellii trichome, Cornell U... 189 2e-47
 emb|AI896756|AI896756 EST266199 tomato callus, TAMU Lycopersicon... 188 4e-47
 emb|AW030559|AW030559 EST273814 tomato callus, TAMU Lycopersicon... 188 4e-47
 emb|AI773854|AI773854 EST254954 tomato resistant, Cornell Lycop... 133 2e-44
 emb|AW832123|AW832123 sm30h02.y1 Gm-c1028 Glycine max cDNA clone... 178 3e-44
 40 emb|AI894447|AI894447 EST263902 tomato callus, TAMU Lycopersicon... 177 9e-44
 emb|AI778651|AI778651 EST259530 tomato susceptible, Cornell Lyco... 177 9e-44
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 emb|AW568464|AW568464 si59b03.y1 Gm-r1030 Glycine max cDNA clone... 163 2e-39
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	gb BE123900 BE123900 EST394025 DSIL Medicago truncatula cDNA clo...	58	7e-08
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5	emb AW184959 AW184959 se84d10.y1 Gm-c1023 Glycine max cDNA clone...	52	6e-06
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	emb AW349705 AW349705 GM210005B21C6R Gm-r1021 Glycine max cDNA 3...	33	2.6
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 http://www3.ncbi.nlm.nih.gov/htbin-
 10 post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac006587| /ncgi
 http://www.ncgr.org/cgi-bin/ff?ac006587
 (504 letters)

Database: plantfungal
 15 661,018 sequences; 426,114,510 total letters

Searching.....done

Score E

20 Sequences producing significant alignments: (bits) Value

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 25 emb|AC005139|AC005139 Plasmodium falciparum chromosome 12, *** S... 36 0.22
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 emb|AL034559|PFMAL3P7 Plasmodium falciparum MAL3P7, complete seq... 35 0.30
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 emb|AE001384|AE001384 Plasmodium falciparum chromosome 2, sectio... 35 0.30
 30 gb|BE034256|BE034256 MH02B11 MH Mesembryanthemum crystallinum cD... 35 0.41
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 35 emb|Z97348|PFMAL3P1 Plasmodium falciparum MAL3P1, complete seque... 35 0.41
 emb|X56950|PFCALM P. falciparum gene for calmodulin. 35 0.41
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 emb|AL034557|PFMAL4P1 Plasmodium falciparum chromosome 4 strain ... 33 1.5
 60 emb|AA550506|AA550506 1663m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 33 1.5
 emb|AW286549|AW286549 LG1_334_C05.g1_A002 Light Grown 1 (LG1) So... 33 1.5

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 5 emb|AL034556|PFMAL3P5 *Plasmodium falciparum* MAL3P5, complete seq... 33 1.5
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 10 emb|AV419396|AV419396 AV419396 *Lotus japonicus* young plants (two... 33 2.0
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 15 emb|AL096783|PFMAL13P9 *Plasmodium falciparum* chromosome 13 strai... 33 2.0
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 emb|AL031744|PFMAL1P1 *Plasmodium falciparum* chromosome 1 strain ... 32 2.8
 emb|AF093584|AF093584 *Plasmodium vivax* merozoite surface protein... 32 2.8
 emb|AC006280|AC006280 *Plasmodium falciparum* chromosome 12 clone ... 32 2.8
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 emb|AE001410|AE001410 *Plasmodium falciparum* chromosome 2, sectio... 32 2.8
 emb|X74069|SCALP1 *S.cerevisiae* APL1 gene for basic-amino-acid pe... 32 2.8
 emb|AC005504|AC005504 *Plasmodium falciparum* chromosome 12, *** S... 32 2.8
 emb|AW727908|AW727908 GA_Ea0028M15 *Gossypium arboreum* 7-10 dpa ... 32 2.8
 25 emb|AE001395|AE001395 *Plasmodium falciparum* chromosome 2, sectio... 32 2.8
 emb|AF030694|AF030694 *Plasmodium falciparum* strain Dd2 heat shoc... 32 2.8
 emb|AQ647469|AQ647469 RPCI93-EcoRI-6E20.TJ RPCI93-EcoRI Trypanos... 32 2.8
 emb|Z38061|SC9168 *S.cerevisiae* chromosome IX cosmid 9168. 32 2.8
 emb|AL110675|CNS018QK *Botrytis cinerea* strain T4 cDNA library un... 32 2.8
 30 emb|AL008970|PFMAL3P4 *Plasmodium falciparum* MAL3P4, complete seq... 31 2.9
 emb|AW035978|AW035978 EST282837 tomato callus, TAMU *Lycopersicon*... 32 3.8
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 emb|AW030017|AW030017 EST273272 tomato callus, TAMU *Lycopersicon*... 32 3.8
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 40 emb|AQ906056|AQ906056 GSSTc07178 Trypanosome cruzi random genom... 32 3.8
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 emb|X16104|SBKAFGK1 *Sorghum* DNA for kafirin, pGK1. 32 3.8
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 emb|AC011016|AC011016 *Leishmania major* chromosome 35 clone L218 ... 32 3.8
 45 emb|AL033503|CAC49C4 *C.albicans* cosmid Ca49C4. 32 3.8
 emb|AW761381|AW761381 sl66g01.y1 Gm-cl027 *Glycine max* cDNA clone... 32 3.8
 emb|AW220823|AW220823 EST297292 tomato fruit mature green, TAMU ... 32 3.8
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 50 emb|AA557046|AA557046 888 Loblolly pine N *Pinus taeda* cDNA clone... 32 3.8
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 emb|AQ935320|AQ935320 CpG2407A *CpIOWAgDNA1* *Cryptosporidium parvu*... 31 5.2
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 55 emb|AE001401|AE001401 *Plasmodium falciparum* chromosome 2, sectio... 31 5.2
 emb|AE001380|AE001380 *Plasmodium falciparum* chromosome 2, sectio... 31 5.2
 emb|AC004157|AC004157 *Plasmodium falciparum* chromosome 12 clone ... 31 5.2
 emb|AE001376|AE001376 *Plasmodium falciparum* chromosome 2, sectio... 31 5.2
 emb|AQ941118|AQ941118 Sheared DNA-35E12.TF Sheared DNA Trypanoso... 31 5.2
 60 emb|AQ949411|AQ949411 Sheared DNA-38N10.TF Sheared DNA Trypanoso... 31 5.2

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 (375 letters)

Database: plantfungal
 10 661,018 sequences; 426,114,510 total letters

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20	emb AI943438 AI943438 MF02E10 MF Mesembryanthemum crystallinum c...	158	2e-38	
	gb BE033541 BE033541 MF02E10 MF Mesembryanthemum crystallinum cD...	158	2e-38	
	emb AW667752 AW667752 GA_Ea0010I06 Gossypium arboreum 7-10 dpa ...	155	1e-37	
	emb AW747419 AW747419 WSI_68_E10.b1_A002 Water-stressed 1 (WS1) ...	155	2e-37	
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	emb AW441269 AW441269 EST310665 tomato fruit red ripe, TAMU Lyco...	153	5e-37	
25	emb AW223703 AW223703 EST300514 tomato fruit red ripe, TAMU Lyco...	153	5e-37	
	emb AW034892 AW034892 EST279121 tomato callus, TAMU Lycopersicon...	153	5e-37	
	emb AW224013 AW224013 EST300824 tomato fruit red ripe, TAMU Lyco...	153	5e-37	
	emb AW907232 AW907232 EST343355 potato stolon, Cornell Universit...	153	7e-37	
	emb AW747501 AW747501 WSI_68_E10.g1_A002 Water-stressed 1 (WS1) ...	152	9e-37	
30	emb AW730496 AW730496 GA_Ea0026O23 Gossypium arboreum 7-10 dpa ...	152	9e-37	
	emb AW760599 AW760599 sl52d09.y1 Gm-c1027 Glycine max cDNA clone...	151	2e-36	
	emb AI960575 AI960575 sc86c01.y1 Gm-c1018 Glycine max cDNA clone...	151	2e-36	
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35	emb AI443884 AI443884 sa44f06.y1 Gm-c1004 Glycine max cDNA clone...	149	6e-36	
	emb AW568285 AW568285 si69g11.y1 Gm-r1030 Glycine max cDNA clone...	149	6e-36	
	emb AW186193 AW186193 se64g04.y1 Gm-c1019 Glycine max cDNA clone...	149	6e-36	
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40	emb AW132618 AW132618 se06f04.y1 Gm-c1013 Glycine max cDNA clone...	148	2e-35	
	emb AI777814 AI777814 EST258693 tomato susceptible, Cornell Lyco...	146	8e-35	
	emb AV408412 AV408412 AV408412 Lotus japonicus young plants (two...	141	2e-33	
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	emb AL160493 LMFLCHR26 Leishmania major Friedlin assembled chrom...	102	1e-21	
	emb AW738874 AW738874 gb03e09.y1 Moss EST library PPN Physcomitr...	99	2e-20	
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50	emb AL049558 SPBC216 S.pombe chromosome II cosmid c216.	67	2e-19	
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	emb AI822525 AI822525 L0-1030T3 Ice plant Lambda Uni-Zap XR expr...	95	3e-19	
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	emb AW222361 AW222361 EST299172 tomato fruit red ripe, TAMU Lyco...	90	5e-18	
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60	emb AW220746 AW220746 EST297215 tomato fruit mature green, TAMU ...	90	5e-18	
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 emb|AI026521|AI026521 TENU0733 T. cruzi epimastigote normalized ... 73 1e-16
 5 emb|X59720|SCCHRIII S.cerevisiae chromosome III complete DNA seq... 85 2e-16
 gb|T36700|T36700 EST101687 S. cerevisiae strain X2180-1A Sacchar... 79 1e-14
 emb|AW650769|AW650769 EST329223 tomato germinating seedlings, TA... 79 1e-14
 emb|AW739119|AW739119 gb26a12.y1 Moss EST library PPN Physcomitr... 79 1e-14
 emb|AT000681|AT000681 AT000681 Brassica rapa guard cell Brassica... 62 4e-14
 10 gb|N81594|N81594 TgESTzy60e01.r1 TgRH Tachyzoite cDNA Toxoplasma... 55 1e-12
 emb|AA740047|AA740047 812 PtIFG2 Pinus taeda cDNA clone 9275M 3'... 62 4e-12
 emb|AW907238|AW907238 EST343361 potato stolon, Cornell Universit... 68 2e-11
 emb|AA948748|AA948748 L0-267M13R Ice plant Lambda Uni-Zap XR exp... 66 1e-10
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 15 emb|AW351206|AW351206 GM210011A20E12R Gm-r1021 Glycine max cDNA ... 61 5e-09
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 20 emb|AW931744|AW931744 EST357587 tomato fruit mature green, TAMU ... 46 9e-05
 emb|AW459770|AW459770 sh91h03.y1 Gm-c1016 Glycine max cDNA clone... 42 0.002
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 emb|AL136235|SPAC664 S.pombe chromosome I cosmid c664. 32 1.8
 30 emb|AU013634|AU013634 AU013634 Schizosaccharomyces pombe late lo... 32 1.8
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 35 emb|AW310022|AW310022 sf28e03.x1 Gm-c1028 Glycine max cDNA clone... 31 3.3
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 45 emb|X90948|ANRNAHSP7 A.nodosum mRNA for HSP70 protein. 31 4.6
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 emb|AW738897|AW738897 gb03h02.y1 Moss EST library PPN Physcomitr... 31 4.6
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 50 emb|Z99262|SPAC9E9 S.pombe chromosome I cosmid c9E9. 30 6.3
 emb|X79192|FBPDK F.brownii pdk gene. 30 6.3
 emb|AI164197|AI164197 A056p02u Hybrid aspen plasmid library Popu... 30 6.3
 emb|AW156147|AW156147 se20b05.y1 Gm-c1015 Glycine max cDNA clone... 30 6.3
 emb|X75516|FPPDK F.pringlei mRNA for pyruvate, orthophosphate di... 30 6.3
 55 gb|U08399|FBU08399 Flaveria brownii cold stable pyruvate, orthop... 30 6.3

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(844 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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	emb AW733754 AW733754	sk77g11.y1	Gm-cl016 Glycine max cDNA clone...	290 9e-78
15	emb AW561007 AW561007	EST316055	DSIR Medicago truncatula cDNA cl...	287 8e-77
	emb AI489189 AI489189	EST247528	tomato ovary, TAMU Lycopersicon ...	273 1e-72
	emb AI488043 AI488043	EST246365	tomato ovary, TAMU Lycopersicon ...	269 2e-71
	emb AW625207 AW625207	EST319114	tomato radicle, 5 d post-imbibit...	258 5e-68
	emb AW559910 AW559910	EST314958	DSIR Medicago truncatula cDNA cl...	258 5e-68
20	emb AW559909 AW559909	EST314957	DSIR Medicago truncatula cDNA cl...	245 4e-64
	emb AI487722 AI487722	EST246044	tomato ovary, TAMU Lycopersicon ...	241 5e-63
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	emb AW624963 AW624963	EST313792	tomato radicle, 5 d post-imbibit...	234 8e-61
	emb AW774997 AW774997	EST334148	KV3 Medicago truncatula cDNA clo...	217 1e-55
25	emb AA495616 AA495616	c425 Zhou and Ragan 1993	Gracilaria gracil...	118 3e-52
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35	emb Z48639 SC9920	S.cerevisiae chromosome XIII	cosmid 9920.	67 2e-34
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40	emb Z72939 SCYGR154C	S.cerevisiae chromosome VII	reading frame O...	51 2e-23
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45	emb AI327824 AI327824	j0c06a1.r1	Aspergillus nidulans 24hr asexu...	77 1e-17
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	emb AA966531 AA966531	w5h12a1.r1	Aspergillus nidulans 24hr asexu...	82 5e-15
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50	emb AW442112 AW442112	EST311508	tomato fruit red ripe, TAMU Lyco...	80 2e-14
	emb AW704348 AW704348	sk18b11.y1	Gm-cl028 Glycine max cDNA clone...	77 2e-13
	emb AW221318 AW221318	EST297787	tomato fruit mature green, TAMU ...	68 9e-11
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	emb AQ492097 AQ492097	V111F10 mTn-3xHA/lacZ	Insertion Library Sa...	55 9e-07
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 5 emb|X71362|HVDHN7 H.vulgare gene for dehydrin 7. 34 1.5
 emb|X88851|SCESTGENE S.cerevisiae DNA for hypothetical proteins a... 34 1.5
 emb|AF043087|AF043087 Hordeum vulgare dehydrin 1 (dhn1) gene, co... 34 1.5
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 emb|Y10224|CMAO1 C.melo aol gene, partial. 34 2.1
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 15 emb|AW730699|AW730699 GA_Ea0027C11 Gossypium arboreum 7-10 dpa ... 33 3.9
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 emb|X68577|SC114 S. cerevisiae 11.4kb segment of chromosome II. 32 5.3
 25 gb|M31036|YSCACH1A S.cerevisiae acetyl-CoA hydrolase (ACH1) mRNA... 32 5.3
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- Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters
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| 50 Sequences producing significant alignments: | | (bits) | Value |
| emb AF053127 AF053127 Malus domestica leucine-rich receptor-like... | 169 | 8e-99 | |
| emb AW930866 AW930866 EST356709 tomato fruit mature green, TAMU ... | 152 | 2e-83 | |
| emb AF197947 AF197947 Glycine max receptor protein kinase-like p... | 160 | 3e-83 | |
| 55 emb AF197946 AF197946 Glycine max receptor protein kinase-like p... | 154 | 8e-81 | |
| emb AI897516 AI897516 EST266959 tomato ovary, TAMU Lycopersicon ... | 133 | 2e-73 | |
| emb AF053998 AF053998 Lycopersicon esculentum Hcr2-5D (Hcr2-5D) ... | 143 | 2e-72 | |
| emb A67434 A67434 Sequence 7 from Patent WO9743429. | 143 | 2e-72 | |
| emb AW650851 AW650851 EST329305 tomato germinating seedlings, TA... | 123 | 4e-72 | |
| 60 emb AF053995 AF053995 Lycopersicon esculentum Hcr2-0B (Hcr2-0B) ... | 144 | 2e-71 | |
| emb AF053993 AF053993 Lycopersicon esculentum disease resistance... | 145 | 4e-71 | |

	emb A67429 A67429 Sequence 2 from Patent WO9743429.	145 4e-71
	emb A67428 A67428 Sequence 1 from Patent WO9743429.	145 4e-71
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	emb A57130 A57130 Sequence 1 from Patent WO9531564.	150 4e-70
5	gb U42445 U42445 Lycopersicon pimpinellifolium leucine rich repe...	150 4e-70
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	emb AW560797 AW560797 EST315845 DSIR Medicago truncatula cDNA cl...	240 5e-62
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10	emb A67432 A67432 Sequence 5 from Patent WO9743429.	144 7e-60
	emb AW033860 AW033860 EST277431 tomato callus, TAMU Lycopersicon...	117 2e-59
	gb U77888 INU77888 Ipomoea nil receptor-like protein kinase (irr...	136 1e-55
	emb AJ486612 AJ486612 EST244933 tomato ovary, TAMU Lycopersicon ...	133 2e-53
	emb AW979740 AW979740 EST341365 tomato root deficiency, Cornell ...	105 5e-53
15	emb AF053996 AF053996 Lycopersicon pimpinellifolium Hcr2-2A (Hcr...	142 2e-52
	emb AW726024 AW726024 GA__Ea0020G24 Gossypium arboreum 7-10 dpa ...	149 1e-51
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20	emb AW693988 AW693988 NF071C05ST1F1037 Developing stem Medicago ...	190 6e-47
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	emb AW650232 AW650232 EST328686 tomato germinating seedlings, TA...	96 7e-45
	emb AJ895242 AJ895242 EST264685 tomato callus, TAMU Lycopersicon...	154 1e-44
	gb BE060160 BE060160 HVSMEg0011B12f Hordeum vulgare pre-anthesis...	90 4e-44
25	emb AW621923 AW621923 EST312721 tomato root during/after fruit s...	94 2e-43
	emb AW428824 AW428824 Ljirmp24-927-c5 Ljirmp Lambda HybriZap ...	120 8e-43
	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	85 2e-42
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30	emb AW668493 AW668493 GA__Ea0014C20 Gossypium arboreum 7-10 dpa ...	92 6e-41
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	83 7e-41
	emb AW929662 AW929662 EST338450 tomato flower buds 8 mm to pre-a...	92 8e-41
	gb U51741 ITU51741 Ipomoea trifida receptor protein kinase 2 (IR...	128 1e-40
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35	emb Z73295 CRPK1 Croseus mRNA for receptor-like protein kinase.	136 1e-40
	emb AW684304 AW684304 NF015C05NR1F1000 Nodulated root Medicago t...	108 1e-40
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	gb U20948 ITU20948 Ipomoea trifida receptor protein kinase (IRK1...	129 2e-40
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40	emb AW036763 AW036763 EST252152 tomato ovary, TAMU Lycopersicon ...	85 2e-40
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	emb AW704459 AW704459 sk53c10.y1 Gm-c1019 Glycine max cDNA clone...	100 3e-40
	emb AW036762 AW036762 EST252151 tomato ovary, TAMU Lycopersicon ...	85 4e-40
	emb AV427160 AV427160 AV427160 Lotus japonicus young plants (two...	117 4e-39
45	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	84 4e-39
	emb AA557073 AA557073 915 Loblolly pine N Pinus taeda cDNA clone...	96 4e-39
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	emb AW299180 AW299180 EST305990 KV2 Medicago truncatula cDNA clo...	122 7e-39
	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	85 3e-38
50	emb AW727470 AW727470 GA__Ea0012H16 Gossypium arboreum 7-10 dpa ...	93 3e-38
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55	emb AW040672 AW040672 EST283536 tomato mixed elicitor, BTI Lycop...	102 4e-38
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 10 emb|AW185015|AW185015 se85e10.y1 Gm-c1023 Glycine max cDNA clone... 100 2e-36
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 15 emb|AA738545|AA738545 SbRLK3 Sorghum bicolor cv. TX430 leaf Sorg... 85 8e-36
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 emb|AJ245479|BNA245479 Brassica napus SI3, slk, srk, CePP, Fmt,... 84 2e-35
 emb|AW734633|AW734633 sk97d07.y1 Gm-c1035 Glycine max cDNA clone... 101 2e-35
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 20 emb|AW736597|AW736597 EST333089 KV3 Medicago truncatula cDNA clo... 91 4e-35
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 emb|Y14286|BOY14286 Brassica oleracea SFR3 gene, partial. 82 3e-34

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 35 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al031187|/ncgi)
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 (2553 letters)

40 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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45	Score	E
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	emb X98520 BOSFR2 B.oleracea mRNA for receptor-like kinase, SFR2.	820 0.0
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50	emb AB008191 AB008191 Brassica rapa mRNA for SRK29, complete cds.	510 0.0
	gb M97667 BNASTKR Brassica napus ssp. oleifera serine/threonine ...	505 0.0
	emb Y18259 BOY18259 Brassica oleracea mRNA for SRK5 protein, par...	504 0.0
	emb AB024416 AB024416 Brassica oleracea SRK2-b mRNA, complete cds.	501 0.0
	gb M76647 BNASKR6A Brassica oleracea receptor protein kinase (SK...	490 0.0
55	emb AB032473 AB032473 Brassica oleracea SRK18 mRNA for S18 S-loc...	489 0.0
	dbj D38563 BOLRPKB Brassica campestris mRNA for receptor protein...	488 0.0
	emb Y18260 BOY18260 Brassica oleracea mRNA for SRK15 protein, pa...	485 0.0
	emb AB013720 AB013720 Brassica oleracea mRNA for SRK23Bol, parti...	483 0.0
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60	emb AB012106 AB012106 Brassica rapa mRNA for SRK45, complete cds.	458 0.0
	gb U00443 BNU00443 Brassica napus cultivar T2 S-receptor kinase ...	455 0.0

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 5 emb|Y12530|BOARLKG B.oleraceae gene encoding serine/threonine ... 652 0.0
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 emb|AB000970|AB000970 Brassica campestris gene for receptor kina... 481 0.0
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 10 emb|AB024418|AB024418 Brassica oleracea SLG13-b gene, partial cds. 506 0.0
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 emb|AB009680|AB009680 Raphanus sativus SLG(S4) gene for S glycop... 493 e-179
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 15 dbj|D85206|D85206 Brassica oleracea DNA for S glycoprotein, part... 406 e-177
 dbj|D85215|D85215 Brassica campestris DNA for S glycoprotein, pa... 295 e-176
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 25 emb|X55274|BCSLG8 B.campestris SLG-8 gene for S-locus glycoprotein. 482 e-175
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 30 emb|AB009681|AB009681 Raphanus sativus SLG(S5) gene for S glycop... 406 e-173
 gb|S70937|S70937 self-incompatibility gene [Brassica campestris,... 283 e-173
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 emb|AB009683|AB009683 Raphanus sativus SLG(S8) gene for S glycop... 284 e-173
 35 dbj|D85227|D85227 Brassica campestris DNA for S glycoprotein, pa... 293 e-172
 dbj|D85211|D85211 Brassica oleracea DNA for S glycoprotein, part... 281 e-172
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 40 dbj|D85216|D85216 Brassica campestris DNA for S glycoprotein, pa... 409 e-171
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 45 dbj|D85208|D85208 Brassica oleracea DNA for S glycoprotein, part... 282 e-171
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 50 dbj|D85205|D85205 Brassica oleracea DNA for S glycoprotein, part... 395 e-170
 dbj|D85221|D85221 Brassica campestris DNA for S glycoprotein, pa... 348 e-170
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 55 emb|Z21608|BNESLOGPA B.napus mRNA for endogenous S-locus glycopr... 477 e-168
 gb|L10736|BNASLGGA Brassica napus S-locus related glycoprotein (... 477 e-168
 dbj|D85222|D85222 Brassica campestris DNA for S glycoprotein, pa... 243 e-166
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 emb|AB009679|AB009679 Raphanus sativus SLG(S3) gene for S glycop... 285 e-166
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 dbj|D85214|D85214 Brassica campestris DNA for S glycoprotein, pa... 395 e-163

- emb|AB009677|AB009677 *Raphanus sativus* SLG(S1) gene for S glycop... 266 e-163
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 10 dbj|D85223|D85223 *Brassica campestris* DNA for S glycoprotein, pa... 224 e-160
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 20 emb|Y12321|BOY12321 *Brassica oleracea* SLG-Sc and SLA-Sc genes an... 285 e-149
 emb|AB009872|AB009872 *Orychophragmus violaceus* gene for SLR1, pa... 413 e-149
 emb|X57673|BOSLR2RNA *B. oleracea* RNA for S-locus-related glycopr... 167 e-149
 emb|AB009873|AB009873 *Cheiranthus cheiri* gene for SLR1, partial ... 163 e-147
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 25 emb|X52089|BOSLRG *Brassica* gene for S locus related glycoprotein. 272 e-143

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<http://www.ncgr.org/cgi-bin/ff?ac003974>
 (2673 letters)

35 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

40 Searching.....done

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	Sequences producing significant alignments:		(bits) Value
45	emb AF053998 AF053998 <i>Lycopersicon esculentum</i> Hcr2-5D (Hcr2-5D) ...	148	4e-74
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	emb AF053993 AF053993 <i>Lycopersicon esculentum</i> disease resistance...	148	4e-74
	emb A67429 A67429 Sequence 2 from Patent WO9743429.	148	4e-74
	emb A67428 A67428 Sequence 1 from Patent WO9743429.	148	4e-74
50	emb AF053995 AF053995 <i>Lycopersicon esculentum</i> Hcr2-0B (Hcr2-0B) ...	150	4e-74
	emb AF053997 AF053997 <i>Lycopersicon esculentum</i> Hcr2-5B (Hcr2-5B) ...	146	1e-72
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	emb AF053996 AF053996 <i>Lycopersicon pimpinellifolium</i> Hcr2-2A (Hcr...	144	3e-35
60	emb AF119041 AF119041 <i>Lycopersicon esculentum</i> haplotype Southern...	139	2e-33
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- emb|AJ002236|LPJ002236 *Lycopersicon pimpinellifolium* Cf-9 resist... 140 4e-33
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- 10 emb|X81370|TAAWJL236 *T. aestivum* (subclone pAWJL236) AWJL236 gene. 115 8e-27
emb|AF140552|AF140552 *Lycopersicon esculentum* plant disease resi... 121 2e-26
emb|AI895949|AI895949 EST265392 tomato callus, TAMU *Lycopersicon*... 70 5e-25
emb|AW624314|AW624314 EST322175 tomato flower buds 3-8 mm, Corne... 113 5e-24
emb|X81369|TAAWJL218 *T. aestivum* (subclone pAWJL218) AWJL218 gene. 104 1e-23
- 15 emb|X81367|TAAWJL172 *T. aestivum* (subclone pAWJL172) AWJL172 gene. 99 7e-23
emb|X81368|TAAWJL175 *T. aestivum* (subclone pAWJL175) AWJL175 gene. 101 2e-22
emb|AW705275|AW705275 sk59a10.y1 Gm-cl019 *Glycine max* cDNA clone... 108 2e-22
emb|AF166121|AF166121 *Hordeum vulgare* Cf2/Cf5 disease resistance... 94 3e-22
emb|AI779817|AI779817 EST260696 tomato susceptible, Cornell Lyco... 100 1e-21
- 20 emb|AW888094|AW888094 NXNV_108_E11_F Nsf Xylem Normal wood Verti... 105 2e-21
emb|AQ917191|AQ917191 T233043b *Medicago truncatula* BAC library M... 93 1e-20
gb|U77888|INU77888 *Ipomoea nil* receptor-like protein kinase (inr... 79 2e-20
emb|AQ367638|AQ367638 tox0002D20f CUGI Tomato BAC Library Lycop... 101 3e-20
emb|AZ044600|AZ044600 Gm_UMB001_116_G01.R UMN Soybean BAC Librar... 73 2e-19
- 25 emb|AW064561|AW064561 ST33A08 Pine TriplEx shoot tip library Pin... 98 3e-19
emb|AI484441|AI484441 EST242451 tomato ovary, TAMU *Lycopersicon* ... 98 3e-19
emb|AW279193|AW279193 sf67g09.y1 Gm-cl013 *Glycine max* cDNA clone... 98 4e-19
emb|AI900597|AI900597 sc13d11.y1 Gm-cl013 *Glycine max* cDNA clone... 97 5e-19
emb|AF197946|AF197946 *Glycine max* receptor protein kinase-like p... 82 1e-18
- 30 emb|AW032163|AW032163 EST275617 tomato callus, TAMU *Lycopersicon*... 64 1e-18
emb|AW979663|AW979663 EST341269 tomato root deficiency, Cornell ... 61 1e-18
emb|AW650508|AW650508 EST328962 tomato germinating seedlings, TA... 91 1e-18
emb|AI488023|AI488023 EST246345 tomato ovary, TAMU *Lycopersicon* ... 91 1e-18
emb|AI896676|AI896676 EST266119 tomato callus, TAMU *Lycopersicon*... 91 1e-18
- 35 emb|AW307311|AW307311 sf55d03.y1 Gm-cl009 *Glycine max* cDNA clone... 66 2e-18
emb|AV415568|AV415568 AV415568 *Lotus japonicus* young plants (two... 85 2e-18
emb|AI895309|AI895309 EST264752 tomato callus, TAMU *Lycopersicon*... 95 2e-18
emb|AI727073|AI727073 BNLGHi7256 Six-day Cotton fiber *Gossypium* ... 95 2e-18
emb|AW306675|AW306675 se53h08.y1 Gm-cl017 *Glycine max* cDNA clone... 95 3e-18
- 40 emb|X79130|TSLRRR *Triticum* sp. (pAWJL3) leucine rich repeat regi... 84 4e-18
emb|AW031498|AW031498 EST274952 tomato callus, TAMU *Lycopersicon*... 94 5e-18
emb|AW775087|AW775087 EST334238 KV3 *Medicago truncatula* cDNA clo... 94 6e-18
emb|AW690301|AW690301 NF029C05ST1F1000 Developing stem *Medicago* ... 81 7e-18
emb|AW267958|AW267958 EST306300 DSIR *Medicago truncatula* cDNA cl... 80 7e-18
- 45 emb|AI895893|AI895893 EST265336 tomato callus, TAMU *Lycopersicon*... 61 9e-18
emb|AW647847|AW647847 EST326301 tomato germinating seedlings, TA... 91 1e-17
emb|AW929189|AW929189 EST337977 tomato flower buds 8 mm to pre-a... 92 2e-17
emb|AW689506|AW689506 NF021E06ST1F1000 Developing stem *Medicago* ... 92 2e-17
emb|AF197947|AF197947 *Glycine max* receptor protein kinase-like p... 82 2e-17
- 50 emb|AW929854|AW929854 EST354124 tomato flower buds 8 mm to pre-a... 91 4e-17
emb|AW929780|AW929780 EST354050 tomato flower buds 8 mm to pre-a... 91 4e-17
emb|AW031218|AW031218 EST274756 tomato callus, TAMU *Lycopersicon*... 91 4e-17
emb|AW033367|AW033367 EST276938 tomato callus, TAMU *Lycopersicon*... 89 1e-16
emb|AI443128|AI443128 sa84f10.y1 Gm-cl004 *Glycine max* cDNA clone... 89 1e-16
- 55 emb|AI896313|AI896313 EST265756 tomato callus, TAMU *Lycopersicon*... 60 1e-16
emb|AW735867|AW735867 EST336635 tomato flower buds 0-3 mm, Corne... 89 2e-16
emb|AW980804|AW980804 EST391957 GVN *Medicago truncatula* cDNA clo... 69 2e-16
emb|AI488443|AI488443 EST246782 tomato ovary, TAMU *Lycopersicon* ... 88 3e-16
emb|AW033129|AW033129 EST276688 tomato callus, TAMU *Lycopersicon*... 78 3e-16
- 60 emb|AW127035|AW127035 ga20c02.y1 Moss EST library PPU *Physcomitr...* 88 4e-16
emb|AI895669|AI895669 EST265112 tomato callus, TAMU *Lycopersicon*... 88 4e-16

- emb|AW618685|AW618685 EST320671 *L. pennellii* trichome, Cornell U... 88 4e-16
 emb|AI894989|AI894989 EST264432 tomato callus, TAMU Lycopersicon... 88 4e-16
 emb|AI782076|AI782076 EST262955 tomato susceptible, Cornell Lyco... 87 5e-16
 emb|AW648795|AW648795 EST327249 tomato germinating seedlings, TA... 87 5e-16
 5 emb|AW694942|AW694942 NF081G02ST1F1018 Developing stem Medicago ... 78 6e-16
 emb|AV415057|AV415057 AV415057 *Lotus japonicus* young plants (two... 87 7e-16
 emb|AW399097|AW399097 EST309597 *L. pennellii* trichome, Cornell U... 63 8e-16
 emb|AW761367|AW761367 sl66e07.y1 Gm-c1027 Glycine max cDNA clone... 86 1e-15
 emb|AW649208|AW649208 EST327662 tomato germinating seedlings, TA... 86 1e-15
 10 emb|AV428126|AV428126 AV428126 *Lotus japonicus* young plants (two... 85 2e-15
 emb|AW290705|AW290705 NXNV045C11F Nsf Xylem Normal wood Vertical... 85 2e-15
 emb|AI352869|AI352869 MB70-4A PZ204.BNlib Brassica napus cDNA cl... 85 2e-15
 emb|AA661049|AA661049 00946 MtrHE Medicago truncatula cDNA 5' si... 85 2e-15
 emb|AW455303|AW455303 EST311841 tomato root during/after fruit s... 85 3e-15
 15 emb|AW869870|AW869870 NXNV_122_E02_F Nsf Xylem Normal wood Verti... 85 3e-15
 emb|AW398651|AW398651 EST309151 *L. pennellii* trichome, Cornell U... 84 4e-15
 emb|AW398661|AW398661 EST309161 *L. pennellii* trichome, Cornell U... 84 4e-15
 emb|AF049920|AF049920 *Petunia x hybrida* PGPS/D4 (PGPS/D4) mRNA, ... 84 4e-15
 emb|AW624634|AW624634 EST322579 tomato flower buds 3-8 mm, Corne... 59 4e-15
 20 emb|AW618879|AW618879 EST320865 *L. pennellii* trichome, Cornell U... 62 4e-15
 gb|BE035885|BE035885 MO11F02 MO Mesembryanthemum crystallinum cD... 84 5e-15

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- 25 emb|cab51412.1| (al096882) acc synthase (atacs-6) [arabidopsis
 thaliana] /blast_score 0 /ec_number /family /chip nova /gb_link
 /ncgi
 (1488 letters)

Database: plantfungal

- 30 661,018 sequences; 426,114,510 total letters

Searching.....done

- | | | Score | E |
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| | Sequences producing significant alignments: | (bits) | Value |
| | emb X82273 BOACCS B.oleracea mRNA for ACC synthase. | 986 | 0.0 |
| | emb X72676 BJMACC B. juncea mRNA for 1-Aminocyclopropane-1-carbo... | 875 | 0.0 |
| | emb AF057563 AF057563 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-... | 765 | 0.0 |
| 40 | emb AJ005002 NTAJ5002 <i>Nicotiana tabacum</i> mRNA for 1-aminocyclopro... | 761 | 0.0 |
| | emb AB034992 AB034992 <i>Malus domestica</i> MdACS-5A mRNA for 1-aminoc... | 754 | 0.0 |
| | emb AB034993 AB034993 <i>Malus domestica</i> MdACS-5B mRNA for 1-aminoc... | 755 | 0.0 |
| | gb U72389 LEU72389 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1... | 756 | 0.0 |
| | gb U72390 LEU72390 <i>Lycopersicon esculentum</i> 1-aminocyclopropane-1... | 753 | 0.0 |
| 45 | emb AB033503 AB033503 <i>Populus euramericana</i> peacs-2 mRNA for 1-am... | 741 | 0.0 |
| | gb U68216 CPU68216 <i>Carica papaya</i> ACC synthase mRNA, complete cds. | 461 | 0.0 |
| | emb AF061605 AF061605 <i>Nicotiana glutinosa</i> ACC synthase mRNA, com... | 742 | 0.0 |
| | emb AB013100 AB013100 <i>Lycopersicon esculentum</i> LE-ACS6 mRNA for 1... | 741 | 0.0 |
| | emb AJ012551 CSI012551 <i>Citrus sinensis</i> mRNA for ACC synthase. | 449 | 0.0 |
| 50 | emb AB013346 AB013346 <i>Lycopersicon esculentum</i> mRNA for 1-aminocy... | 739 | 0.0 |
| | emb AB033502 AB033502 <i>Populus euphratica</i> peacs-1 mRNA for 1-amin... | 620 | 0.0 |
| | gb U88971 PHU88971 <i>Pelargonium hortorum</i> 1-aminocyclopropane-1-ca... | 455 | 0.0 |
| | emb Z11613 VRACCSYNM V.radiata mRNA for ACC synthase. | 456 | 0.0 |
| | emb X98492 NTACCS <i>Nicotiana tabacum</i> mRNA for ACC-synthase (clone... | 455 | 0.0 |
| 55 | emb X67100 GMCACCS1 G.max mRNA for ACC synthase. | 454 | 0.0 |
| | emb Z18952 DCAMCRBSY D.caryophyllus mRNA for 1-aminocyclopropane... | 716 | 0.0 |
| | emb AJ012696 CSI012696 <i>Citrus sinensis</i> mRNA for ACC synthase (AC... | 449 | 0.0 |
| | emb AJ011095 CSI011095 <i>Citrus sinensis</i> mRNA for ACC synthase (ac... | 452 | 0.0 |
| | emb Z18953 PHAMCRBSY P.hybrida mRNA for 1-aminocyclopropane 1-ca... | 450 | 0.0 |
| 60 | emb AB006804 AB006804 <i>Cucumis sativus</i> CS-ACS2 mRNA for ACC synth... | 451 | 0.0 |
| | emb AF080258 AF080258 <i>Musa acuminata</i> 1-aminocyclopropane-1-carbo... | 711 | 0.0 |

- emb|AF016459|AF016459 *Pisum sativum* 1-aminocyclopropane-1-carbox... 445 0.0
emb|AF109927|AF109927 *Musa acuminata* 1-aminocyclopropane-1-carbo... 707 0.0
dbj|D30805|CUS1A1CS Melon mRNA for 1-aminocyclopropane-1-carboxy... 705 0.0
emb|AB021906|AB021906 *Musa acuminata* MA-ACS1 mRNA for ACC syntha... 703 0.0
5 emb|AB006803|AB006803 *Cucumis sativus* CS-ACS1 mRNA for ACC synth... 703 0.0
emb|AF129508|AF129508 *Musa acuminata* 1-aminocyclopropane-1-carbo... 702 0.0
emb|X65982|NTXACCSYN *N.tabacum* mRNA for 1-aminocyclopropane-1-ca... 438 0.0
emb|AB031026|AB031026 *Prunus mume* PM-ACS1 mRNA for ACC synthase,... 434 0.0
emb|AB015625|AB015625 *Pyrus pyrifolia* pPPACS3 mRNA for 1-aminocy... 418 0.0
10 dbj|D01032|CUCACCW *Cucurbita maxima* mRNA for 1-aminocyclopropane... 695 0.0
dbj|E03724|E03724 cDNA encoding detriment induced type 1-aminocy... 695 0.0
gb|M58323|CUCACCSYN *Cucurbita pepo* 1-aminocyclopropane-1-carboxy... 692 0.0
emb|Y11357|CP1A1CS *C.papaya* mRNA for 1-aminocyclopropane-1-carbo... 430 0.0
emb|X62536|LEACC *L.esculentum* mRNA for ACC synthase. 327 0.0
15 emb|AF057562|AF057562 *Nicotiana glutinosa* 1-aminocyclopropane-1-... 437 0.0
emb|X59145|LEACC2MR *Lycopersicon esculentum* LE-ASCC2 mRNA (ptACC... 326 0.0
gb|U79999|MAU79999 *Musa acuminata* ACC synthase (acs3) mRNA, comp... 687 0.0
emb|Y15739|MAACSYNTH *Musa acuminata* mRNA for 1-aminocyclopropane... 687 0.0
gb|M34289|TOMACS *Tomato* 1-aminocyclopropane-1-carboxylate syntha... 327 0.0
20 gb|M63490|TOMACCS *Tomato* 1-aminocyclopropane-1-carboxylate synth... 682 0.0
emb|X59146|LEACC4MR *Lycopersicon esculentum* LE-ACC4 mRNA (ptACC4... 681 0.0
gb|U17229|PHU17229 *Pelargonium hortorum* clone pGAC-1 1-aminocycl... 438 0.0
gb|U17231|PHU17231 *Pelargonium hortorum* clone pGAC-2 1-aminocycl... 423 0.0
emb|AF038945|AF038945 *Rumex palustris* 1-aminocyclopropane-1-carb... 407 0.0
25 gb|L20634|POTACCSYN *Solanum tuberosum* 1-aminocyclopropane-1-carb... 403 0.0
emb|AJ276295|CSI276295 *Citrus sinensis* partial mRNA for ACC synt... 446 0.0
emb|AF239987|AF239987 *Prunus persica* ACC synthase ACS1 mRNA, par... 662 0.0
emb|AF178076|AF178076 *Carica papaya* 1-aminocyclopropane-1-carbox... 395 0.0
emb|X82265|CAACC1 *C.anuum* mRNA for 1-aminocyclopropane-1-carboxyl... 639 0.0
30 gb|U70842|STU70842 *Solanum tuberosum* 1-aminocyclopropane-1-carbo... 637 0.0
emb|AF144746|AF144746 *Solanum melongena* 1-aminocyclopropane-1-ca... 636 0.0
emb|AJ012577|CPA012577 *Carica papaya* mRNA for 1-aminocyclopropan... 387 e-180
gb|U73815|MDU73815 *Malus domestica* ACC synthase (MdACS-2) mRNA, ... 623 e-178
dbj|D37937|D37937 *Cucumis melo* mRNA for 1-aminocyclopropane-1-ca... 380 e-177
35 emb|Z11562|VRACCSYN *V.radiata* mRNA for 1-aminocyclopropane-1-car... 375 e-176
emb|AF177769|AF177769 *Carica papaya* 1-aminocyclopropane-1-carbox... 369 e-175
emb|AF083814|AF083814 *Antirrhinum majus* ACC synthase 1 (ACS1) mR... 605 e-172
emb|AF178077|AF178077 *Carica papaya* 1-aminocyclopropane-1-carbox... 316 e-172
emb|AF239989|AF239989 *Prunus persica* ACC synthase ACS25 mRNA, pa... 597 e-170
40 gb|U22523|MIU22523 *Mangifera indica* 1-aminocyclopropane-carboxyl... 359 e-169
emb|X66605|DCACCS *D.caryophyllus* mRNA for 1-aminocyclopropane-1-... 396 e-168
gb|L31347|MAUACCSYN *Malus domestica* 1-aminocyclopropane-1-carbox... 378 e-168
emb|AB015624|AB015624 *Pyrus pyrifolia* mRNA for 1-aminocyclopropan... 377 e-168
emb|AF049137|AF049137 *Dianthus caryophyllus* 1-aminocyclopropane-... 338 e-167
45 emb|AF170705|AF170705 *Mangifera indica* 1-aminocyclopropane-1-car... 290 e-167
gb|U03294|MSU03294 *Malus sylvestris* 1-aminocyclopropane-1-carbox... 372 e-166
emb|Z77854|PSPACS1 *Phalaenopsis species* mRNA for 1-aminocyclopro... 513 e-166
emb|AJ277160|CPA277160 *Carica papaya* partial paccs1A gene for 1-... 266 e-165
gb|U73816|MDU73816 *Malus domestica* ACC synthase (MdACS-3) mRNA, ... 505 e-164
50 emb|AB007449|AB007449 *Actinidia deliciosa* mRNA for 1-aminocyclop... 355 e-164
emb|AB007639|AB007639 *Pyrus pyrifolia* mRNA for 1-aminocyclopropan... 502 e-164
dbj|D01033|CUCACCA *Cucurbita maxima* mRNA for 1-aminocyclopropane... 366 e-164
emb|X87112|PCPCACS1G *P.communis* mRNA for 1-aminocyclopropane-1-c... 363 e-163
gb|U17972|LEU17972 *Lycopersicon esculentum* 1-aminocyclopropane-1... 362 e-163
55 emb|AB015495|AB015495 *Passiflora edulis* PE-ACS2 mRNA for ACC syn... 368 e-162
emb|AB006805|AB006805 *Cucumis sativus* CS-ACS3 mRNA for ACC synth... 360 e-160
emb|AB000679|AB000679 *Vigna radiata* mRNA for 1-aminocyclopropane... 365 e-158
gb|U34987|VRU34987 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 325 e-157
gb|M66619|DINCARACC *D.caryophyllus* 1-aminocyclopropane-1-carboxy... 496 e-156
60 gb|U34986|VRU34986 *Vigna radiata* 1-aminocyclopropane-1-carboxyli... 362 e-156
gb|U64031|DCU64031 *Dendrobium crumenatum* ACC synthase gene, comp... 259 e-154

- emb|AF016458|AF016458 *Pisum sativum* 1-aminocyclopropane-1-carbox... 355 e-154
 emb|Z27233|STACCAS1 *S.tuberosum* (STAC1) gene for amino cycloprop... 237 e-152
 emb|Z27234|STACCAS2 *S.tuberosum* STACS2 gene for 1-Aminocycloprop... 232 e-152
 5 emb|AF043122|AF043122 *Lycopersicon esculentum* ACC synthase (LE-A... 236 e-150
 gb|U37774|CMU37774 *Cucurbita maxima* 1-aminocyclopropane-1-carbox... 234 e-150
 gb|L34171|TOMACS3A *Lycopersicon esculentum* 1-aminocyclopropane-1... 235 e-149
 gb|U18055|LEU18055 *Lycopersicon esculentum* 1-aminocyclopropane-1... 235 e-149
 emb|AF151961|AF151961 *Vigna radiata* 1-aminocyclopropane-1-carbox... 232 e-146
 10 emb|Z12135|VRACCSYN4 *V.radiata* gene for ACC synthase (pMAC-4). 376 e-145
 gb|L07883|DORAMICARB *Moth orchid* 1-aminocyclopropane-1-carboxyla... 243 e-144
 emb|AF074927|AF074927 *Sinapis arvensis* 1-aminocyclopropane-1-car... 330 e-142
 emb|AF083815|AF083815 *Antirrhinum majus* ACC synthase 2 (ACS2) mR... 482 e-141
 emb|AB021907|AB021907 *Musa acuminata* MA-ACS2 mRNA for ACC syntha... 310 e-140
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 20 http://www.ncgr.org/cgi-bin/ff?ac000107
 (1950 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

25

Searching.....done

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| Sequences producing significant alignments: | (bits) | Value |
| 30 gb U79958 PSU79958 <i>Pisum sativum</i> BP-80 vacuolar sorting receptor... 630 0.0 | | |
| emb AB006809 AB006809 <i>Cucurbita</i> sp. mRNA for PV72, complete cds. 606 0.0 | | |
| emb AW267745 AW267745 EST305873 <i>DSIR Medicago truncatula</i> cDNA cl... 350 e-124 | | |
| emb AW931583 AW931583 EST357426 tomato fruit mature green, TAMU ... 165 e-112 | | |
| 35 emb AW309187 AW309187 sg05d06.y1 <i>Gm-cl019 Glycine max</i> cDNA clone... 326 e-108 | | |
| emb AW622833 AW622833 EST306903 tomato flower buds 3-8 mm, Corne... 387 e-106 | | |
| emb AW774434 AW774434 EST333585 <i>KV3 Medicago truncatula</i> cDNA clo... 294 e-100 | | |
| emb AW689392 AW689392 NF018F12ST1F1000 Developing stem <i>Medicago</i> ... 338 e-100 | | |
| gb BE054150 BE054150 GA_Ea0034H17f <i>Gossypium arboreum</i> 7-10 dpa ... 195 2e-99 | | |
| 40 emb AI782787 AI782787 EST263666 tomato susceptible, Cornell Lyco... 332 6e-90 | | |
| emb AW737948 AW737948 EST339375 tomato flower buds, anthesis, Co... 225 1e-89 | | |
| emb AW615949 AW615949 EST325315 tomato flower buds 0-3 mm, Corne... 217 3e-86 | | |
| emb AW932529 AW932529 EST358372 tomato fruit mature green, TAMU ... 303 1e-83 | | |
| emb AW685785 AW685785 NF030C07NR1F1000 Nodulated root <i>Medicago</i> t... 157 2e-81 | | |
| 45 emb AW747297 AW747297 WS1_67_G06.b1_A002 Water-stressed 1 (WS1) ... 286 4e-76 | | |
| emb AI443067 AI443067 sa47a01.y1 <i>Gm-cl1004 Glycine max</i> cDNA clone... 265 6e-76 | | |
| emb AI728635 AI728635 BNLGHi11276 Six-day Cotton fiber <i>Gossypium</i> ... 135 1e-75 | | |
| emb AI484571 AI484571 EST242801 tomato ovary, TAMU <i>Lycopersicon</i> ... 278 1e-73 | | |
| emb AI727826 AI727826 BNLGHi9195 Six-day Cotton fiber <i>Gossypium</i> ... 135 9e-71 | | |
| 50 emb AW695542 AW695542 NF096C05ST1F1037 Developing stem <i>Medicago</i> ... 153 2e-65 | | |
| emb AV406766 AV406766 AV406766 <i>Lotus japonicus</i> young plants (two... 170 5e-65 | | |
| emb AW509740 AW509740 ga63h11.y1 Moss EST library PPU <i>Physcomitr...</i> 226 6e-63 | | |
| emb AW256542 AW256542 EST304679 <i>KV2 Medicago truncatula</i> cDNA clo... 181 8e-60 | | |
| emb AW397829 AW397829 sg68h03.y1 <i>Gm-cl1007 Glycine max</i> cDNA clone... 225 1e-57 | | |
| 55 emb AW289687 AW289687 NXNV004E04F Nsf Xylem Normal wood Vertical... 182 7e-55 | | |
| emb AW690002 AW690002 NF026G04ST1F1000 Developing stem <i>Medicago</i> ... 143 4e-54 | | |
| emb AA660289 AA660289 00158 MtRHE <i>Medicago truncatula</i> cDNA 5', m... 138 2e-53 | | |
| emb AW064744 AW064744 ST35C06 Pine TriplEx shoot tip library Pin... 141 6e-53 | | |
| emb AV428420 AV428420 AV428420 <i>Lotus japonicus</i> young plants (two... 134 1e-51 | | |
| 60 emb AW623959 AW623959 EST321904 tomato flower buds 3-8 mm, Corne... 74 1e-49 | | |
| emb AW568619 AW568619 si60a11.y1 <i>Gm-r1030 Glycine max</i> cDNA clone... 165 2e-47 | | |

- emb|AI967865|AI967865 Ljirnp14-100-f3 Ljirnp Lambda HybriZap ... 180 5e-47
emb|AW309191|AW309191 sg05d10.y1 Gm-cl019 Glycine max cDNA clone... 105 2e-46
emb|AW398931|AW398931 EST309431 L. pennellii trichome, Cornell U... 132 2e-45
emb|AW737369|AW737369 EST338892 tomato flower buds, anthesis, Co... 182 6e-45
5 emb|AW096632|AW096632 EST289812 tomato mixed elicitor, BTI Lycop... 81 7e-45
emb|AF209910|AF209910 Prunus dulcis vacuolar sorting receptor pr... 76 8e-44
emb|AW056624|AW056624 ST53G07 Pine TriplEx shoot tip library Pin... 178 1e-43
emb|AW680054|AW680054 WS1_3_A01.g1_A002 Water-stressed 1 (WS1) S... 77 1e-41
emb|AW290400|AW290400 NXNV019G06F Nsf Xylem Normal wood Vertical... 170 4e-41
10 gb|BE125908|BE125908 DG1_59_E01.b1_A002 Dark Grown 1 (DG1) Sorgh... 164 2e-39
emb|AI161766|AI161766 A006P54U Hybrid aspen plasmid library Popu... 76 3e-39
emb|AI162330|AI162330 A016P01U Hybrid aspen plasmid library Popu... 130 2e-37
gb|BE049814|BE049814 NXNV_144_F04_F Nsf Xylem Normal wood Vertic... 156 4e-37
emb|AW508719|AW508719 si35f03.y1 Gm-r1030 Glycine max cDNA clone... 155 8e-37
15 gb|L38113|L38113 BNAF0628E Mustard flower buds Brassica rapa cDN... 153 4e-36
emb|AW616461|AW616461 EST322872 L. hirsutum trichome, Cornell Un... 102 4e-33
emb|AA660955|AA660955 00852 MtrHE Medicago truncatula cDNA 5' si... 72 4e-31
emb|AW774190|AW774190 EST333273 KV3 Medicago truncatula cDNA clo... 134 2e-30
emb|AW201441|AW201441 sf03b09.y1 Gm-cl027 Glycine max cDNA clone... 73 5e-30
20 emb|AW906386|AW906386 EST342508 potato stolon, Cornell Universit... 78 2e-27
emb|AW126100|AW126100 N100297e rootphos(-) Medicago truncatula c... 73 9e-27
emb|AW620693|AW620693 sj08d10.y1 Gm-cl032 Glycine max cDNA clone... 77 1e-26
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emb|AW706755|AW706755 sk02f10.y1 Gm-cl023 Glycine max cDNA clone... 117 3e-25
25 emb|AW125944|AW125944 N100139e rootphos(-) Medicago truncatula c... 71 1e-23
emb|AW932524|AW932524 EST358367 tomato fruit mature green, TAMU ... 69 1e-22
emb|AW348825|AW348825 GM210003B11E6R Gm-r1021 Glycine max cDNA 3... 66 2e-22
emb|AW093844|AW093844 EST287024 tomato mixed elicitor, BTI Lycop... 98 3e-19
emb|AW691052|AW691052 NF037B05ST1F1000 Developing stem Medicago ... 79 6e-17
30 emb|AW119909|AW119909 sd54d08.y1 Gm-cl016 Glycine max cDNA clone... 88 2e-16
emb|AW685952|AW685952 NF036G09NR1F1000 Nodulated root Medicago t... 50 1e-15
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emb|AI794754|AI794754 sb68f11.y1 Gm-cl019 Glycine max cDNA clone... 82 1e-14
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35 emb|AW760128|AW760128 sl58d09.y1 Gm-cl027 Glycine max cDNA clone... 66 8e-14
emb|AW037563|AW037563 EST278890 tomato mixed elicitor, BTI Lycop... 77 6e-13
emb|AW256398|AW256398 EST304465 KV2 Medicago truncatula cDNA clo... 72 7e-13
emb|AW686287|AW686287 NF040A08NR1F1000 Nodulated root Medicago t... 67 6e-10
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40 emb|AW747372|AW747372 WS1_67_G06.g1_A002 Water-stressed 1 (WS1) ... 64 4e-09
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emb|AI939286|AI939286 sc69h02.y1 Gm-cl016 Glycine max cDNA clone... 48 2e-04
emb|AQ652964|AQ652964 Sheared DNA-1M1.TR Sheared DNA Trypanosoma... 39 0.16
gb|C95899|C95899 C95899 Marchantia polymorpha immature sex organ... 38 0.31
45 gb|B67199|B67199 CpG0015B CpIOWAgDNA1 Cryptosporidium parvum gen... 38 0.31
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emb|AF083502|AF083502 Plasmodium vivax ookinete surface protein ... 37 0.42
emb|AW626172|AW626172 EST320079 tomato radicle, 5 d post-imbibit... 37 0.42
emb|AC008054|AC008054 Leishmania major chromosome 35 clone L8453... 36 0.55
50 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 35 1.5
emb|AB033343|AB033343 Plasmodium vivax gene for ookinete surface... 35 1.5
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55 emb|AB033339|AB033339 Plasmodium vivax gene for ookinete surface... 35 1.5
emb|AV410215|AV410215 AV410215 Lotus japonicus young plants (two... 35 2.1
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emb|AQ649743|AQ649743 Sheared DNA-17O2.TR Sheared DNA Trypanosom... 35 2.8
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60 emb|AZ216543|AZ216543 Sheared DNA-116G5.TR Sheared DNA Trypanoso... 35 2.8
emb|AC004157|AC004157 Plasmodium falciparum chromosome 12 clone ... 35 2.8

- gb|U18916|SCE9781 *Saccharomyces cerevisiae* chromosome V cosmids ... 35 2.8
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 emb|AI778616|AI778616 EST259495 tomato susceptible, Cornell Lyco... 33 3.3
 5 emb|AA749476|AA749476 L30-23M13T3 Ice plant Lambda Uni-Zap XR ex... 31 3.3
 emb|AA938798|AA938798 L0-249M13R Ice plant Lambda Uni-Zap XR exp... 31 3.3
 emb|AI822187|AI822187 L0-664T3 Ice plant Lambda Uni-Zap XR expre... 31 3.3
 emb|AI822671|AI822671 L0-1192T3 Ice plant Lambda Uni-Zap XR expr... 31 3.3
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- 25 emb|X97606|MSRNAAAA *M. sativa* mRNA translated from abscisic activ... 306 e-115
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 emb|AW692860|AW692860 NF056E06ST1F1000 Developing stem *Medicago* ... 309 2e-89
 gb|BE123903|BE123903 EST394028 DSIL *Medicago truncatula* cDNA clo... 304 7e-88
 emb|AW774316|AW774316 EST333467 KV3 *Medicago truncatula* cDNA clo... 308 5e-83
 emb|AW728361|AW728361 GA_Ea0016H09 *Gossypium arboreum* 7-10 dpa ... 306 2e-82
 30 emb|AW267789|AW267789 EST305917 DSIR *Medicago truncatula* cDNA cl... 169 4e-81
 emb|AW329160|AW329160 N200369e rootphos(-) *Medicago truncatula* c... 224 2e-80
 emb|AW696127|AW696127 NF102F09ST1F1078 Developing stem *Medicago* ... 298 4e-80
 emb|AI794650|AI794650 sb67a05.y1 Gm-c1019 *Glycine max* cDNA clone... 286 2e-76
 gb|BE037103|BE037103 MP15A03 *MP Mesembryanthemum crystallinum* cD... 139 8e-76
 35 emb|AW399617|AW399617 EST310117 *L. pennellii* trichome, Cornell U... 281 5e-75
 emb|AW564270|AW564270 LG1_289_E10.b1_A002 Light Grown 1 (LG1) So... 162 6e-72
 emb|AW756208|AW756208 sl17d10.y1 Gm-c1036 *Glycine max* cDNA clone... 264 5e-70
 emb|AW760494|AW760494 sl51a09.y1 Gm-c1027 *Glycine max* cDNA clone... 178 1e-69
 emb|AW831516|AW831516 sm27a02.y1 Gm-c1028 *Glycine max* cDNA clone... 261 4e-69
 40 emb|AJ223291|SRAJ3291 *Sesbania rostrata* mRNA for putative chalco... 115 2e-64
 emb|AW830327|AW830327 sm25f04.y1 Gm-c1028 *Glycine max* cDNA clone... 242 2e-63
 emb|AW688330|AW688330 NF006B06ST1F1000 Developing stem *Medicago* ... 169 6e-63
 gb|BE020597|BE020597 sm51b07.y1 Gm-c1028 *Glycine max* cDNA clone ... 239 2e-62
 emb|X82368|MSCHR2A *M. sativa* mRNA for chalcone reductase (1134 bp). 117 6e-61
 45 gb|U13925|MSU13925 *Medicago sativa* Apollo clone CHR7 chalcone re... 117 6e-61
 emb|X57526|HVALREDR *H. vulgare* gene for aldose reductase-related ... 92 1e-60
 emb|X82367|MSCHR1B *M. sativa* mRNA for chalcone reductase (1115 bp). 116 1e-60
 emb|X82366|MSCHR1A *M. sativa* mRNA for chalcone reductase (1202 bp). 116 2e-60
 emb|AF133841|AF133841 *Xerophyta viscosa* aldose reductase ALDRXV4... 97 2e-60
 50 gb|U13924|MSU13924 *Medicago sativa* Apollo clone CHR12 chalcone r... 114 8e-60
 emb|X55730|GMREDUC *Soybean* mRNA for reductase involved in deoxyc... 111 1e-59
 emb|AF108438|AF108438 *Papaver somniferum* putative NADPH-dependen... 154 1e-59
 gb|L12042|BMUSUSCUL *Bromus inermis* aldose reductase-related prot... 86 2e-59
 emb|AW694657|AW694657 NF078G04ST1F1035 Developing stem *Medicago* ... 164 3e-59
 55 emb|X59465|PSXYL1RE *P. stipitis* XYL1-gene for NAD(P)H-dependent X... 125 2e-58
 emb|AF020040|AF020040 *Pichia guilliermondii* xylose reductase mRN... 121 2e-58
 emb|AF039182|AF039182 *Fragaria x ananassa* probable aldo-keto red... 105 5e-58
 emb|AB002105|AB002105 *Candida tropicalis* DNA for D-xylose reduct... 127 6e-58
 emb|AW991001|AW991001 *Suaeda salsa* ZAP cDNA library Suae... 184 1e-57
 60 emb|AB002106|AB002106 *Candida tropicalis* DNA for D-xylose reduct... 124 2e-57
 emb|AW830449|AW830449 sm27b05.y1 Gm-c1028 *Glycine max* cDNA clone... 223 2e-57

- dbj|D83718|GYCPKR *Glycyrrhiza echinata* mRNA for polyketide reduc... 111 6e-57
 gb|U40706|PTU40706 *Pachysolen tannophilus* aldose reductase gene... 123 8e-57
 dbj|D86559|D86559 *Glycyrrhiza glabra* mRNA for polyketide reducta... 110 1e-56
 dbj|D86558|D86558 *Glycyrrhiza glabra* mRNA for polyketide reducta... 110 1e-56
 5 emb|AF074484|AF074484 *Candida tenuis* xylose reductase (xylr) gen... 127 2e-54
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 emb|Z73100|SPAC26F1 *S.pombe* chromosome I cosmid c26F1. 92 1e-51
 emb|AW730093|AW730093 GA_Ea0027M16 *Gossypium arboreum* 7-10 dpa ... 128 1e-51
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 10 gb|U83687|AGU83687 *Apium graveolens* NADPH-dependent mannose 6-ph... 80 2e-51
 emb|AF108432|AF108432 *Papaver somniferum* NADPH-dependent codeino... 141 4e-51
 gb|U00059|YSCH8263 *Saccharomyces cerevisiae* chromosome VIII cosm... 116 2e-50
 dbj|D11080|MAUS6PDH Apple S6PDH mRNA for NADP-dependent D-sorbit... 78 2e-49
 emb|AF219625|AF219625 *Aspergillus niger* D-xylose reductase (xylA... 86 6e-49
 15 emb|AF108435|AF108435 *Papaver somniferum* NADPH-dependent codeino... 85 1e-48
 emb|AF108434|AF108434 *Papaver somniferum* NADPH-dependent codeino... 83 1e-48
 emb|AW773597|AW773597 EST332583 KV3 *Medicago truncatula* cDNA clo... 161 2e-48
 emb|AF108433|AF108433 *Papaver somniferum* NADPH-dependent codeino... 85 2e-47
 emb|AW982655|AW982655 HVSMEg0003N17f *Hordeum vulgare* pre-anthesi... 156 2e-47
 20 emb|AL021815|SPBC8E4 *S.pombe* chromosome I cosmid c8E4. 84 3e-47
 gb|J04483|LEIP10011E *Leishmania major* reductase (P100/11E) mRNA,... 83 5e-47
 emb|AW266162|AW266162 L30-2855T3 Ice plant Lambda Uni-Zap XR exp... 185 7e-47
 emb|AW351113|AW351113 GM210010B20E10R Gm-r1021 *Glycine max* cDNA ... 122 2e-46
 emb|AW267703|AW267703 EST305831 DSIR *Medicago truncatula* cDNA cl... 114 3e-46
 25 emb|AL110661|CNS018Q6 *Botrytis cinerea* strain T4 cDNA library un... 108 2e-45
 emb|AB014493|AB014493 *Gibberella zeae* gene for reductase, partia... 91 5e-45
 emb|X94335|SC130KBXV *S.cerevisiae* 130kb DNA fragment from chromo... 57 2e-44
 emb|X90518|SCXVORFS *S.cerevisiae* DNA of 51 Kb from chromosome XV... 57 2e-44
 emb|Z75028|SCYOR120W *S.cerevisiae* chromosome XV reading frame OR... 57 2e-44
 30 emb|X13228|SCGCY Yeast GCY gene (homologous to vertebrate eye le... 57 2e-44
 emb|X96740|SCGCY1 *S.cerevisiae* GCY1 gene. 57 2e-44
 emb|AW775175|AW775175 EST334326 KV3 *Medicago truncatula* cDNA clo... 101 5e-44
 emb|AW776733|AW776733 EST335798 DSIL *Medicago truncatula* cDNA cl... 177 9e-44
 gb|BE036780|BE036780 MP05F01 MP *Mesembryanthemum crystallinum* cD... 84 9e-43
 35 gb|BE036644|BE036644 MP03B08 MP *Mesembryanthemum crystallinum* cD... 80 9e-43
 emb|AW706251|AW706251 sj54a08.yl Gm-c1033 *Glycine max* cDNA clone... 106 2e-42
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 emb|AW686854|AW686854 NF003B10RT1F1000 Developing root *Medicago* ... 114 4e-42
 40 gb|U21747|AFU21747 *Avena fatua* aldose reductase-related protein ... 91 4e-41
 emb|AW981220|AW981220 EST392310 DSIL *Medicago truncatula* cDNA cl... 83 5e-41
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 45 emb|AW568008|AW568008 si56c03.yl Gm-r1030 *Glycine max* cDNA clone... 166 3e-40
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 emb|AW310318|AW310318 sf34d05.xl Gm-c1028 *Glycine max* cDNA clone... 124 1e-38
 emb|AL115070|CNS01C4M *Botrytis cinerea* strain T4 cDNA library un... 90 2e-38
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 50 emb|AW306925|AW306925 sf50e02.yl Gm-c1009 *Glycine max* cDNA clone... 93 2e-38
 emb|AW564756|AW564756 LG1_301_B12.b1_A002 Light Grown 1 (LG1) So... 147 6e-38
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 55 emb|AW728632|AW728632 GA_Ea0017G17 *Gossypium arboreum* 7-10 dpa ... 80 3e-36
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 emb|AI939278|AI939278 sc69f11.yl Gm-c1016 *Glycine max* cDNA clone... 150 1e-35
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 60 emb|AW756704|AW756704 sl26b12.yl Gm-c1027 *Glycine max* cDNA clone... 79 2e-35
 gb|U26463|SSU26463 *Sporidiobolus salmonicolor* NADPH-dependent al... 86 3e-35

emb|AW234076|AW234076 sf34a01.y1 Gm-c1028 Glycine max cDNA clone... 111 7e-35

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25	emb AW832261 AW832261	sm21g08.y1 Gm-c1027 Glycine max cDNA clone...	372 e-102
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	emb AV421952 AV421952	AV421952 Lotus japonicus young plants (two...	304 1e-81
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35	emb X67045 STTPTMR	S.tuberosum mRNA TPT for triose phosphate tra...	183 1e-67
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40	emb AW926251 AW926251	HVSMEg0006L14 Hordeum vulgare pre-anthesis...	226 2e-58
	emb AW472436 AW472436	si25b11.y1 Gm-c1029 Glycine max cDNA clone...	221 2e-57
	emb AF173679 AF173679	Beta vulgaris phosphat translocator (pt) m...	135 2e-53
	emb AW560889 AW560889	EST315937 DSIR Medicago truncatula cDNA cl...	205 2e-53
	emb AI939281 AI939281	sc69g06.y1 Gm-c1016 Glycine max cDNA clone...	204 1e-51
45	emb AW688995 AW688995	NF014B11ST1F1000 Developing stem Medicago ...	150 2e-50
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	emb AI772801 AI772801	EST253901 tomato resistant, Cornell Lycopen...	188 8e-47
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60	emb AI812950 AI812950	22G7 Pine Lambda Zap Xylem library Pinus t...	176 3e-43
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emb|AW933284|AW933284 EST359127 tomato fruit mature green, TAMU ... 175 8e-43
emb|AW399333|AW399333 EST309833 L. pennellii trichome, Cornell U... 175 8e-43
emb|AW626582|AW626582 NXNV067A01 Nsf Xylem Normal wood Vertical ... 107 2e-42
5 emb|AW671381|AW671381 LG1_335_G10.b1_A002 Light Grown 1 (LG1) So... 173 3e-42
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emb|AW559735|AW559735 EST314727 DSIR Medicago truncatula cDNA cl... 167 3e-42
gb|BE034606|BE034606 MK02F02 MK Mesembryanthemum crystallinum cD... 170 2e-41
10 emb|AW690541|AW690541 NF035G02ST1F1000 Developing stem Medicago ... 166 5e-41
gb|U13632|BOU13632 Brassica oleracea var. botrytis non-green pla... 166 2e-40
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15 emb|AW776623|AW776623 EST335688 DSIL Medicago truncatula cDNA cl... 162 4e-39
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20 emb|AW930290|AW930290 EST340747 tomato fruit mature green, TAMU ... 157 2e-37
emb|AV415709|AV415709 AV415709 Lotus japonicus young plants (two... 153 2e-36
emb|AW201212|AW201212 se99c01.y1 Gm-c1027 Glycine max cDNA clone... 93 3e-36
emb|AI736196|AI736196 sb24f10.y1 Gm-c1008 Glycine max cDNA clone... 151 8e-36
emb|AV426398|AV426398 AV426398 Lotus japonicus young plants (two... 149 6e-35
25 emb|AV422882|AV422882 AV422882 Lotus japonicus young plants (two... 147 2e-34
emb|AF173660|AF173660 Beta vulgaris clone GPTI109UNI glucose-6-p... 146 4e-34
emb|AI822397|AI822397 L0-856T3 Ice plant Lambda Uni-Zap XR expre... 125 7e-34
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30 gb|BE059998|BE059998 sn39f10.y1 Gm-c1027 Glycine max cDNA clone ... 143 3e-33
emb|AW671168|AW671168 LG1_330_E06.b1_A002 Light Grown 1 (LG1) So... 142 5e-33
emb|AW667825|AW667825 GA_Ea0010N10 Gossypium arboreum 7-10 dpa ... 141 9e-33
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35 emb|AW781979|AW781979 sl99a06.y1 Gm-c1027 Glycine max cDNA clone... 138 8e-32
emb|AV426209|AV426209 AV426209 Lotus japonicus young plants (two... 135 6e-31
emb|AW287694|AW287694 LG1_271_C05.b1_A002 Light Grown 1 (LG1) So... 135 8e-31
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emb|AW564618|AW564618 LG1_297_G09.b1_A002 Light Grown 1 (LG1) So... 134 1e-30
40 emb|AW924990|AW924990 WS1_74_A05.b1_A002 Water-stressed 1 (WS1) ... 134 1e-30
emb|AW888070|AW888070 NXNV_126_H09_F Nsf Xylem Normal wood Verti... 134 1e-30
emb|AW694653|AW694653 NF078G03ST1F1023 Developing stem Medicago ... 108 2e-30
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emb|AW030490|AW030490 EST273745 tomato callus, TAMU Lycopersicon... 132 7e-30
45 emb|AW738715|AW738715 EST340142 tomato flower buds, anthesis, Co... 132 7e-30
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emb|AW780617|AW780617 sl73c03.y1 Gm-c1027 Glycine max cDNA clone... 131 1e-29
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50 emb|AW286886|AW286886 LG1_222_F11.b1_A002 Light Grown 1 (LG1) So... 129 3e-29
emb|AW399232|AW399232 EST309732 L. pennellii trichome, Cornell U... 129 5e-29
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55 emb|AW759175|AW759175 sl38a01.y1 Gm-c1027 Glycine max cDNA clone... 128 7e-29
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emb|AW596590|AW596590 sj14c04.y1 Gm-c1032 Glycine max cDNA clone... 128 9e-29
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60 emb|AV415908|AV415908 AV415908 Lotus japonicus young plants (two... 127 2e-28

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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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10

Score E
Sequences producing significant alignments: (bits) Value

15 gb|U21848|BNU21848 Brassica napus chitinase class IV (LSC222) mR... 225 e-134
emb|X61488|BNCHITIN B.napus mRNA for chitinase. 156 7e-88
gb|U97521|VVU97521 Vitis vinifera class IV endochitinase (VvChi4... 173 3e-77
gb|U97522|VVU97522 Vitis vinifera class IV endochitinase (VvChi4... 174 2e-76
emb|X57187|PVCHITIN P.vulgaris mRNA for chitinase. 149 2e-74
20 emb|AF112966|AF112966 Triticum aestivum chitinase IV precursor (... 157 5e-70
dbj|D45181|D45181 Chenopodium amaranticolor mRNA for chitinase, ... 100 5e-67
gb|U52845|DCU52845 Daucus carota class IV chitinase EP3-1/H5 (EP... 114 7e-67
gb|U52846|DCU52846 Daucus carota class IV chitinase EP3-2/H1 (EP... 111 9e-66
gb|BE034166|BE034166 MG05H02 MG Mesembryanthemum crystallinum cD... 129 1e-65
gb|U52847|DCU52847 Daucus carota class IV chitinase EP3-3/E7 (EP... 110 8e-65
25 gb|U52848|DCU52848 Daucus carota class IV chitinase EP3B/E6 (EP3... 111 2e-64
gb|BE034975|BE034975 ML07H10 ML Mesembryanthemum crystallinum cD... 125 2e-64
gb|BE034428|BE034428 MH04G02 MH Mesembryanthemum crystallinum cD... 123 2e-63
gb|BE034976|BE034976 ML07H11 ML Mesembryanthemum crystallinum cD... 120 6e-63
dbj|D45183|D45183 Chenopodium amaranticolor mRNA for chitinase, ... 96 1e-62
30 dbj|D45184|D45184 Chenopodium amaranticolor mRNA for chitinase, ... 100 3e-62
dbj|D45182|D45182 Chenopodium amaranticolor mRNA for chitinase, ... 100 4e-60
emb|X75945|BVCH4RNA B.vulgaris Ch4 mRNA for chitinase. 92 6e-60
emb|A23392|A23392 B.vulgaris mRNA for chitinase 4 (B15). 92 6e-60
emb|X88803|VURNACHI4 V.unguiculata mRNA for chitinase class 4 (p... 118 3e-59
35 emb|AI897733|AI897733 EST267176 tomato ovary, TAMU Lycopersicon ... 110 1e-58
gb|BE034406|BE034406 MH04D10 MH Mesembryanthemum crystallinum cD... 105 2e-58
gb|L25826|BEUSP2X Sugar beet chitinase (SP2) mRNA, complete cds. 158 3e-58
gb|BE034497|BE034497 MH05H03 MH Mesembryanthemum crystallinum cD... 89 8e-58
gb|L42467|PIACHI Picea glauca chitinase (chi) mRNA, complete cds. 93 2e-57
40 emb|AF090336|AF090336 Citrus sinensis chitinase CHI1 (chi1) mRNA... 166 2e-57
emb|AI897843|AI897843 EST267286 tomato ovary, TAMU Lycopersicon ... 103 1e-56
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gb|BE035287|BE035287 MM04H04 MM Mesembryanthemum crystallinum cD... 162 4e-54
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45 gb|BE033502|BE033502 ME03F10-ME Mesembryanthemum crystallinum cD... 87 4e-50
gb|M94105|ALCCHITIN Allium sativum chitinase mRNA, 3' end. 100 6e-49
emb|AI898279|AI898279 EST267722 tomato ovary, TAMU Lycopersicon ... 83 1e-48
gb|U83592|MSU83592 Medicago sativa class I chitinase mRNA, compl... 109 1e-48
gb|U83591|MSU83591 Medicago sativa class I chitinase mRNA, compl... 109 1e-48
50 emb|AW030814|AW030814 EST274069 tomato callus, TAMU Lycopersicon... 83 3e-48
emb|AW035013|AW035013 EST279284 tomato callus, TAMU Lycopersicon... 83 3e-48
emb|AW029733|AW029733 EST272988 tomato callus, TAMU Lycopersicon... 83 3e-48
gb|BE034481|BE034481 MH05F02 MH Mesembryanthemum crystallinum cD... 162 5e-48
emb|AW924422|AW924422 WS1_69_C06.b1_A002 Water-stressed I (WS1) ... 140 7e-48
55 emb|AI485982|AI485982 EST244303 tomato ovary, TAMU Lycopersicon ... 83 1e-47
emb|AF061805|AF061805 Elaeagnus umbellata acidic chitinase mRNA,... 99 1e-47
emb|AW648023|AW648023 EST326477 tomato germinating seedlings, TA... 83 3e-47
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60 emb|X15494|STCHITIN Potato endochitinase gene (EC 3.2.1.14). 95 6e-47
emb|X07130|STCHIT Solanum tuberosum mRNA for endochitinase (EC 3... 95 6e-47

- gb|M13968|PHVCHM *P.vulgaris* chitinase mRNA, complete cds. 106 1e-46
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 gb|S43926|S43926 CH5B=chitinase [*Phaseolus vulgaris*=beans, cv Sa... 106 5e-46
 emb|X88800|VURNACHI1 *V.unguiculata* mRNA for chitinase class 1 (p... 105 1e-45
 5 emb|AJ012821|CAR012821 *Cicer arietinum* mRNA for class I chitinase. 108 6e-45
 emb|AW691007|AW691007 NF036E09ST1F1000 Developing stem Medicago ... 78 8e-45
 emb|Y10373|MTCHITIN1 *M.truncatula* mRNA for chitinase. 109 8e-45
 emb|AW033122|AW033122 EST276681 tomato callus, TAMU Lycopersicon... 83 2e-44
 gb|M94106|ALCCHINTIA *Allium sativum* chitinase mRNA, 3' end. 102 3e-44
 10 emb|AW746018|AW746018 WS1_38_H11.g1_A002 Water-stressed 1 (WS1) ... 170 3e-44
 emb|AW922735|AW922735 DG1_45_B06.g1_A002 Dark Grown 1 (DG1) Sorg... 178 4e-44
 emb|AW746695|AW746695 WS1_54_E02.g1_A002 Water-stressed 1 (WS1) ... 178 4e-44
 emb|A16119|A16119 Intracellular chitinase mRNA (SEQ ID NO: 2). 95 5e-44
 gb|M15173|TOBECH Tobacco (*N.tabacum*) endochitinase mRNA, partial... 95 5e-44
 15 emb|AF061806|AF061806 *Elaeagnus umbellata* basic chitinase mRNA, ... 105 1e-43
 emb|Z54234|VVCHIT1MR *V.vinifera* mRNA for chitinase. 98 1e-43
 gb|S44869|S44869 basic chitinase [*Nicotiana tabacum*=tobacco, cv ... 95 2e-43
 emb|X16939|NTECHITR *Nicotiana tabacum* mRNA for endochitinase (EC... 95 2e-43
 emb|X76041|TACHIG *T.aestivum* (Chinese spring) chi gene for endoc... 93 4e-43
 20 emb|AB015655|AB015655 *Cucurbita* sp. mRNA for chitinase, complete... 97 6e-43
 emb|Z46948|SNCHJET15 *S.nigra* mRNA for chitinase, pathogenesis-re... 104 2e-42
 gb|U02605|STU02605 *Solanum tuberosum* chitinase (chtB1) mRNA, par... 95 3e-42
 gb|U02606|STU02606 *Solanum tuberosum* chitinase (chtB2) mRNA, par... 95 4e-42
 emb|Z46950|SNCHJET19 *S.nigra* mRNA chitinase class II, pathogenes... 104 6e-42
 25 gb|U78888|GHU78888 *Gossypium hirsutum* class I endochitinase mRNA... 102 1e-41
 gb|BE034450|BE034450 MH05B01 MH *Mesembryanthemum crystallinum* cD... 81 3e-41
 emb|Z15140|LECHI9 *L.esculentum* mRNA for chitinase. 95 3e-41
 gb|U02607|STU02607 *Solanum tuberosum* chitinase (chtB3) mRNA, par... 95 6e-41
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 30 emb|AF034566|AF034566 *Gossypium hirsutum* class I chitinase mRNA,... 100 6e-41
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 gb|M25337|POPCHIB *Populus* sp. chitinase (win8) mRNA, complete cds. 89 8e-41
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 emb|AI897217|AI897217 EST266756 tomato ovary, TAMU Lycopersicon ... 110 4e-40
 35 emb|AF000965|AF000965 *Poa pratensis* chitinase (Chi3) pseudogene ... 91 4e-40
 emb|X95610|CSHITIB *C.sativa* mRNA for chitinase Ib. 88 9e-40
 gb|U48687|CSU48687 *Castanea sativa* endochitinase mRNA, complete ... 88 9e-40
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 emb|Z78202|PACHI1 *Persea americana* mRNA for endochitinase. 96 2e-39
 40 emb|AW745819|AW745819 WS1_37_H11.g1_A002 Water-stressed 1 (WS1) ... 163 2e-39
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 gb|L22032|ULMCHITIN *Ulmus americana* chitinase (pHS2) mRNA, compl... 106 6e-39
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 45 emb|AW560048|AW560048 EST315096 DSIR Medicago truncatula cDNA cl... 109 7e-39
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 emb|AI897657|AI897657 EST267100 tomato ovary, TAMU Lycopersicon ... 101 1e-37
 50 emb|AF098302|AF098302 *Brassica juncea* chitinase mRNA, complete cds. 106 1e-37
 emb|AW746429|AW746429 WS1_53_G09.b1_A002 Water-stressed 1 (WS1) ... 97 4e-37
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(1548 letters)

60 Database: plantfungal
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	emb AB001379 AB001379	Glycyrrhiza echinata CYP81E1 mRNA for cyto...	323	e-137
	emb AJ238439 CAR238439	Cicer arietinum mRNA for a cytochrome P45...	328	e-136
	emb AB022732 AB022732	Glycyrrhiza echinata CYP Ge-31 mRNA for cy...	322	e-136
10	emb AB025016 AB025016	Lotus japonicus mRNA for cytochrome P450, ...	291	e-134
	emb AJ012581 CAR012581	Cicer arietinum mRNA for cytochrome P450.	324	e-134
	emb AJ000478 HTCYP81L	Helianthus tuberosus mRNA for cytochrome P...	227	e-124
	emb AJ000477 HTCYP81C	Helianthus tuberosus mRNA for cytochrome P...	227	e-124
	emb AJ239051 CAR239051	Cicer arietinum mRNA for cytochrome P450 ...	237	3e-82
15	emb AJ249800 CAR249800	Cicer arietinum partial mRNA for cytochro...	290	3e-79
	emb AW185361 AW185361	se90e02.y1 Gm-cl027 Glycine max cDNA clone...	280	3e-74
	emb AW775904 AW775904	EST334969 DSIL Medicago truncatula cDNA cl...	228	1e-70
	emb AF082028 AF082028	Hemerocallis hybrid cultivar senescence-as...	189	2e-70
	emb AW234443 AW234443	sf25c03.y1 Gm-cl028 Glycine max cDNA clone...	264	1e-69
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	emb AW171738 AW171738	N100632e rootphos(-) Medicago truncatula c...	251	1e-65
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	emb AI729126 AI729126	BNLGH12694 Six-day Cotton fiber Gossypium...	180	4e-58
25	emb AW329224 AW329224	N200436e rootphos(-) Medicago truncatula c...	224	1e-57
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30	emb AI774414 AI774414	EST255514 tomato resistant, Cornell Lycopen...	144	5e-54
	emb AW171672 AW171672	N100566e rootphos(-) Medicago truncatula c...	212	7e-54
	emb AW932147 AW932147	EST357990 tomato fruit mature green, TAMU ...	211	1e-53
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	emb AI731081 AI731081	BNLGH18648 Six-day Cotton fiber Gossypium ...	200	2e-50
35	emb AI728374 AI728374	BNLGH10609 Six-day Cotton fiber Gossypium...	163	9e-50
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	emb AF156976 AF156976	Gerbera hybrida flavone synthase II (CYP93...	100	8e-46
	dbj E13663 E13663	cDNA encoding cytochrome P450 which is induced...	104	1e-45
40	dbj D83968 SOYCYP93A1	Soybean mRNA for cytochrome P450 (CYP93A1)...	104	1e-45
	emb Y10492 GMC450CP5	G.max mRNA for putative cytochrome P450, cl...	106	6e-44
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45	emb AI973839 AI973839	sd11c06.y1 Gm-cl020 Glycine max cDNA clone...	104	2e-43
	emb AF155332 AF155332	Petunia x hybrida flavonoid 3'-hydroxylase...	158	2e-43
	emb AW734404 AW734404	sk19f09.y1 Gm-cl028 Glycine max cDNA clone...	157	2e-43
	gb U29333 PSU29333	Pisum sativum novel wound-inducible cytochrom...	160	5e-43
	emb AF124372 AF124372	Nicotiana tabacum NT7 mRNA, partial cds.	134	6e-43
50	gb U72654 EGU72654	Eustoma grandiflorum flavonoid 3'-hydroxyla...	149	2e-42
	dbj D86351 D86351	Glycine max CYP93A2 mRNA for cytochrome P-450,...	102	2e-42
	emb AW688601 AW688601	NF009D12ST1F1000 Developing stem Medicago ...	173	4e-42
	emb AW616170 AW616170	EST307209 L. hirsutum trichome, Cornell Un...	148	5e-42
	dbj D14589 D14589	Eustoma russellianum mRNA for flavonoid 3',5'-...	148	6e-42
55	emb AJ011862 CRO011862	Catharanthus roseus mRNA for flavonoid 3'...	155	6e-42
	emb Z22545 PHFLAHYDB	P.hybrida flavonoid 3',5'-hydroxylase mRNA.	148	8e-42
	dbj D14588 PETHF1	Petunia hybrida Hfl mRNA for flavonoid-3',5'-h...	148	8e-42
	emb AW616482 AW616482	EST322893 L. hirsutum trichome, Cornell Un...	148	1e-41
	emb AW617814 AW617814	EST324213 L. hirsutum trichome, Cornell Un...	148	1e-41
60	emb AW309826 AW309826	sf25c03.x1 Gm-cl028 Glycine max cDNA clone...	166	1e-41
	emb AB024931 AB024931	Lotus japonicus mRNA for cytochrome P450, ...	100	2e-41

- emb|AW299084|AW299084 EST305758 KV2 Medicago truncatula cDNA clo... 171 2e-41
 emb|AW728587|AW728587 GA_Ea0017C12 Gossypium arboreum 7-10 dpa ... 170 2e-41
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 emb|AW616075|AW616075 EST296834 L. hirsutum trichome, Cornell Un... 148 3e-41
 5 emb|AF195800|AF195800 Medicago sativa isoflavone synthase 1 (ifs... 99 4e-41
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 emb|AI776121|AI776121 EST257209 tomato resistant, Cornell Lycop... 111 5e-41
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 10 emb|AF195810|AF195810 Trifolium pratense isoflavone synthase 1 (... 98 6e-41
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 15 emb|Y10982|GMP450CP6 Glycine max mRNA for cytochrome P450-like p... 149 7e-41
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 emb|AW651341|AW651341 EST329795 tomato germinating seedlings, TA... 148 7e-41
 emb|AF195798|AF195798 Glycine max isoflavone synthase 1 (ifs1) m... 98 8e-41
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 20 emb|AI782402|AI782402 EST263281 tomato susceptible, Cornell Lyco... 144 2e-40
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 25 emb|AF195817|AF195817 Beta vulgaris isoflavone synthase 2 (ifs2)... 97 2e-40
 emb|AW687247|AW687247 NF007E11RT1F1086 Developing root Medicago ... 167 2e-40
 emb|AF096998|AF096998 Pinus taeda trans-cinnamate 4-hydroxylase ... 143 2e-40
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 30 emb|AW034115|AW034115 EST277610 tomato callus, TAMU Lycopersicon... 147 4e-40
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 emb|AF195813|AF195813 Lupinus albus isoflavone synthase 1 (ifs1)... 96 5e-40
 35 emb|AW616066|AW616066 EST296823 L. hirsutum trichome, Cornell Un... 145 5e-40
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 45 emb|AF195816|AF195816 Beta vulgaris isoflavone synthase 1 (ifs1)... 97 1e-39

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 (2805 letters)

55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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60 Score E
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- emb|AF109392|AF109392 Brassica napus ligand gated channel-like p... 142 3e-57
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5 emb|AI759920|AI759920 sb66c06.y1 Gm-c1017 Glycine max cDNA clone... 84 4e-15
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10 emb|AW928584|AW928584 EST337372 tomato flower buds 8 mm to pre-a... 66 1e-09
emb|AW622410|AW622410 EST313197 tomato root during/after fruit s... 40 3e-06
emb|AW160184|AW160184 EST290041 L. pennellii trichome, Cornell U... 40 4e-06
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emb|AW031815|AW031815 EST275269 tomato callus, TAMU Lycopersicon... 31 0.42
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30 emb|AW224605|AW224605 EST303048 tomato root, plants pre-anthesis... 31 0.42
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35 emb|AW455351|AW455351 EST311889 tomato root during/after fruit s... 31 0.42
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emb|AW038338|AW038338 EST280021 tomato mixed elicitor, BTI Lycop... 31 0.43
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emb|AW982678|AW982678 HVSMEg0003O16f Hordeum vulgare pre-anthesi... 35 1.0
50 emb|AW933175|AW933175 EST359018 tomato fruit mature green, TAMU ... 36 1.6
emb|Z50171|TBBSLARN T.brucei brucei SLA RNA gene. 36 1.6
emb|AI484282|AI484282 EST248834 tomato susceptible, Cornell Lyco... 31 2.0
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55 emb|AB008750|AB008750 Schizosaccharomyces pombe gene for Alp11, ... 35 2.2
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 emb|AI965479|AI965479 sc72e01.y1 Gm-c1018 Glycine max cDNA clone... 35 4.2
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 10 emb|AC004710|AC004710 Plasmodium falciparum chromosome 12, *** S... 35 4.2
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 40 post/entrez/query?db=n&form=6&dopt=g&uid=gb|af071527|/ncgi
 http://www.ncgr.org/cgi-bin/ff?af071527
 (1926 letters)
 Database: plantfungal
 45 661,018 sequences; 426,114,510 total letters
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 55 emb|AI729861|AI729861 BNLGHi5428 Six-day Cotton fiber Gossypium ... 52 2e-05
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 emb|AV420300|AV420300 AV420300 Lotus japonicus young plants (two... 49 1e-04
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 60 emb|AI896054|AI896054 EST265497 tomato callus, TAMU Lycopersicon... 47 4e-04
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10	emb AQ638202 AQ638202 927P1-9H10.TP 927P1 Trypanosoma brucei gen...	41	0.033
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15	emb AW256577 AW256577 EST304714 KV2 Medicago truncatula cDNA clo...	30	0.064
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	emb Z49595 SCYJR095W S.cerevisiae chromosome X reading frame ORF...	35	2.0
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40	gb L20566 ASNACDP Aspergillus niger acid phosphatase complete cds.	27	4.0
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45	emb AQ639089 AQ639089 927P1-1D11.TP 927P1 Trypanosoma brucei gen...	33	7.2
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	emb AW623353 AW623353 EST321298 tomato flower buds 3-8 mm, Corne...	33	7.2
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50	emb AQ656501 AQ656501 Sheared DNA-12B14.TF Sheared DNA Trypanoso...	33	7.2
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60	emb X87941 SCDNAGENS S.cerevisiae CRM1, YML9, PET54, SMI1, PHO81...	28	7.5
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- emb|AI213023|AI213023 y6e12a1.fl *Aspergillus nidulans* 24hr asexu... 33 9.9
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 emb|AW991081|AW991081 SsS0293 *Suaeda salsa* ZAP cDNA library Suae... 33 9.9
 10 emb|AW399343|AW399343 EST309843 *L. pennellii* trichome, Cornell U... 33 9.9
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 20 (1062 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

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| 30 | emb AI486803 AI486803 EST245125 tomato ovary, TAMU <i>Lycopersicon</i> ... | 358 | 6e-98 | |
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| | emb AW574302 AW574302 EST316893 GVN <i>Medicago truncatula</i> cDNA clo... | 255 | 1e-76 | |
| | emb AW459665 AW459665 sh90c10.y1 Gm-cl016 <i>Glycine max</i> cDNA clone... | 285 | 5e-76 | |
| | emb AI898341 AI898341 EST267784 tomato ovary, TAMU <i>Lycopersicon</i> ... | 282 | 3e-75 | |
| 35 | gb L42466 PIAEFE <i>Picea glauca</i> ethylene-forming enzyme (EFE) mRNA... | 156 | 4e-75 | |
| | emb AW981190 AW981190 EST392384 <i>DSIL Medicago truncatula</i> cDNA cl... | 262 | 2e-73 | |
| | emb AI777799 AI777799 EST258678 tomato susceptible, Cornell Lyco... | 267 | 1e-70 | |
| | emb AW574101 AW574101 EST316692 GVN <i>Medicago truncatula</i> cDNA clo... | 198 | 2e-67 | |
| | emb AW268031 AW268031 EST306309 <i>DSIR Medicago truncatula</i> cDNA cl... | 126 | 6e-65 | |
| 40 | emb AW775553 AW775553 EST334618 <i>DSIL Medicago truncatula</i> cDNA cl... | 210 | 3e-63 | |
| | emb AW509400 AW509400 si22f08.y1 Gm-cl029 <i>Glycine max</i> cDNA clone... | 237 | 8e-62 | |
| | emb AB003779 AB003779 <i>Perilla frutescens</i> mRNA for leucoanthocyan... | 115 | 5e-59 | |
| | emb AW349732 AW349732 GM210006A11F12R Gm-r1021 <i>Glycine max</i> cDNA ... | 228 | 6e-59 | |
| | gb U97530 PAU97530 <i>Prunus armeniaca</i> ethylene-forming-enzyme-like... | 143 | 1e-58 | |
| 45 | emb AF082862 AF082862 <i>Pisum sativum</i> unknown mRNA, partial cds. | 220 | 2e-56 | |
| | emb Z22543 PHFLASYNA <i>P.hybrida</i> flavonol synthase mRNA. | 99 | 1e-55 | |
| | emb X83229 NTRNA1A1C <i>N.tabacum</i> mRNA for 1-aminocyclopropane-1-ca... | 176 | 1e-54 | |
| | emb AF184273 AF184273 <i>Daucus carota</i> leucoanthocyanidin dioxygena... | 110 | 9e-54 | |
| | emb AW030000 AW030000 EST273255 tomato callus, TAMU <i>Lycopersicon</i> ... | 186 | 1e-53 | |
| 50 | emb AF026058 AF026058 <i>Matthiola incana</i> anthocyanidin synthase mR... | 116 | 2e-53 | |
| | emb AF184274 AF184274 <i>Daucus carota</i> leucoanthocyanidin dioxygena... | 110 | 2e-53 | |
| | emb AF117269 AF117269 <i>Malus domestica</i> anthocyanidin synthase (AN... | 114 | 3e-53 | |
| | emb X71360 MSPANTHHY <i>Malus sp.</i> mRNA for anthocyanidin hydroxylase. | 114 | 3e-53 | |
| | emb AW686531 AW686531 NF042D05NR1F1000 Nodulated root <i>Medicago t...</i> | 166 | 2e-52 | |
| 55 | gb U54566 NGU54566 <i>Nicotiana glutinosa</i> 1-aminocyclopropane-1-car... | 174 | 2e-52 | |
| | emb AF001391 AF001391 <i>Matthiola incana</i> putative flavonol synthas... | 118 | 3e-52 | |
| | emb AF119095 AF119095 <i>Malus domestica</i> flavonol synthase (FLS) mR... | 91 | 2e-51 | |
| | emb X70786 PHFLV3HDX <i>P.hybrida</i> mRNA for putative flavanone 3-hyd... | 112 | 5e-51 | |
| | emb AB012205 AB012205 <i>Lactuca sativa</i> Ls3h1 mRNA for gibberelin 3... | 137 | 9e-51 | |
| 60 | emb AF028602 AF028602 <i>Ipomoea purpurea</i> anthocyanidin synthase (A... | 108 | 1e-50 | |
| | emb AB013101 AB013101 <i>Lycopersicon esculentum</i> LE-ACO4 mRNA for 1... | 157 | 2e-50 | |

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5 emb|A35021|A35021 *L. esculentum* pTOM13. 159 1e-49
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emb|AB003514|AB003514 *Actinidia deliciosa* mRNA for 1-aminocyclop... 157 4e-49
10 gb|U68215|CPU68215 *Carica papaya* ACC oxidase mRNA, complete cds. 152 5e-49
emb|AF117270|AF117270 *Malus domestica* flavanone 3-hydroxylase (F... 100 5e-49
emb|X69664|MSF3HA *Malus* sp. mRNA for naringenin, 2-oxoglutarate, 3... 100 5e-49
gb|M97961|ACTACCOXI *Actinidia deliciosa* ACC oxidase homologue pr... 154 7e-49
emb|AB010991|AB010991 *Lycopersicon esculentum* Le3OH-1 mRNA for 3... 133 7e-49
15 emb|AF115262|AF115262 *Trifolium repens* mature green leaf 1-amino... 158 7e-49
gb|U19856|PHU19856 *Pelargonium hortorum* 1-aminocyclopropane-1-ca... 153 1e-48
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20 gb|U74081|IPU74081 *Ipomoea purpurea* flavanone 3-hydroxylase (F3H... 99 2e-48
emb|AF254125|AF254125 *Carica papaya* ACC oxidase mRNA, complete cds. 150 2e-48
emb|AB012857|AB012857 *Nicotiana tabacum* mRNA for ACC oxidase, co... 155 2e-48
emb|AB002667|AB002667 *Vigna angularis* mRNA for ACC-oxidase, comp... 158 2e-48
emb|AB023789|AB023789 *Ipomoea batatas* f3h II mRNA for flavanone ... 96 2e-48
25 emb|AB023790|AB023790 *Ipomoea batatas* f3h III mRNA for flavanone... 96 2e-48
gb|U06047|VRU06047 *Vigna radiata* clone pVR-ACO2 1-aminocycloprop... 157 3e-48
gb|BE058138|BE058138 sn11h05.y1 Gm-c1016 *Glycine max* cDNA clone ... 193 3e-48
emb|Y10749|BPACORNA *B. pendula* ACO mRNA. 150 3e-48
gb|U67861|PHU67861 *Pelargonium hortorum* 1-aminocyclopropane-1-ca... 154 5e-48
30 emb|X87097|PCPCACO1G *P. communis* mRNA for 1-aminocyclopropane-1-c... 155 5e-48
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emb|AB023788|AB023788 *Ipomoea batatas* f3h I mRNA for flavanone 3... 95 6e-48
35 gb|U23066|PAU23066 *Persea americana* flavanone 3-hydroxylase mRNA... 100 6e-48
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emb|X98493|NTACCO *Nicotiana tabacum* mRNA for ACC-oxidase (clone ... 154 9e-48
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gb|L35152|DINACCA *Dianthus caryophyllus* amino-cyclopropane carbo... 158 1e-47
40 emb|AW685110|AW685110 NF025C04NR1F1000 *Nodulated root Medicago* t... 158 1e-47
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45 emb|Y10034|PP1AMCSYN *R. palustris* mRNA for 1-aminocyclopropane-1-... 159 2e-47
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55 emb|Z46349|NTACCDEAM *N. tabacum* mRNA for 1-aminocyclopropane-1-ca... 150 8e-47
gb|L07912|DORACCOXID *Moth orchid* ACC oxidase mRNA, complete cds. 129 1e-46
emb|X77232|PPPAO1 *P. persica* PAO1 mRNA for 1-aminocyclopropane-1-... 156 1e-46
emb|Z11750|BJEFEMR *B. juncea* mRNA for ethylene-forming enzyme. 146 1e-46
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60 emb|X72594|MIFHT *M. incana* mRNA for flavanone 3-beta-hydroxylase. 94 2e-46
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- emb|AB010992|AB010992 Lycopersicon esculentum Le3OH-2 mRNA for 3... 133 2e-46
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 15 (1731 letters)

Database: plantfungal
 661,018 sequences; 426,114,510 total letters

- 20 Searching.....done

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| 25 emb AF023472 AF023472 Hordeum vulgare peptide transporter (ptr1)... | 162 | e-119 | |
| emb AW929517 AW929517 EST338305 tomato flower buds 8 mm to pre-a... | 162 | 3e-90 | |
| emb AF016713 AF016713 Lycopersicon esculentum oligopeptide trans... | 138 | 3e-89 | |
| emb AF213936 AF213936 Prunus dulcis amino acid/peptide transport... | 132 | 2e-87 | |
| emb Y13862 NTENRT1 Nicotiana tabacum enr-T1 gene. | 173 | 9e-81 | |
| 30 emb X92852 LENIT2 L.esculentum exon 1 of NIT2 gene. | 140 | 1e-80 | |
| emb AW773639 AW773639 EST332625 KV3 Medicago truncatula cDNA clo... | 298 | 9e-80 | |
| emb X92853 LEMIT1 L.esculentum exon 1 of NIT1 gene. | 150 | 9e-74 | |
| gb U17987 BNU17987 Brassica napus RCH2 protein mRNA, complete cds. | 80 | 5e-73 | |
| emb AW929740 AW929740 EST354010 tomato flower buds 8 mm to pre-a... | 163 | 3e-58 | |
| 35 emb AW278758 AW278758 sf97b05.y1 Gm-c1019 Glycine max cDNA clone... | 127 | 2e-47 | |
| emb AW186088 AW186088 se63e01.y1 Gm-c1019 Glycine max cDNA clone... | 176 | 4e-43 | |
| emb AQ917114 AQ917114 T233143b Medicago truncatula BAC library M... | 112 | 6e-42 | |
| emb AF080545 AF080545 Nepenthes alata peptide transporter (PTR1)... | 111 | 1e-41 | |
| emb AW677489 AW677489 DG1_8_A08.b1_A002 Dark Grown 1 (DG1) Sorgh... | 126 | 2e-35 | |
| 40 emb AW219289 AW219289 EST301771 tomato root during/after fruit s... | 144 | 3e-34 | |
| emb Z69370 CSNITR1 C.sativus mRNA for nitrite transporter. | 76 | 3e-34 | |
| emb AW310175 AW310175 sf32c04.x1 Gm-c1028 Glycine max cDNA clone... | 146 | 5e-34 | |
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| emb AW455271 AW455271 EST311931 tomato root during/after fruit s... | 144 | 3e-33 | |
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| 50 emb AI488938 AI488938 EST247277 tomato ovary, TAMU Lycopersicon ... | 85 | 2e-31 | |
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| emb AI485754 AI485754 EST244075 tomato ovary, TAMU Lycopersicon ... | 107 | 9e-30 | |
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| 60 emb AW707240 AW707240 sk22e06.y1 Gm-c1028 Glycine max cDNA clone... | 111 | 7e-28 | |
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- emb|AW688241|AW688241 NF005B02ST1F1000 Developing stem Medicago ... 77 9e-28
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5 emb|AW201920|AW201920 sf08g07.yl Gm-c1027 Glycine max cDNA clone... 105 4e-27
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10 emb|AW692300|AW692300 NF054C11ST1F1000 Developing stem Medicago ... 77 1e-25
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45 emb|AW257541|AW257541 EST305678 KV2 Medicago truncatula cDNA clo... 58 1e-19
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 10 http://www.ncgr.org/cgi-bin/ff?ac006580
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

15

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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 60 emb|AW668121|AW668121 GA_Ea0012N05 Gossypium arboreum 7-10.dpa ... 154 1e-46
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- emb|AI898263|AI898263 EST267706 tomato ovary, TAMU Lycopersicon ... 185 5e-46
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25 emb|AJ010830|TSP010830 Triticum sp. mRNA for GRAB2 protein. 133 3e-44
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5

Database: plantfungal
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Score E
 Sequences producing significant alignments: (bits) Value

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 20 emb|AW509358|AW509358 si22a10.y1 Gm-c1029 Glycine max cDNA clone... 272 3e-72
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 25 emb|AI774300|AI774300 EST255316 tomato resistant, Cornell Lycopen... 210 1e-53
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60 Database: plantfungal
661,018 sequences; 426,114,510 total letters

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55 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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60 Score E
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- 5 gb|BE052481|BE052481 GA_Ea0034B15f *Gossypium arboreum* 7-10 dpa ... 248 8e-65
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 5 emb|AI055630|AI055630 coau0004J11 Cotton Boll Abscission Zone cD... 113 4e-24
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 10 emb|AW726477|AW726477 GA_Ea0021M14 *Gossypium arboreum* 7-10 dpa ... 60 5e-10
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 emb|AW091888|AW091888 EST285068 tomato mixed elicitor, BTI *Lycop*... 53 5e-08
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 15 emb|AW221657|AW221657 EST298468 tomato fruit red ripe, TAMU *Lyc*... 58 2e-07
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 30 gb|U32307|SCU32307 *Saccharomyces cerevisiae* oligosaccharyltransf... 35 1.6
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 (711 letters)

5 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

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	gb BE124796 BE124796	EST393831	GVN Medicago truncatula cDNA clon...	72	2e-19
	emb AW399006 AW399006	EST309506	L. pennellii trichome, Cornell U...	77	1e-17
	emb AW442210 AW442210	EST311606	tomato fruit red ripe, TAMU Lyco...	75	2e-17
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	emb AI729941 AI729941	BNLGH15757	Six-day Cotton fiber Gossypium ...	79	3e-14
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 10 emb|AI484163|AI484163 EST248970 tomato resistant, Cornell Lycopersicon... 69 1e-11
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 emb|AW031045|AW031045 EST274352 tomato callus, TAMU Lycopersicon... 68 7e-11
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 45 emb|AW980667|AW980667 EST391820 *GVN Medicago truncatula* cDNA clo... 67 1e-10
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Database: plantfungal

661,018 sequences; 426,114,510 total letters

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Sequences producing significant alignments: (bits) Value

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 10 emb|AW034255|AW034255 EST277826 tomato callus, TAMU Lycopersicon... 74 6e-14
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 15 emb|AW694732|AW694732 NF079D07ST1F1061 Developing stem Medicago ... 73 8e-14
 emb|AW621923|AW621923 EST312721 tomato root during/after fruit s... 73 8e-14
 emb|A67797|A67797 Sequence 2 from Patent WO9743427. 73 8e-14
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 20 emb|AW621294|AW621294 EST312092 tomato root during/after fruit s... 73 8e-14
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 25 gb|T14833|T14833 crs280 lambdaZAPST Ricinus communis cDNA clone ... 47 1e-13
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 30 emb|AW201545|AW201545 sf04d10.y1 Gm-c1027 Glycine max cDNA clone... 72 1e-13
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 emb|A67796|A67796 Sequence 1 from Patent WO9743427. 72 2e-13
 emb|AW429258|AW429258 EST306714 tomato flower buds 0-3 mm, Corne... 72 2e-13
 emb|AI898120|AI898120 EST267563 tomato ovary, TAMU Lycopersicon ... 48 3e-13
 35 emb|AW617954|AW617954 EST314028 L. pennellii trichome, Cornell U... 71 3e-13
 emb|AW029819|AW029819 EST273074 tomato callus, TAMU Lycopersicon... 48 3e-13
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55 Database: plantfungal
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- emb|AW687938|AW687938 NF001B11ST1F1000 Developing stem Medicago ... 393 e-108
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 5 emb|AW688778|AW688778 NF011E05ST1F1000 Developing stem Medicago ... 244 1e-65
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 emb|AW041025|AW041025 EST283889 tomato mixed elicitor, BTI Lycop... 171 2e-41
 10 emb|AL023554|SPBC16G5 S.pombe chromosome II cosmid c16G5. 81 1e-31
 gb|BE053060|BE053060 GA_Ea0020N16f Gossypium arboreum 7-10 dpa ... 132 7e-30
 gb|BE035432|BE035432 MO05D07 MO Mesembryanthemum crystallinum cD... 111 1e-23
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 15 emb|AV421776|AV421776 AV421776 Lotus japonicus young plants (two... 72 4e-13
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 20 emb|AW220409|AW220409 EST302892 tomato root during/after fruit s... 53 5e-06
 emb|AW737074|AW737074 CAF50 Peronospora parasitica cDNA-AFLP fra... 46 8e-04
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 gb|U10274|SCU10274 Saccharomyces cerevisiae thioredoxin reductas... 44 0.004
 emb|AW933535|AW933535 EST359294 tomato fruit mature green, TAMU ... 38 0.016
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 50 gb|U15935|CWKAS3A Cuphea wrightii beta-ketoacyl-ACP synthase III... 34 4.3
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- gb|U18839|SCE9747 *Saccharomyces cerevisiae* chromosome V cosmids ... 33 8.1
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 5 emb|AI441951|AI441951 sa83b07.y1 Gm-c1004 *Glycine max* cDNA clone... 33 8.1
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 10 emb|Z69368|SPAC27F1 *S.pombe* chromosome I cosmid c27F1. 33 8.1
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 http://www3.ncbi.nlm.nih.gov/htbin-
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 20 http://www.ncgr.org/cgi-bin/ff?x98676
 (643 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

25

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| | gb L46574 L46574 BNAF1975 Mustard flower buds <i>Brassica rapa</i> cDNA... | 84 | 2e-29 | |
| | emb AB006600 AB006600 <i>Petunia x hybrida</i> mRNA for ZPT2-13, comple... | 57 | 2e-25 | |
| | emb AB006599 AB006599 <i>Petunia x hybrida</i> mRNA for ZPT2-12, comple... | 57 | 5e-23 | |
| | emb AI485362 AI485362 EST243683 tomato ovary, TAMU Lycopersicon ... | 64 | 4e-22 | |
| 35 | emb AI898309 AI898309 EST267752 tomato ovary, TAMU Lycopersicon ... | 63 | 8e-22 | |
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| | emb AB006604 AB006604 <i>Petunia x hybrida</i> mRNA for ZPT2-9, complet... | 102 | 2e-21 | |
| | emb AW030869 AW030869 EST274159 tomato callus, TAMU Lycopersicon... | 61 | 4e-21 | |
| | emb AI485555 AI485555 EST243876 tomato ovary, TAMU Lycopersicon ... | 55 | 7e-21 | |
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| | emb AI486228 AI486228 EST244549 tomato ovary, TAMU Lycopersicon ... | 55 | 2e-20 | |
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| 45 | emb AI488341 AI488341 EST246663 tomato ovary, TAMU Lycopersicon ... | 55 | 8e-20 | |
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| | emb AI966235 AI966235 sc35g05.y1 Gm-c1014 <i>Glycine max</i> cDNA clone... | 60 | 1e-19 | |
| | emb AI897376 AI897376 EST266819 tomato ovary, TAMU Lycopersicon ... | 64 | 2e-19 | |
| | emb AB006603 AB006603 <i>Petunia x hybrida</i> mRNA for ZPT2-8, complet... | 61 | 4e-19 | |
| 50 | emb AW033868 AW033868 EST277439 tomato callus, TAMU Lycopersicon... | 62 | 1e-18 | |
| | emb AI894711 AI894711 EST264154 tomato callus, TAMU Lycopersicon... | 61 | 1e-18 | |
| | emb AI485123 AI485123 EST243427 tomato ovary, TAMU Lycopersicon ... | 60 | 2e-18 | |
| | emb AI771824 AI771824 EST252924 tomato ovary, TAMU Lycopersicon ... | 59 | 5e-18 | |
| | emb AW685937 AW685937 NF031H10NR1F1000 Nodulated root <i>Medicago t...</i> | 59 | 9e-18 | |
| 55 | emb AW216442 AW216442 EST295072 tomato callus, TAMU Lycopersicon... | 57 | 1e-17 | |
| | emb AW684455 AW684455 NF017B06NR1F1000 Nodulated root <i>Medicago t...</i> | 62 | 5e-17 | |
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| | emb AV422177 AV422177 AV422177 <i>Lotus japonicus</i> young plants (two... | 56 | 8e-17 | |
| | emb AB006602 AB006602 <i>Petunia x hybrida</i> mRNA for ZPT2-7, complet... | 60 | 2e-16 | |
| 60 | dbj D26083 PETZFDB1 <i>Petunia hybrida</i> gene for zinc-finger DNA bin... | 56 | 3e-16 | |
| | dbj D26084 PETZFDB2 <i>Petunia</i> mRNA for zinc-finger DNA binding pro... | 56 | 3e-16 | |

- emb|AW680050|AW680050 WS1_3_G12.g1_A002 Water-stressed 1 (WS1) S... 57 1e-15
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5 emb|AI896031|AI896031 EST265474 tomato callus, TAMU Lycopersicon... 53 3e-15
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emb|AW153229|AW153229 sc37f05.y1 Gm-c1015 Glycine max cDNA clone... 51 3e-12
emb|AW625323|AW625323 EST319146 tomato radicle, 5 d post-imbibit... 52 3e-12
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30 emb|AB035132|AB035132 Petunia x hybrida gene for C2H2 zinc-finge... 50 4e-12
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35 emb|AW560934|AW560934 EST315982 DSIR Medicago truncatula cDNA cl... 49 6e-12
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40 dbj|D26086|PETZFP4 Petunia zinc-finger protein gene. 50 1e-11
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- emb|AV426673|AV426673 AV426673 Lotus japonicus young plants (two... 48 4e-08
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 5 emb|X60700|PHEPF1 P.hybrida EPF1 gene for DNA-binding protein. 55 7e-07
 emb|AW620780|AW620780 sj09e02.y1 Gm-c1032 Glycine max cDNA clone... 54 9e-07
 emb|AI960244|AI960244 sc80g07.y1 Gm-c1018 Glycine max cDNA clone... 54 9e-07
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 (643 letters)
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 25 emb|AB006599|AB006599 Petunia x hybrida mRNA for ZPT2-12, comple... 57 5e-23
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 emb|AI898309|AI898309 EST267752 tomato ovary, TAMU Lycopersicon ... 63 8e-22
 emb|AI483886|AI483886 EST249757 tomato ovary, TAMU Lycopersicon ... 64 2e-21
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 30 emb|AW030869|AW030869 EST274159 tomato callus, TAMU Lycopersicon... 61 4e-21
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 emb|AB000451|AB000451 Petunia hybrida mRNA for PETHy;ZPT2-5, com... 62 2e-20
 emb|AI486627|AI486627 EST244948 tomato ovary, TAMU Lycopersicon ... 55 2e-20
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 45 emb|AI771824|AI771824 EST252924 tomato ovary, TAMU Lycopersicon ... 59 5e-18
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 60 emb|AW033257|AW033257 EST276828 tomato callus, TAMU Lycopersicon... 53 3e-15
 emb|AI771191|AI771191 EST252387 tomato ovary, TAMU Lycopersicon ... 53 3e-15

- emb|AW032357|AW032357 EST275811 tomato callus, TAMU Lycopersicon... 53 3e-15
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 5 emb|AI488445|AI488445 EST246784 tomato ovary, TAMU Lycopersicon ... 55 2e-13
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 20 emb|AW924443|AW924443 WS1_69_C08.g1_A002 Water-stressed 1 (WS1) ... 57 3e-12
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 35 emb|AW729218|AW729218 GA_Ea0024G18 *Gossypium arboreum* 7-10 dpa ... 48 2e-11
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 50 emb|AW216968|AW216968 EST295682 tomato callus, TAMU Lycopersicon... 53 4e-09
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5

(639 letters)

Database: plantfungal

661,018 sequences; 426,114,510 total letters

10

Searching.....done

Score E

Sequences producing significant alignments: (bits) Value

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emb|Y11607|MSMP2C M.sativa mRNA for protein phosphatase 2C... 164 7e-70
emb|AJ242803|SST242803 Sporobolus stapfianus partial mRNA for pu... 154 4e-61
emb|AJ055336|AJ055336 coau0003L08 Cotton Boll Abscission Zone cD... 163 7e-56
emb|AJ488711|AJ488711 EST247050 tomato ovary, TAMU Lycopersicon ... 158 5e-46
20 emb|AJ489841|AJ489841 EST248180 tomato ovary, TAMU Lycopersicon ... 173 1e-42
emb|AW832587|AW832587 sm14b05.y1 Gm-cl027 Glycine max cDNA clone... 119 5e-40
emb|AW676724|AW676724 DG1_13_B08.g1_A002 Dark Grown 1 (DG1) Sorg... 152 2e-36
emb|AW423616|AW423616 sh69d07.y1 Gm-cl015 Glycine max cDNA clone... 110 3e-36
emb|AW278110|AW278110 sf39h03.y1 Gm-cl009 Glycine max cDNA clone... 119 2e-35
25 emb|AW698103|AW698103 NXNV_066_C09_F Nsf Xylem Normal wood Verti... 120 2e-33
emb|AI489730|AI489730 EST248069 tomato ovary, TAMU Lycopersicon ... 62 3e-29
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emb|AF092432|AF092432 Lotus japonicus protein phosphatase type 2... 73 8e-18
30 emb|AI731667|AI731667 BNLGHi10427 Six-day Cotton fiber Gossypium... 80 4e-16
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35 emb|AW776573|AW776573 EST335638 DSIL Medicago truncatula cDNA cl... 78 2e-15
emb|AW164504|AW164504 se73e07.y1 Gm-cl023 Glycine max cDNA clone... 76 5e-15
gb|H07534|H07534 cbn054 BNL2 Brassica napus cDNA 5'/3', mRNA seq... 82 5e-15
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55 emb|AW126261|AW126261 N100368e rootphos(-) Medicago truncatula c... 71 3e-13
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5 emb|AW934653|AW934653 EST353545 tomato flower buds 0-3 mm, Corne... 69 3e-11
emb|AW736469|AW736469 EST332483 KV3 Medicago truncatula cDNA clo... 69 3e-11
emb|AI052979|AI052979 Mpc9 Ice plant seedlings, RT-PCR, pCRII M... 63 3e-11
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emb|AW224147|AW224147 EST300958 tomato fruit red ripe, TAMU Lyco... 69 3e-11
10 emb|AW623772|AW623772 EST321717 tomato flower buds 3-8 mm, Corne... 68 5e-11
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25 emb|AI167089|AI167089 xylem.est.857 Poplar xylem Lambda ZAPII li... 48 6e-10
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35 emb|AW739238|AW739238 gb39a01.y1 Moss EST library PPN Physcomitr... 59 3e-08
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60 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|ac004138|/ncgi)
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<http://www.ncgr.org/cgi-bin/ff?ac004138>
(1551 letters)

Database: plantfungal

5 661,018 sequences; 426,114,510 total letters

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	emb AB022319 AB022319	Pisum sativum mRNA for apyrase, complete cds.	64	1e-30
15	emb AB027616 AB027616	Pisum sativum mRNA for apyrase, partial cd...	64	2e-29
	emb AW925295 AW925295	HVSMEg0001H23 Hordeum vulgare pre-anthesis...	69	2e-29
	emb AF156782 AF156782	Medicago sativa nod factor binding lectin...	66	8e-29
	emb AW983120 AW983120	HVSMEg0008D22f Hordeum vulgare pre-anthesi...	70	2e-28
	emb AI771115 AI771115	EST252215 tomato ovary, TAMU Lycopersicon ...	71	4e-28
20	emb AW934554 AW934554	EST353446 tomato flower buds 0-3 mm, Corne...	71	8e-26
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	emb AW618513 AW618513	EST320499 L. pennellii trichome, Cornell U...	67	5e-22
	emb AF139807 AF139807	Dolichos biflorus nod factor binding lecti...	65	6e-22
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40	emb AJ388942 AJ388942	AJ388942 Medicago truncatula R108 Medicago...	63	1e-12
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45	emb AW696828 AW696828	NF109D12ST1F1101 Developing stem Medicago ...	57	2e-11
	gb BE059022 BE059022	sn24b03.y1 Gm-c1016 Glycine max cDNA clone ...	53	4e-11
	emb AW306606 AW306606	se53a03.y1 Gm-c1017 Glycine max cDNA clone...	56	8e-11
	emb AI490444 AI490444	EST248770 tomato ovary, TAMU Lycopersicon ...	61	2e-10
	emb AW564791 AW564791	LG1_301_H10.b1_A002 Light Grown 1 (LG1) So...	51	2e-10
50	emb AI771846 AI771846	EST252946 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI897295 AI897295	EST266654 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AI485852 AI485852	EST244173 tomato ovary, TAMU Lycopersicon...	61	3e-10
	emb AI899079 AI899079	EST268522 tomato ovary, TAMU Lycopersicon ...	61	3e-10
	emb AW922880 AW922880	DG1_47_F10.b1_A002 Dark Grown 1 (DG1) Sorg...	48	4e-10
55	emb AI490499 AI490499	EST249033 tomato ovary, TAMU Lycopersicon ...	61	5e-10
	emb AI488302 AI488302	EST246624 tomato ovary, TAMU Lycopersicon ...	60	1e-09
	emb AV418181 AV418181	AV418181 Lotus japonicus young plants (two...	57	2e-09
	emb AW924275 AW924275	WS1_52_E03.b1_A002 Water-stressed 1 (WS1) ...	64	3e-09
	emb AW257004 AW257004	EST305141 KV2 Medicago truncatula cDNA clo...	48	8e-09
60	emb AI771696 AI771696	EST252796 tomato ovary, TAMU Lycopersicon ...	61	3e-08
	emb AW623313 AW623313	EST321258 tomato flower buds 3-8 mm, Corne...	58	2e-07

- emb|AA231755|AA231755 CDO38.R cDNA from oat Avena sativa cDNA cl... 56 7e-07
 emb|AW736308|AW736308 EST332392 KV3 Medicago truncatula cDNA clo... 54 4e-06
 emb|AW563435|AW563435 LG1_214_E12.b1_A002 Light Grown 1 (LG1) So... 38 4e-05
 emb|AB010444|AB010444 Neospora caninum mRNA for NTPase, complete... 41 1e-04
 5 emb|AL160371|LMFLCHR15 Leishmania major Friedlin assembled chrom... 44 0.004
 emb|AF203695|AF203695 Saccharomyces cerevisiae golgi nucleoside ... 43 0.005
 gb|U18778|SCE9537 Saccharomyces cerevisiae chromosome V cosmids ... 43 0.005
 emb|AZ124337|AZ124337 T223080b Medicago truncatula BAC library M... 41 0.026
 emb|AW225681|AW225681 ST70C07 Pine TriplEx shoot tip library Pin... 41 0.026
 10 emb|AW774350|AW774350 EST333501 KV3 Medicago truncatula cDNA clo... 41 0.026
 emb|AI974272|AI974272 T110271e KV0 Medicago truncatula cDNA clon... 40 0.035
 emb|AL049184|PFMAL13P3 Plasmodium falciparum chromosome 13 strai... 39 0.13
 emb|AI728079|AI728079 BNLGH19928 Six-day Cotton fiber Gossypium ... 29 0.23
 emb|X61608|BNLHCB3A B.napus gene for LHCII Type III chlorophyll ... 37 0.33
 15 emb|AW671082|AW671082 LG1_284_C02.b1_A002 Light Grown 1 (LG1) So... 37 0.33
 emb|AZ124338|AZ124338 T223081b Medicago truncatula BAC library M... 36 0.85
 emb|AF188744|AF188744 Brassica napus high-affinity ammonium tran... 35 1.2
 dbj|D37795|D37795 Ipomoea nil Tpn1 gene. 35 1.2
 dbj|E08493|E08493 gDNA encoding transposable element,Tpn1 which ... 35 1.2
 20 emb|AL356192|NCB24B19 Neurospora crassa DNA linkage group II BAC... 30 1.3
 emb|AF106939|AF106939 Phanerochaete chrysosporium 1,4-benzoquino... 29 1.4
 emb|AL163492|LMFL787 Leishmania major Friedlin chromosome 19 cos... 35 1.5
 emb|AW234282|AW234282 sf23d03.y1 Gm-cl028 Glycine max cDNA clone... 35 1.6
 emb|AL116534|CNS01D9A Botrytis cinerea strain T4 cDNA library un... 35 1.6
 25 emb|AW428880|AW428880 Ljirmp25-999-b7 Ljirmp Lambda HybriZap ... 35 1.6
 gb|N60092|N60092 TgESTzy11d09.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2
 emb|AW056764|AW056764 ST55E11 Pine TriplEx shoot tip library Pin... 35 2.2
 gb|N81562|N81562 TgESTzy59h03.r1 TgRH Tachyzoite cDNA Toxoplasma... 35 2.2
 emb|AW286610|AW286610 LG1_335_A07.g1_A002 Light Grown 1 (LG1) So... 35 2.2
 30 emb|AQ656308|AQ656308 Sheared DNA-27M14.TR Sheared DNA Trypanoso... 35 2.2
 emb|AL162692|SPBP4H10 S.pombe chromosome II P1 clone p4H10. 34 3.0
 emb|AQ652731|AQ652731 Sheared DNA-18C6.TR Sheared DNA Trypanosom... 34 3.0
 emb|AF016222|AF016222 Schizosaccharomyces pombe Rsv1p (rsv1) gen... 34 3.0
 emb|AW350237|AW350237 GM210008A10B2R Gm-r1021 Glycine max cDNA 3... 34 4.1
 35 emb|AQ943814|AQ943814 Sheared DNA-34A9.TF Sheared DNA Trypanosom... 34 4.1
 emb|AW666160|AW666160 sk32h08.y1 Gm-cl028 Glycine max cDNA clone... 34 4.1
 emb|AL109736|SPCC18B5 S.pombe chromosome III cosmid c18B5. 27 4.6
 emb|AW441608|AW441608 EST311004 tomato fruit red ripe, TAMU Lyco... 33 5.7
 emb|AL035476|PFMAL4P3 Plasmodium falciparum chromosome 4 strain ... 33 5.7
 40 emb|AW398001|AW398001 sg71a06.y1 Gm-cl007 Glycine max cDNA clone... 33 5.7
 emb|AW933585|AW933585 EST359428 tomato fruit mature green, TAMU ... 33 5.7
 emb|AI069343|AI069343 mgae0006cG03f Magnaporthe grisea Appressor... 33 5.7
 emb|X62697|NCACU3 N.crassa acu-3 gene for isocitrate lyase. 26 5.7
 emb|AI488866|AI488866 EST247205 tomato ovary, TAMU Lycopersicon ... 31 6.2
 45 emb|Z79690|ANPFA A.niger pfkA gene. 26 7.3
 emb|X13508|HVGHRDSP Barley gene for storage protein gamma-hordein. 28 7.8
 gb|M36378|BLYGIHORDA Barley gamma-1 hordein storage protein gene... 28 7.8
 emb|AF114171|AF114171 Sorghum bicolor BAC clone 25.M18, complete... 33 7.8
 emb|AI900865|AI900865 sb95d08.y1 Gm-cl012 Glycine max cDNA clone... 33 7.8
 50 emb|AZ124341|AZ124341 T223084b Medicago truncatula BAC library M... 33 7.8

Query= AL035679.144_at 17653_at /id_source genbank /description
 emb|cab38823.1| (al035679) putative protein [arabidopsis thaliana]
 /blast_score 0 /ec_number /family /chip nova /gb_link
 55 [http://www3.ncbi.nlm.nih.gov/htbin-](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi)
[post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi](http://www3.ncbi.nlm.nih.gov/htbin-post/entrez/query?db=n&form=6&dopt=g&uid=gb|al035679|/ncgi)
<http://www.ncgr.org/cgi-bin/ff?al035679>
 (1455 letters)

60 Database: plantfungal
 661,018 sequences; 426,114,510 total letters

Searching.....done

	Score	E		(bits)	Value
5	Sequences producing significant alignments:				
	emb AW091895 AW091895	EST285075	tomato mixed elicitor, BTI Lycop...	306	3e-82
	emb AW040183 AW040183	EST282682	tomato mixed elicitor, BTI Lycop...	306	3e-82
	emb AW776130 AW776130	EST335195	DSIL Medicago truncatula cDNA cl...	204	2e-51
10	emb AI897609 AI897609	EST267052	tomato ovary, TAMU Lycopersicon ...	182	4e-45
	emb AI055000 AI055000	coau0002L23	Cotton Boll Abscission Zone cD...	90	1e-42
	emb AI055639 AI055639	coau0004K19	Cotton Boll Abscission Zone cD...	107	2e-22
	emb AW693198 AW693198	NF061D12ST1F1000	Developing stem Medicago ...	66	6e-10
	emb AW684256 AW684256	NF014F09NR1F1000	Nodulated root Medicago t...	43	0.007
15	emb AW667681 AW667681	GA_Ea0010D15	Gossypium arboreum 7-10 dpa ...	43	0.007
	emb AW736130 AW736130	EST332126	KV3 Medicago truncatula cDNA clo...	39	0.12
	emb AW683515 AW683515	NF015C12LF1F1097	Developing leaf Medicago ...	36	0.21
	emb AI781902 AI781902	EST262781	tomato susceptible, Cornell Lyco...	36	0.57
	gb U12141 SCU12141	Saccharomyces cerevisiae	chromosome XIV left ...	35	0.73
20	emb AW277626 AW277626	sf84e07.y1	Gm-c1019 Glycine max cDNA clone...	36	0.79
	emb Z71330 SCYNL054W	S.cerevisiae	chromosome XIV reading frame O...	35	0.80
	emb AW692595 AW692595	NF057C11ST1F1000	Developing stem Medicago ...	35	1.1
	emb X54145 ANPECT	A.niger	gene for pectinesterase.	35	1.5
	emb A35008 A35008	A.niger	PE gene.	35	1.5
25	emb A34997 A34997	A.niger	pectinesterase coding sequence.	35	1.5
	emb AQ162316 AQ162316	mgxb0012I08r	CUGI Rice Blast BAC Library P...	34	2.8
	emb AF132029 AF132029	Hortonia floribunda	chloroplast atpB-rbcL ...	34	2.8
	emb AW567917 AW567917	si67c02.y1	Gm-r1030 Glycine max cDNA clone...	34	2.8
	emb AQ951657 AQ951657	Sheared DNA-48F5	TR Sheared DNA Trypanosom...	34	2.8
30	gb U81520 CIU81520	Cichorium intybus	sucrose:sucrose 1-fructosyl...	34	3.9
	emb AZ047925 AZ047925	LMAJFV1_lm68e11.x1	Leishmania major FV1 ra...	34	3.9
	emb AI730144 AI730144	BNLGH16313	Six-day Cotton fiber Gossypium ...	34	3.9
	emb AQ942723 AQ942723	Sheared DNA-42J12	TR Sheared DNA Trypanoso...	34	3.9
	gb U05812 HMU05812	Herpetomonas muscarum	ATCC 30261 kinetoplast ...	34	3.9
35	emb AW681095 AW681095	WS1_8_B09.g1	A002 Water-stressed 1 (WS1) S...	34	3.9
	emb AL049180 PFMAL13P1	Plasmodium falciparum	chromosome 13 strai...	27	4.9
	emb AW832107 AW832107	sm30e05.y1	Gm-c1028 Glycine max cDNA clone...	33	5.3
	gb N82224 N82224	TgESTzy37d01.r1	TgRH Tachyzoite cDNA Toxoplasma...	33	5.3
	emb A94222 A94222	Sequence 5 from Patent	EP0952222.	33	5.3
40	emb AA741851 AA741851	LmLv39p3/584B	Leishmania major promastigot...	33	5.3
	emb AW728096 AW728096	GA_Ea0029O02	Gossypium arboreum 7-10 dpa ...	33	7.3
	emb AW278032 AW278032	sf89g07.y1	Gm-c1019 Glycine max cDNA clone...	33	7.3
	gb N82117 N82117	TgESTzy36b06.r1	TgRH Tachyzoite cDNA Toxoplasma...	33	7.3
	emb AL355930 NCB208	Neurospora crassa	DNA linkage group II BAC c...	32	10.0
45	emb AW688738 AW688738	NF011A11ST1F1000	Developing stem Medicago ...	32	10.0
	emb AI781529 AI781529	EST262408	tomato susceptible, Cornell Lyco...	32	10.0
	emb AI397765 AI397765	NCC5A11T7	Conidial Neurospora crassa cDNA ...	32	10.0
	emb AF127239 AF127239	Nicotiana tabacum	cultivar Burley 21 argin...	32	10.0
	emb AW180260 AW180260	MgA0351f	MgA Library Mycosphaerella gramin...	32	10.0
50	emb AF127240 AF127240	Nicotiana tabacum	cultivar Xanthi arginine...	32	10.0
	gb BE055666 BE055666	GA_Ea0009H20f	Gossypium arboreum 7-10 dpa ...	32	10.0
	gb BE036548 BE036548	MP01C02	MP Mesembryanthemum crystallinum cD...	32	10.0
	emb AW038750 AW038750	EST280611	tomato mixed elicitor, BTI Lycop...	32	10.0
	emb AL133484 LMFL236	Leishmania major	Friedlin chromosome 19 cos...	32	10.0
55	gb BE123936 BE123936	EST394061	DSIL Medicago truncatula cDNA clo...	32	10.0

Example 4

Immediate Early Transcriptional Responses Controlled by a Salicylic Acid Dependent Local Resistance Pathway

Salicylic Acid (SA) is an important mediator of local and systemic defense responses. In *Arabidopsis*, accumulation of SA is essential for local resistance against many pathogens including *Peronospora parasitica* (*Peronospora*) isolates. Furthermore, numerous defense-related genes can be activated by SA treatment. In addition to local resistance, SA-accumulation is required for systemic acquired resistance (SAR). In the SAR pathway, SA has been shown to act upstream of *NPR1*, which is also essential for SAR. Short application of the SA analog BTH (e.g., 4 hours) to plant tissue appears to simulate local defense responses to *Peronospora parasitica*, whereas sustained SA treatment (e.g., 48 hours) elicits SAR-related plant responses (Maleck et al., 2000).

A previous cDNA microarray study identified a cluster of roughly 30 co-regulated genes that appear to be specifically involved in resistance of the *Arabidopsis* ecotype WS against the *Peronospora* isolate Noco2 (Maleck et al., 2000). These genes are strongly activated in response to infection with Noco2 (incompatible interaction) and 4 hours after BTH treatment. However, these genes were not markedly activated during a compatible interaction with the *Peronospora* isolate Emwa1 or an incompatible interaction with *Pseudomonas syringae* (DC3000 avrRpt2) bacteria. BTH treatment for 48 hours (that simulates SAR) even strongly repressed these genes. Thus, a rapid and transient SA peak may control Noco2 triggered defense genes.

Resistance of the *Arabidopsis* ecotype Col-0 against the *Peronospora* isolate Emoy2 appears to be regulated by a similar pathway that also is dependent on accumulation of SA. Emoy2 resistance in Col-0 is controlled by the resistance gene *RPP4*. To further explore early SA-dependent gene regulatory events and to relate these to *Peronospora*-induced resistance responses, immediate-early target genes of SA were identified using Affymetrix chip experiments with the protein biosynthesis inhibitor cycloheximide (CHX). Genes of this category likely are linked to transcriptional regulators acting closely downstream of SA. Results from these "SA-chip" experiments were combined with those from a set of chip experiments examining expression

profiles triggered in the *Arabidopsis* ecotype Col-0 by the *Peronospora* isolate Emoy2 to identify clusters of co-regulated *RPP4* controlled SA-dependent immediate early genes.

Results

5 To identify genes controlled by the *RPP4* pathway, interactions between the *Peronospora* isolate Emoy2 and Col-0 wild type plants, the defense mutants *ndr1*, *npr1* and *pad4* as well as transgenic NahG plants were examined by chip experiments. The interactions between Emoy2 and Col-0, *ndr1* or *npr1* are incompatible (plant is disease resistant), whereas the interactions involving *pad4* and NahG are compatible (plant is susceptible, i.e., disease develops). For each interaction three different time points were analyzed: 0, 12 and 48 hours post infection with 50,000 Emoy2 spores/ml. Genes that were at one or more time points more strongly expressed in Col-0, *ndr1* and *npr1* as compared to *pad4* and NahG were considered as controlled by the *RPP4* pathway. Genes represented by 271 probe sets showed at least one 2-fold expression difference in comparison between Col-0 and *pad4* or NahG and were selected for further analysis.

To identify immediate early target genes of SA, Col-0 wt seedlings were pretreated with CHX or mock treated 15 minutes before spraying with 2 mM SA or water and harvested 2 hours later (Table 28).

Table 28

<u>Plants</u>	<u>Treatment</u>
Col-0	untreated (mock)
25 Col-0	+ SA
Col-0	+ SA + CHX
Col-0	+ CHX

271 probe sets were found to be upregulated in a *RPP4* pathway-specific manner (SEQ ID NOs: 400-684). Emoy2-induced upregulation of these genes is compromised in *pad4* and *NahG* plants. These *RPP4* controlled genes were further analyzed concerning their responses to SA, CHX and SA + CHX. The 271 probe sets were subcategorized by K-means clustering over the SA/CHX data set. Nine K-means clusters comprised three subgraphs. For each of these subgraphs, the first data point represented the untreated control value, the second data point represented the response to combined SA/CHX treatment, the third

data point represented CHX treatment alone and the fourth data point represented SA treatment alone. K-means clustering defined two categories of RPP4 controlled CHX/SA-responsive genes: immediate early genes (SA-responsive, not CHX affected) and super-induced genes (additive effects of SA and CHX).

Two K-means clusters represent *RPP4*-controlled SA-induced immediate early genes (Table 29; SEQ ID NOs: 150, 159, 117, 126, 208, 428, 426, 436, 430, 434, 478, 641, 609, 615 and 526). *RPP4*-controlled upregulation of these genes is SA dependent and SA induction is not compromised by CHX, which blocks or reduces protein biosynthesis. Thus, all essential regulators that mediate SA-responsiveness of these genes must be already preformed and, hence, are likely to act closely downstream of SA. This set of 15 genes includes seven potential regulator genes that may be involved in the control of secondary response genes (which require protein biosynthesis) or other late responses.

Table 29

12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
14978_at	gb AAB64024.1 (AC002333) putative glucosyltransferase
15479_at	emb CAB39671.1 (AL049483) putative protein
15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
16061_s_at	gb AAB97145.1 (AF000977) MEK1
16109_s_at	gb AAC05342.1 (AC002521) putative protein kinase
16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
16603_s_at	gb AAB58497.1 (U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase
17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
17930_s_at	emb CAA07352.1 (AJ006960) peroxidase
18966_at	gb AAC95196.1 (AC004561) putative glutathione S-transferase
20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak similarity to NF-kappa-B
20685_at	emb CAB41928.1 (AL049751) short-chain alcohol dehydrogenase like protein
13702_s_at	emb CAA19683.1 (AL024486) putative protein
14704_s_at	gb AAD15461.1 (AC006067) unknown protein

To further subcategorize these genes and to more precisely define a cluster of strictly co-regulated genes, the set of 15 genes was analyzed by K-means clustering over the *RPP4* data set (Emoy2 infections). This allows to use *RPP4* triggered expression timing as an additional criterion for subclustering. Normalized absolute expression levels at 0, 12 and 48 hpi in Emoy2 infected

Col-0 (w.t.), *ndr1*, *npr1*, *pad4* and *NahG* plants are displayed. Genes that share a pronounced almost linear and sustained expression increase were chosen for further analysis. These 5 genes (Table 30, which show a pronounced Emoy2-induced SA-dependent but *npr1*-independent linear expression increase and which encode potential regulators) are upregulated by the *RPP4* pathway, respond to Emoy2 recognition with a steep, sustained, almost linear expression increase. This pronounced "upregulation" is SA dependent and independent of *de novo* protein biosynthesis. Transcription factors that mediate this response must be present when SA is perceived and may act closely downstream of SA.

The mechanism that switches these genes on may involve posttranslational modifications of such preformed transcription factors.

Table 30

12354_g_at	gb AAC23641.1 (AC004684) putative receptor-like protein kinase
15616_s_at	emb CAA08794.1 (AJ009696) wall-associated kinase 1
16140_s_at	emb CAB42872.1 (AJ012423) wall-associated kinase 2
17499_s_at	gb AAD19610.1 (AF107726) cyclic nucleotide gated channel
20429_s_at	emb CAB10219.1 (Z97336) hypothetical protein - weak similarity to NF-kappa-B

To identify the potential binding sites of such key transcription factors, the promoters of these five genes were searched for conserved compact sequence motifs (Table 31; SEQ ID NOs: 757-764; SEQ ID NO:765 is a consensus sequence). Using the program "AlignACE", a strikingly conserved motif was found that is present in all five promoters. This motif resembles the described consensus binding site of WRKY transcription factors, W box. However, the W box core motif, TGAC, is followed by an "A". The permutation TGACA has never been associated with WRKY binding. In addition to this, four more positions are highly conserved. This motif may be the specific binding site of an unconventional WRKY transcription factor or a factor of a novel so far unknown type. Yeast one hybrid screens can reveal the identity of this factor.

Table 31

W box-like Motif		
MAP Score: 4.4		
ACAGTGACA 0 391 1	(12345)	SEQ ID NO:757
ACAGTGACA 1 236 1	(16140)	SEQ ID NO:758

ACAGTGACA 1 317 1 (16140) SEQ ID NO:759
 ACAGTGACA 2 281 1 (15616) SEQ ID NO:760
 ACAGTAACA 3 84 1 (17498) SEQ ID NO:761
 AAAGTAACA 3 1557 0 (17498) SEQ ID NO:762
 5 AAAGTGACA 4 1840 0 (20429) SEQ ID NO:763
 AAAGTGACA 4 2131 0 (20429) SEQ ID NO:764

 ACAGTGACA SEQ ID NO:765
 A
 10 Expt. Frequency: 0.02/1kb
 Obs. in SOMc7: 0.06/1kb
 Obs. in this cluster: 0.50/1kb

15 One K-means cluster of the 271 RPP4 controlled probe sets represents
RPP4-controlled SA/CHX super-induced genes (Table 32; SEQ ID NOs: 214,
 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551).
RPP4-controlled upregulation of these genes is SA-dependent; these genes are
 weakly inducible upon both SA and CHX treatment alone. The response to
 20 combined treatment with SA and CHX is stronger than the response to either
 single treatment. Induction of genes in response to CHX alone has been
 described before and has been attributed to hypothetical proteins that are rapidly
 turned over and either repress transcription of the respective gene or control
 degradation of the respective mRNA. Block of synthesis of such hypothetical
 25 proteins may lead to increased mRNA levels by either increased transcription or
 reduced mRNA degradation. Like the set of immediate early SA responsive
 genes shown before, genes of this set also appear not to require *de novo* protein
 biosynthesis for their response to SA. In contrast to the previous gene set,
 however, the observed CHX-induced up-regulation may point to a de-repression
 30 mechanism.

Table 32

	12505_s_at	gb AAC63643.1 (AC005309) putative CONSTANS-like B-box zinc finger protein
35	13656_at	gb AAD22649.1 AC007138_13 (AC007138) predicted protein of unknown function
	14116_at	gb AAC26243.1 (AF077407) contains similarity to sugar transporters
	14170_at	gb AAF29406.1 AC022354_5 (AC022354) unknown protein
40	14223_at	emb CAA19683.1 (AL024486) putative protein

14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450
14608_at	gb AAD31074.1 AC007357_23 (AC007357) Similar to gb AF038007 FIC1, member of the PF 00122 E1-E2 ATPase family.
14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase
15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase
16054_s_at	emb CAA74639.1 (Y14251) glutathione S-transferase
16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4
16968_at	emb CAA17559.1 (AL021961) glucosyltransferase -like protein
18235_at	gb AAB61480.1 (AC000348) T7N9.4
18567_at	gb AAC34217.1 (AC004411) putative alcohol dehydrogenase
18591_at	emb CAA52772.1 (X74756) ATAF2
19845_g_at	emb CAB37510.1 (AL035540) monooxygenase 2 (MO2)
20017_at	gb AAC16079.1 (AC004521) unknown protein

To further subcategorize these genes based on *RPP4* triggered expression timing, the set of 17 SA/CHX super induced genes was K-means clustered over the *RPP4* (Emoy2) data set (Table 33; SEQ ID NOs: 214, 621, 71, 439, 78, 80, 264, 265, 613, 583, 594, 616, 355, 503, 168, 447, and 551). A group of five genes was identified that consistently respond quickly ("fast", within 12 hpi) and that have elevated expression ground states in the *npr1* mutant. The fast response is SA dependent (is abolished or attenuated in *pad4* and *NahG*). The elevated expression ground states in *npr1* together with the observed CHX inducibility may point to an *NPRI*-dependent repression mechanism. Since *NPRI* has been shown previously to act closely at the level of transcriptional regulation, a *NPRI* dependent repressor may shut expression of these genes down. Upon CHX treatment this hypothetical repressor is not synthesized anymore and expression of these genes is elevated. This repressor may also participate in *RPP4* triggered activation of these genes and allow Emoy2-induced de-repression.

Table 33

18591_at	emb CAA52772.1 (X74756) ATAF2
14248_at	gb AAD31062.1 AC007357_11 (AC007357) Strong similarity to gb X97864 cytochrome P450
14614_at	gb AAC16958.1 (AC004165) putative glucosyltransferase
15646_s_at	gb AAC37474.1 (L42212) serine acetyltransferase
16105_s_at	gb AAC31756.1 (U68017) heat shock transcription factor 4

To identify binding sites of activating or repressing factors responsible for the co-regulation of this small cluster, the promoters of these genes were searched for conserved compact motifs with "AlignACE" (Table 34; SEQ ID NOs: 766-772, SEQ ID NO:773 is a consensus sequence). One strictly conserved octameric motif was found, which, however, is absent in one of the promoters. Yeast one hybrid screens can identify factors binding to this motif.

Table 34

Motif 15		
10	MAP Score: 1.23758	
	AATCGAAT 0 40 0	(18591) SEQ ID NO:766
	AATCGAAT 0 1741 1	(18591) SEQ ID NO:767
	AATCGAAT 1 386 1	(PAD3, 14248) SEQ ID NO:768
	AATCGAAT 2 334 1	(14614) SEQ ID NO:769
15	AATCGAAT 2 660 1	(14614) SEQ ID NO:770
	AATCGAAT 2 2105 1	(14614) SEQ ID NO:771
	AATCGAAT 3 1570 1	(15646) SEQ ID NO:772

	AATCGAAT	SEQ ID NO:773
20	expt.: 0.08/kb	
	obs.: 0.70/kb	
	SOMc7: 0.06/kb	
	Random20: 0.00/kb	
25	SOMc3: 0.10/kb	
	SOMc1: 0.10/kb	

As described hereinbelow, sets of genes specifically controlled by the *RPP7* and *RPP8* pathways were defined. Similarly a set of *RPP4* pathway controlled genes was defined (see Figure 4). Figure 4 shows a "Venn diagram" including only the transcription factor genes of these *RPP4*, *RPP7* and *RPP8* controlled genes. Three transcription factor genes were found to be specifically upregulated by each of the three *Peronospora* defense pathways: AtERF1, HSF4, ATAF2. Furthermore, ERF transcription factors appear to play an important role in controlling defense responses directed against *Peronospora* in general. Table 35 gives four potential target genes of ERF transcription factors. These genes contain ERF binding motifs in their promoters.

Table 35

40 Genes with potential ERF binding sites (GCCGCC or GCCGAC):

thioredoxin (13189) RPP7/RPP8 and (weakly) RPP4 controlled
 C2H2 zinc finger (15665) RPP7/RPP4 and (weakly) RPP8 controlled
 SigA binding protein (14148) RPP7/RPP4 controlled
 HSP70 (13284) RPP7/RPP8 controlled

5

These genes are specifically controlled by at least two different *Peronospora* defense pathways and show an almost linear increase of transcript levels during incompatible Hiks1 interactions (K-means clusters 3+5).

6 potential ERF binding sites in K-means cluster 3+5: 0.5 motifs /

10 1kbExpected: 0.1 motif / 1kb; Enrichment in K-means cluster 3+5: 5-fold

SEQ ID NO:789

MPTSATAVAPSTGQKQDQDWRILSPEQFRVLREKGTENRGKGEYT
 KLFDDGIYSCAGCATPLYKSTTKFDSGCGWPSFFDAIPGAIKQTD MFSGN
 15 AADGSIVTSGLDYILISINEKLKAYT

SEQ ID NO:790

1 tgcattcttt tgaggggttt aattttctgc atagctttgt ctaatctctt agagctcaat
 61 aagagaagat ggatgttcca cggccagctt tcaaatgttt tgatgacgat ggccggctta
 20 121 aacgttcagg gacggtttgg accgcgagtg cgcatacat aaccgccgtg attggatctg
 181 gtgttctatc gcttgcgtgg gctataggtc aactcgggtg gatcgcaggt cctacagtga
 241 tgttgttgtt ctcttttgc acttactact ctccacgct tcttagcgac tgctacagaa
 301 ccggagatcc tgtctctggg aagagaaact atacttcat ggacgctgtc ccatcaatcc
 361 taggtggctt taggtcaag atttggggc tgattcagta ttgaatctg ttggtatca
 25 421 cggtcgggta cacaatcgca gcatctataa gtatgatggc gatcaagagg tccaactgtt
 481 tccacgagag cggagggaaa aaccgcgtgc acatgtcgag caatccatac atgatcatg
 541 ttggtgtgac cgagatcttg ctctctcaga tcaagattt tgaccagatt tgggtgctct
 601 ccattgtcgc tgctatcatg tcttccatc actctgcaat cggtttagct ctcggaatca
 661 ttcaagtcgc ggcaaatgga gttgtcaagg gaagtctcac cggaattagc atcggcgcag
 30 721 tgactcagac ccaaaaaata tggagaacct tcaagcact tggagacatt gcctttgctt
 781 attcatactc tgttgttctt attgaaattc aggacactgt aagatctcca ccagcagaat
 841 caaaaacgat gaagatcgcc acaagaatca gcatcgctgt tacaacgaca ttttcatg
 901 tatgtggttg tatgggctat gcggccttcg gagataaagc accgggaaac ctcttaaccg
 961 gttttgttt ctacaatccg ttttgctcc ttgacgtggc taacgctgcc atagttatcc
 35 1021 acctttagg agcttatcaa gtctttgctc agcccatctt cgcctttatt gagaacaac
 1081 tggccgctag gtttccgac agtgacttgg tgaccaagga atacgaaatc cgaatccctg
 1141 gttttaggtc accgtacaaa gtcaacgtt tcagagcagt ttaccgaagc gggtttggg
 1201 ttttgaccac tgtgatatcc atgcttatgc cgtttttcaa cgacgtcgta gggattttag
 1261 gtgcgttagg gttttggcct ttgacgggtt acttccggg ggagatgtat ataagacaga
 40 1321 ggaaggttga gagatggagt atgaagtggg ttgtctgca gatgttgagc tgtgttgg
 1381 tgatgatcac gttgtgcgcc ggagttggct ccatcgccgg agtaagtcta gaccttaagg
 1441 tttaacagcc gttcaagact acttactaaa caaacatga tgatagatga agaagaagaa
 1501 ggtggtggag aaaaaaaca aaagatataa attttaatga tgatttcat tggggaaatg
 1561 tgaataatgt aaaagtctt cgttcgtat aattttatc ttgcgtaatt tatatacat
 45

SEQ ID NO:791

MVKNLKVDP LAKVTASTTSMVILSSLFITDDSYVLVSAKENKNQSEAE
 PSYYETLETYQGLPCPYGGYYGYYPGLDGSVGEAKDNGYYGYGTEVQ
 YPVMQGENGSVIYLMPGFQSYDASQTYMPINPVGVSQALHSPMYAAQ
 GYYQNQFGYADVSSPTYLWDPVGDYVYGVASYTPPLKQNISSSSHNH
 5 NNYYSKSKNSFTGHGMGDRPKTPRKASQNSYAPPLLNQEKGRIAYPM
 DPVKKKSGALNRDETEKAKARTKENGTSMDLANGQDHITNGECESCS
 LDAEGNERSNGVGSVIRRDQYNLPSFQTKYEEAIFVKSYSEDDIHKS
 YNVWSSTLNGNKKLDSAYQESQKKAADKSGKCPVFLFFSVNASGQFCG
 VAEMIGRVDYEKSMFEWQQDKWTGYFPVKWHIHKDVPNPQLRHIEN
 10 NENKPVNTSRDTQEVRLPQGNEVLNIFKNYAAKTSILDDDFDYENREKV
 MVQKKLRFPPVLKKKEEDLVADFKTMEMSNTVEEGNTELTGTVS

SEQ ID NO:792

1 cgatcacgga tctggcttgg ttcatacaaa accgccgttg ccgcggcacg ggcctacgat.
 15 61 accgctgtgt ttacttacg tggctctcg gcgagactca attccctga agaggtcttt
 121 aaggatggaa acggcgggta aggccttagga ggagatatgt ctccgacgtt gatacgggaa
 181 aaggcggctg aggtgggagc tagagtcgac gcagagttgc ggtagagaa taggatgggt
 241 gagaacttag acatgaataa gttgccggag gcatatggat tgtaattat agtttggtag
 301 ttataggtt ggagattgcc cggagacaga gtaaacaga ggttctctga ctcatatgag
 20 361 gcataatata gtaatatag taattttgt ttgagcata gtaattatgt cataacc

SEQ ID NO:793

1 gggcaatgat taticgttcg ccggaaccag aagcaaaat ttggttagat agggatccca
 61 taaaaacttc tttagaggaa tgggctaaac ccggtcattt ctcaagaaca atagctaagg
 25 121 gacctgatac taccacttgg atctggaacc tacatgctga tgctcacgat ttgatagtc
 181 ataccagtga tttagaggaa atctctcgaa aagtatttag tggccatttc ggccaactct
 241 ctatcatctt tcttggctg agtggcatgt attccatgg tgctcgttt tccaattatg
 301 aagcatggct gattgacct actcacattg gacctagtgc tcaggtgggt tggccaatag
 361 tgggccaaga aatcctgaat ggagtagtgg gcggaggcct ccgaggaata caaataacct
 30 421 caggctttt tcagatttgg cgagcatccg gaataactag tgaattaca ctttattgta
 481 ccgaattgg cgcattggc ttcgcagcct taatgcttt tgctgggttg ttccattatc
 541 acaaagcagc tcaaaattg gcttgggtcc aagatgtaga atctatgtg aatcaccatt
 601 tagcagggt actaggactt gggcccttt ctgggcagg acatcaagta catgtatctt
 661 atccgattaa ccaatttcta aacgctggag tagatcctaa agaaataccg ctctcatg
 35 721 aatttatctt gaatcgggat ctttggctc aactttatcc aagtttgc gaaggagcaa
 781 ctccctttt tacctaaat tggcaaaat actcggaatt tctacttt cgtggcggat
 841 tagatccagt gactgggggt ctatggttaa ccgatatagc acatcatcat ttacgtatg
 901 caattcttt tctaactcg ggtcatatgt ataggaccaa ctgggggtatt ggtcatgta
 961 taaaagatat tttagaggct cataaaggc cattacagg ccaaggccat aaaggccat
 40 1021 atgaaattct aacaacatca ttgcc

SEQ ID NO:794

MEGSSSSSSSLISKSDAELEEMLDRLTRLALCDDSKLESLSVSNLLPLTISS
 LSSQSPVVRNKAMCVDFIFQVLEILSHVNKRVKHQHEIGLPLLALWKLY
 45 TDPAAPMVRNFAIVYVEMAFERAPAKVIGECHASKISDDVSAKYRSLIT
 SQDKDLFLDFCLHMLLYQPSSQGGGSSPGLSVFQVNRIGKQALKGDTLT
 RRKLPSNTFLTKNYHFLKINQFLKQLGILNVIGNMDLPGESVYPLYAAS
 VDRVGMDDL VKIHSSQEPVAKRGEELLKKIASGTNLDDPKLINRFLFLN
 GTTGTENVAPENVA PGNISLKMKLMSGFCRSIAAANSFPATLQCIFGC
 50 MYDILFLLNLTFREKTEMAVRLFDALKLETQSLRSTIQEAIVSLAAAYKD

SPENILRDLEVL LANS LAEQNEARFCALRWATSLYN SHHCPSLYICMLS
 AADPKLDIREIALEGLFLKEEGRSIVSNHDHKYPKFIEMLEYILKQQPKLL
 DSSEMRSQKLLFPSQVYLVMIKFLVKCFELEMEESENTQAVGTEFLDSAQ
 KMCSLLEHSLAFEGSAELHACASKALVSVGSYLPENVELYFSRKIVWLR
 5 SLLSHTDLSTRESVSRLLGMASCALSDAESCSLLSELISSISQPKLRFEAQ
 HGGLCAVG FVSAHCLHRIPTVSKAVTQNAV KYLVEVVNLETAPLASVA
 MEALGHIGICGALPFLVNDSSPGTQVLEILQERLSKLLSGDDIKSVQKIAL
 SLGHICSNETSSSHLKIALDLLFSLRSKAEELFAAGEALSFLWGGVPVT
 ADMILKTNYSLSLTD SNFLMKEVKSLSDVKTDTEEDSRTTITRETITGKLF
 10 DTLLYSSRKEERCAGTVWMLSLTMYCGQQPSIQLMLPKIQEAFSHLLGD
 QNELTQELASQGMSIYELGDASMKKSLVDALVNTLTGTSKRKRAIKLV
 EESEVFQEGTIGESPSGGKISTYKELCNLANEMGQPDLYKFMDLANHQA
 SLNSKRGA AFGFSKIAKQAGDALRPHLRLLIPRLIRYQYDPDKNVQDAM
 AHIWKALIQDPKKA VDEHLNHIFDDLLVQCGSRLWRSREASCLALADIQ
 15 GRKFDQVKEHLKKLWIAAFRAMDDIKETVRNAGDKLCRAVTSLTIRICD
 VTLTELADAKQAMDIVLPFLSEGIMSKVNSVRKASIGVVMKLAKFYK
 HEINQFELLASFGELNVLLGNIYDPLSDFLVFVTVCR LHAANIGIETEKLE
 NLRISISKGSPMWETLDLCINIVDIESLEQLPRLTQLVRGGVGLNTRVG
 ASFISLLVQKVGSEIKPFTGM LRLLPVAKEEKSSAAKRAFSSACGIVLK
 20 YSSPSQAQSLIEETAALHSGDRSSQIACASLFKSFSSTAADIMSSHQSAIVP
 AIFISRFEDKQISSLFEEVWEDITSGERVTLQLFLQEIVNHICESITSSSRFK
 LSFSLGKDALLDALGALSVACHEAITKEDPTTPTTILSLICSACKKKLKKY
 RESAFSCLEKVI AFGDPKFFH AVFPM LYEMCNTASIKTNTQVQAASDAV
 KTESENGEDGHVPLEKIMECVKSCIQVATIDDILSAKADLIHVLIISLSPGF
 25 LWTVKMSGISCVGKLCSRFP SLWTD SMDDLSPSDATK FVHEL FHS LVPK
 LLECIHTVKIAQFHVAASQCLLELIELYSTISSLHPVEVDFKAEVVS LLELE
 KSEEAKSLLRKSRDALANLPSLN

SEQ ID NO:795

30 MDKETEILSR LAANHLHLAQFEPLKATLLALRV RNPDLALTILQTIVSNA
 GRFDNVLWSRSCPSPLLSFLSTIELLR FENPTSPWGF DSETLSLRADFL
 MVQVLIDRVTERIKEDEESEDENSG LGNCLRVLQGVLELGVERLK FVVD
 TSSSEGSNKIEEDAVVSLRSIVLDYSDVFDALCCNIQRQLAGCESYGTCL
 VEEVQGEEQRKEMNEATCIGSPELDNINVFALIQRNVQLAQLDAMKTKL
 35 DEGDERGAADRIRYLHLDYGV EKENYH AVLKALLSRVMEKKDEYGDS
 WHMVRQNLLFMYKEALSSNCGDLVQMIQGIQDDMLLPHSQLHLSLDNE
 QIPLPLECFRRYLVDLKTERNIEDKSSPMSRAINSCLRDMYHYARISGSHV
 LECVMCAALSSVKKEKLQEANDVLTLPRLRPLVASMGWDLPLPGKTAT
 RRKLMRLLWTSDSQALRLEESSLYGNQTDELELASFAACVNSGKSWTP
 40 KASFLMHGNVSSAHDDAEVDPFVENLVLERLSAQSPLRVLF DVVPGIKF
 QDAISLISMQPIASTAEAWKRIEDIELMHMRYALEAIVLALGAMEEAMK
 DETDASHRVVFYHLKDLTNHLEAIKNVPRKIMMVNIVISLLHIDDIRLSST
 QSASSACFSEKSNTPGLDPGDLGTEGEKEIVISFTKQLLDVLRRLPSHPIE
 QECQLDGNYSTDGRQALEWRVSM AKRFIEDCEWRLSVMQHLLPLSERQ
 45 WGLKEVLSILRAAPEKLLNLCMQRAKYDIGEEAVNRFALSAEDKATLEL
 AEWVDNAFKGTLVEDVMSRTAEGAAAVQDLDFHSLGSQLSPLAMVLLF
 AQSQVMLSEIYPGGAPKVGFTYWDQVHEVAIISVLRRILKRLQEFLEQDD
 PQILQASFSGDTIISSTESH RQGQKDRALAMLHQMIEDAHRGKRQFLSG
 KLHNLARALADEKPEVDVLKGDGSDMAVEKDGV LGLGLKYTKQSPGS
 50 ANRAVDGNPVSHETEDKGKKSFGPLSNKTSTYLSQFILYTA AIGDIVDGT

DTTHDFNFFSLVYEWPKDLLTRLVFD RSSTDA AAKVAEVM SADFVHEVI
 SACVPPVYPPRSGHGWACIPVIP TTPCSHSEGKVLSPSIEAKPNCYVRSSA
 TPGVPLYPLQLDVIRHLVKISPVR AVLACVFGGSILYNGSDSISSSLNDEF
 PSSPADARLFYEFSLDQSERYP TNLNRWIQMOTNLHRVSEFVVTPKQKPD
 5 DTRIKPDER TGIKRLLEHDS SESDTEETFSKNNIQPALTDGSARDGGSFE
 NGVCRTDPTVFLSFDWENEVPYEKAVNRLIDEGKLMDALALSDRFLRN
 GASDWLLQLLKSREENPSTSGRSQGYGGQSNWQYCLRLKDKQLAAT
 LALKCCIGDKLCRSTATYFRQMI AIIAGKRLSFFLLFEIMFGSWYARCVTL
 KNLNGKQVEAECKEDPEGLALRLAGKGA VSAALEVAESAGLSIDLRLREL
 10 QGRQLVKLLTTDPLNGGGPAEASRFLSSLQDSADALPVMGAMQLLPD
 LRSKQLLILKEFPALRDNNVIMAYAAKAISVTI PPPPREPRITVSASRLRQK
 SRAGPAVKASFTSSLSNFQREARRAFSWAPRNAENRTTSKDVYRK RKNS
 GLGASERAAWEAMTGIQEDQGSSYSADGQDRLP SVSIAEEWMLTGDKT
 KDEGVRASHKYESTPDILFKALLSLCSD ELVSARSAMDLCISQMKNVLS
 15 SKQLSEGASVETIGRAYHATEAFVQGLSYAKSLLRKLLGTTESTNNNGE
 RSRDVDDISSDAGSSSVGSQSTDEPSDVLSLTEIWLGRAELLQSLGSGIS
 TSLDDIADQLSSECLRDRLISDERYSMAVYMCKKCKIDVFPVWKA WGL
 ALLRMERYAQARVKFKQAFQLKGEDIPDVIQE IINTIEGGPPVDVSIVRS
 MYDHLAKSAPTILDDSLSADSYLNV LHMPSTFPR SERSRRSLESEKNSSV
 20 PGSDFEDGPRSNLDTTRYSECTNYLQEHARQNLLGFMFRHGHFKDACM
 LFFPQSGLPPLQTSSVGAVSTSSSPQRTDPLATEYGTIESLCEFCVGYGAI
 SSLEEVITERLESAKNQDQAINQYIAGALTRICAFFEINRHFNYLYKFLVL
 KKDYVTSGYCCIQLFMNSTTQEDAVRHLEHAKKYWSLTILGVQAHFEE
 ALTARHRGSDSKKLVTKGVRGKSAAEKLSEETLVKLSSRVKMQIDVVK
 25 SFSDSEGAPWKHSLFGNPNDSETSRRRCEIVETLVEKNFDLAYSVIYEFK
 LSAVDIYAGVATSLADRKKGSQ LTELFKNIKGTIQDDDWDQVLNIADTG
 KARSVWLIFCEMLQVLGAAINIYANKHKERPDR LIDMLTSSHRKVLACV
 VCGRLKSAFQIASKSGSVADVQYVAHQALHANSHTV LDMCKQWLAKY
 M
 30

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- 30 All publications, patents and patent applications are incorporated herein by
reference. While in the foregoing specification this invention has been described
in relation to certain preferred embodiments thereof, and many details have been
set forth for purposes of illustration, it will be apparent to those skilled in the art
that the invention is susceptible to additional embodiments and that certain of the

details described herein may be varied considerably without departing from the basic principles of the invention.

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a plant or fungal nucleotide sequence encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 or the complement of the open reading frame, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
2. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which is substantially similar to an *Arabidopsis* nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
3. An isolated polynucleotide comprising a plant or fungal nucleotide sequence which hybridizes under high stringency conditions to the complement of a nucleic acid sequence comprising an open reading frame selected from the group consisting of SEQ ID NOs: 1-684 and 789-795, wherein the nucleotide sequence is not one of SEQ ID NOs: 1-684 and 789-795.
4. The isolated polynucleotide of claim 1, 2, or 3 which is DNA.
5. The isolated polynucleotide of claim 1, 2, or 3 which is RNA.
6. The isolated polynucleotide of claim 1 wherein the nucleotide sequence encodes a polypeptide having at least 90% amino acid sequence identity to the *Arabidopsis* polypeptide encoded by the open reading frame.
7. The isolated polynucleotide of claim 1 wherein the nucleotide sequence is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat sequence.

8. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a dicot.
9. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a monocot.
10. The isolated polynucleotide of claim 1, 2, or 3 wherein the nucleotide sequence is from a cereal plant.
11. An isolated polypeptide encoded by the polynucleotide of claim 1, 2, or 3.
12. An expression cassette comprising the polynucleotide of claim 1, 2, or 3 operably linked to suitable regulatory sequences.
13. The expression cassette of claim 12 wherein the polynucleotide is linked to a promoter for expression in a plant.
14. A recombinant vector comprising the polynucleotide of claim 1, 2, or 3.
15. A host cell comprising the expression cassette of claim 12.
16. A host cell comprising the polynucleotide of claim 1, 2, or 3.
17. The host cell of claim 15 or 16 which is selected from the group consisting of yeast, bacteria and plant.
18. A transformed plant, the genome of which is augmented with the polynucleotide of claim 1, 2, or 3 or a polynucleotide which comprises one of SEQ ID NOs: 1-684 and 789-795 which is expressed in an amount which confers resistance or tolerance to the plant to pathogen infection.

19. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene corresponding to the polynucleotide of claim 1, 2, or 3 or a gene corresponding to one of SEQ ID NOs: 1-684 and 789-795.
20. The plant of claim 19 which is altered by T-DNA insertion, transposon insertion, or targeted DNA insertion.
21. The plant of claim 19 in which expression is inhibited by transcription or post-transcriptional mechanisms.
22. The plant of claim 18 or 19 which is a monocot.
23. The plant of claim 18 or 19 which is a dicot.
24. The plant of claim 18 or 19 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
25. A method of expressing a polynucleotide in a cell, comprising: introducing the polynucleotide of claim 1, 2, or 3 into a cell so as to express the open reading frame.
26. The method of claim 25 wherein the cell is a plant cell.
27. The method of claim 25 wherein the cell is a monocot cell.
28. The method of claim 25 wherein the cell is a dicot cell.
29. A composition comprising the polynucleotide of claim 1, 2, or 3 or comprising the polypeptide of claim 11.

30. A method to identify an open reading frame in the genome of a plant cell, the expression of which is altered by oomycete infection of the cell, comprising:
- a) contacting a plurality of isolated nucleic acid samples on a solid substrate with a probe comprising plant nucleic acid corresponding to RNA isolated from plant cells infected with an oomycete, so as to form a complex, wherein each sample comprises a plurality of oligonucleotides corresponding to at least a portion of one plant gene; and
 - b) comparing complex formation in a) to complex formation between a second plurality of isolated nucleic acid samples on a solid substrate with a second probe comprising plant nucleic acid corresponding to RNA from uninfected plant cells or from mutant plant cells which have a response to pathogen infection that is different than the plant cells in a), so as to identify which samples corresponding to genes having an open reading frame, the expression of which is altered in response to oomycete infection, wherein the genes comprise orthologs of *Arabidopsis* genes comprising one of SEQ ID NOs: 1-684 and 789-795.
31. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is induced in response to infection.
32. The method of claim 30 further comprising identifying an open reading frame in the gene, the expression of which is decreased in response to infection.
33. The method of claim 30 wherein the probe comprises nucleic acid from a dicot.
34. The method of claim 30 wherein the probe comprises nucleic acid from a monocot.

35. An isolated polynucleotide comprising an open reading frame of a gene identified by the method of claim 30.
36. A method to confer resistance or tolerance to a plant to a pathogen, comprising:
 - a) contacting plant cells with an expression cassette comprising a polynucleotide encoding a polypeptide that is substantially similar to a polypeptide encoded by a nucleic acid sequence comprising an open reading frame comprising one of SEQ ID NOs: 1-684 and 789-795 so as to yield transformed plant cells; and
 - b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the polynucleotide in the cells of the plant in an amount effective to confer resistance or tolerance to the plant to the pathogen relative to a corresponding plant which does not comprise the expression cassette.
37. The method of claim 36 wherein the polynucleotide hybridizes under moderate hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
38. The method of claim 36 wherein the polynucleotide hybridizes under stringent hybridization conditions to the complement of one of SEQ ID NOs: 1-684 and 789-795.
39. A transformed plant prepared by the method of claim 36.
40. A seed of the plant of claim 39.
41. A progeny plant of the plant of claim 39.
42. A method for identifying a plant cell infected with a pathogen, comprising:

- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with at least one oligonucleotide under conditions effective to specifically amplify a nucleotide sequence substantially similar to one or more of SEQ ID NOs:1-184, 301-494 or 500-803, or a portion thereof so as to yield an amplified product; and
 - b) detecting or determining the presence or amount of the amplified product, wherein the presence or amount of the product is indicative of pathogen infection.
43. An isolated polynucleotide comprising a plant nucleotide sequence that alters transcription of an operatively linked nucleic acid segment in a plant cell after pathogen infection, which plant nucleotide sequence is from a gene encoding a polypeptide which is substantially similar to an *Arabidopsis* polypeptide encoded by a gene comprising at least one of SEQ ID NOs: 685-788.
44. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, which nucleotide sequence hybridizes under high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788 or which nucleotide sequence hybridizes under very high stringency conditions to the complement of at least one of SEQ ID NOs: 685-788.
45. An isolated polynucleotide comprising a plant nucleotide sequence that directs transcription of an operatively linked nucleic acid segment in a plant cell, wherein the plant nucleotide sequence comprises SEQ ID NO: 710, SEQ ID NO: 711, SEQ ID NO: 714, SEQ ID NO: 715, SEQ ID NO: 764 or SEQ ID NO: 773.
46. The isolated polynucleotide of claim 43, 44, 45 or 46 wherein the nucleotide sequence which directs transcription is 25 to 2000 nucleotides in length.

47. A recombinant vector comprising the polynucleotide of claim 43, 44, 45 or 46.
48. The vector of claim 47 which is a plasmid.
49. An expression cassette comprising the polynucleotide of claim 43, 44, 45 or 46 operatively linked to an open reading frame.
50. The expression cassette of claim 49 operably linked to other suitable regulatory sequences.
51. A host cell comprising the expression cassette of claim 49.
52. A transformed plant, the genome of which is augmented with the expression cassette of claim 49.
53. A plant cell containing the expression cassette of claim 49.
54. A transformed plant comprising transformed plant cells, the transformed plant cells containing the expression cassette of claim 49.
55. The transformed plant of claim 54 wherein the plant is a dicot.
56. The cell of claim 53 which is a dicot cell.
57. The transformed plant of claim 54 wherein the plant is a monocot.
58. The cell of claim 53 which is a monocot cell.
59. The transformed plant of claim 54 which is a cereal plant.
60. A method of augmenting a plant genome, comprising:
 - a) contacting plant cells with the expression cassette of claim 49 so as to yield transformed plant cells; and

- b) regenerating the transformed plant cells to provide a differentiated transformed plant, wherein the differentiated transformed plant expresses the open reading frame in the cells of the plant.
61. A transformed plant prepared by the method of claim 60.
62. A seed of the plant of claim 61.
63. A progeny plant of the plant of claim 61.
64. A method of using a plant promoter, comprising: introducing the expression cassette of claim 49 to a plant cell and detecting the expression of the product of the open reading frame.
65. A recombinant vector comprising the expression cassette of claim 49.
66. A plant cell comprising the vector of claim 65.
67. A transformed plant, the cells of which comprise the vector of claim 65.
68. The plant of claim 52, 54, 61 or 67 which is a maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat plant.
69. The expression cassette of claim 49 wherein the open reading frame is in an antisense orientation.
70. The expression cassette of claim 49 wherein the open reading frame is in a sense orientation.
71. A transformed plant, the genome of which is augmented with a polynucleotide which is substantially similar to any one of SEQ ID NOs:

1-684 and 789-795 and which is expressed in an amount which inhibits or prevents pathogen infection.

72. A transformed plant, the genome of which is genetically altered so as to inhibit the expression of a gene comprising a polynucleotide substantially similar to any one of SEQ ID NOs: 1-684 and 789-795.
73. The plant of claim 71 or 72 wherein the polynucleotide is substantially similar to SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 32, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 792, SEQ ID NO: 57, SEQ ID NO: 68, SEQ ID NO: 78, SEQ ID NO: 79, SEQ ID NO: 102, SEQ ID NO: 111, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 682, SEQ ID NO: 129, SEQ ID NO: 137, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 157, SEQ ID NO: 161, SEQ ID NO: 165, SEQ ID NO: 170, SEQ ID NO: 174, SEQ ID NO: 179, SEQ ID NO: 180, SEQ ID NO: 181, SEQ ID NO: 184, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 197, SEQ ID NO: 208 or SEQ ID NO: 211.
74. The method of claim 36 wherein the polynucleotide is substantially similar to SEQ ID NO: 308, SEQ ID NO: 300, SEQ ID NO: 272, SEQ ID NO: 362, SEQ ID NO: 265, SEQ ID NO: 241, SEQ ID NO: 261, SEQ ID NO: 380, SEQ ID NO: 228, SEQ ID NO: 658, SEQ ID NO: 243, SEQ ID NO: 254, SEQ ID NO: 216, SEQ ID NO: 225, or one of SEQ ID NOs: 400-684.
75. The expression cassette of claim 12 wherein the polynucleotide is in antisense orientation.
76. The expression cassette of claim 12 wherein the polynucleotide is in sense orientation.

77. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting a sample comprising polypeptides obtained from a plant cell suspected of being infected with a pathogen with an agent that specifically binds to a polypeptide that is substantially similar to an *Arabidopsis* polypeptide encoded by an open reading comprising sequences selected from the group consisting of SEQ ID NOs: 1-684 and 789-795 so as to form a complex; and
 - b) detecting or determining the presence or amount of the complex, wherein the presence or amount of the complex is indicative of pathogen infection.
78. A method for identifying a plant cell infected with a pathogen, comprising:
- a) contacting isolated nucleic acid obtained from a plant cell suspected of being infected with a pathogen with a probe comprising at least a portion of a polynucleotide that is substantially similar to any one of SEQ ID NOs: 1-684 and 789-795 under conditions effective to form a specific complex between the probe and the nucleic acid; and
 - b) detecting and determining the presence or amount of complex formation wherein the presence or amount of complex formation is indicative of pathogen infection.
79. A computer-readable medium having stored thereon a data structure comprising:
- a) a nucleic acid molecule that has at least 70% nucleic acid sequence identity to a nucleotide molecule selected from the group consisting of SEQ ID NOs: 1-791 or the complement thereof; and
 - b) a module receiving the nucleic acid molecule which compares the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.

80. The computer readable medium of claim 79 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
81. A computer-readable medium having stored thereon computer executable instructions for performing a method comprising:
- a) receiving a nucleic acid molecule having at least 70% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-791 or the complement thereof; and
 - b) comparing the nucleic acid sequence of the molecule to at least one other nucleic acid sequence.
82. The computer readable medium of claim 81 wherein the medium is selected from the group consisting of magnetic tape, optical disk, CD-ROM, random access memory, volatile memory, non-volatile memory and bubble memory.
83. The method of claim 42, 60, 77 or 78 wherein the cells are dicot cells.
84. The method of claim 42, 60, 77 or 78 wherein the cells are monocot cells.
85. The method of claim 42, 60, 77 or 78 wherein the cells are maize, soybean, barley, alfalfa, sunflower, canola, soybean, cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat cells.

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RPP-DEPENDENT DEFENSE PATHWAYS

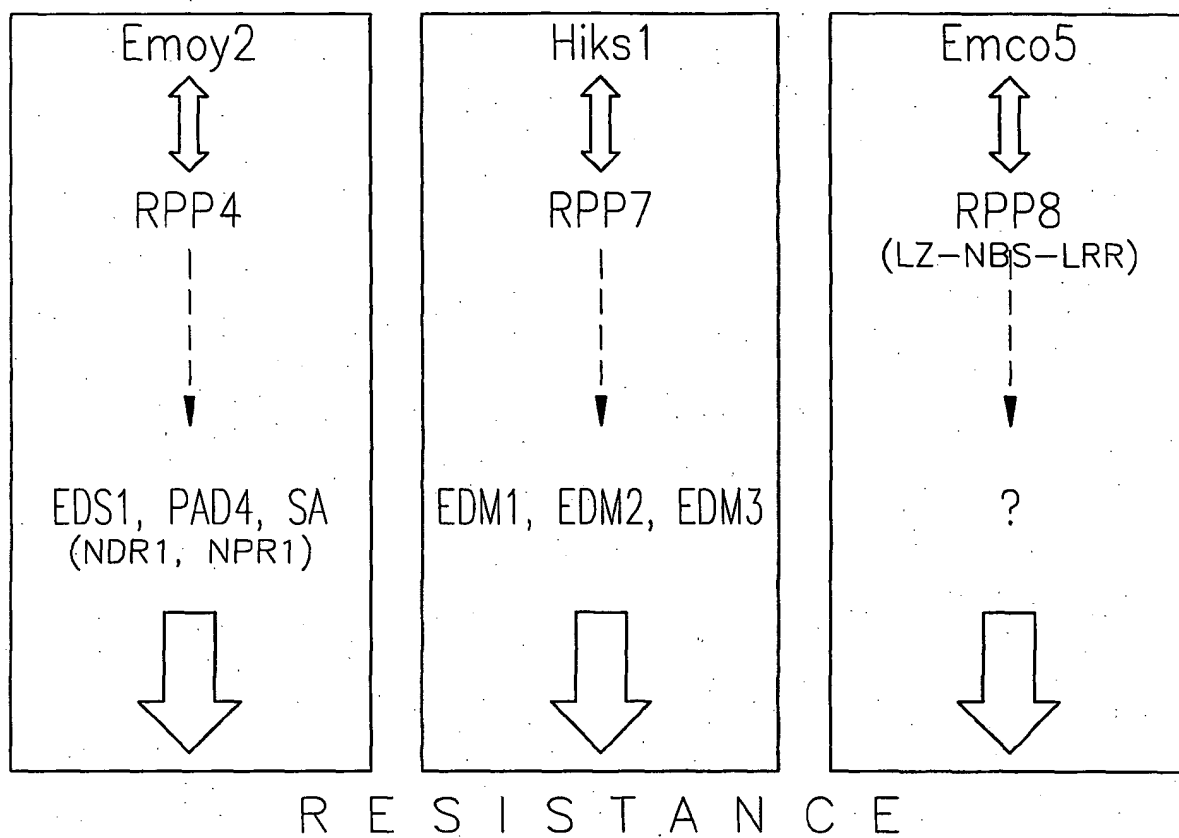


FIG. 1

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motifs:

Motif 1/ MAP Score: 6.87857

CAACAATGAC

TT TT

Motif 2 MAP Score: 2.22382

GATGGGNCNAA

TT A

C

Known stress-responsive cis-elements:

ttgacc, ttgact, ggtcaa and agtcaa W box

ttgaca and tgtcaa W box-like

tgacg and cgtca TGA-bZIP binding site

acgt bZIP binding site core

cacgtg G Box

gccgcc and ggcggc GCC box

| Subcluster A
17014 ribonuclease RNS1

SEQ ID NO:
774

tagaattgaaaaagggtaatgtgaaaagggtattctcaacaattattcaagataaaaat
tgtatagggtgttaaataaatgtgtaaaagagaagacgatgtgaagtattaaaagaaa
aaaaaatggatgttgatatataagtaaccattgtagatagtttaagcaagaaaaattga
tggtgcattggaaattaaaaaatttcaataaaattagaaaagcaactctaaatcattac
ttatttttattattttcaagaagttataaagtattaaacaattcgtTGACAaataagttt
gatcgacattgtgtgacaaattttaaacacatcattaataacaacgaggacaaatacag
ttcagatatcgtctactattaaaacacttcttctataggagcaaagaaaaattgtcggc
aacgaactggggaccaataatattccgagtttgagttcaaactgagtaattttattttg
agaaaatttgccaagtttaacttataattctgggtttACGTgtagtaattttattaagttgt
tataggaaaatgagaaaataactaagacacatccaagaaagtttcacacgaaatttactt
acaaaaagattgtttattttaataacttccgtatatagatatataaatatttaacacatta
attataaagttcaagataattgattatctatctttttttgtcatctgaaattattatcg
ctcaaacgaagtaattctgaggaaagttgtttacaaactagttatttccattattgtcta
cttatataatagaattaaaaaaaattattgcttaatgcaatttagttttagataaaaatc

FIG. 2A

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attaaacttaatagattatataagtttagatatcaataattgggcttgcttaaaaaacata
aatataaaaatattattggggccgttACGTgcatacaaaaacgaaccttctaacaacaagt
gtgaACGTTacgacttcaaaattaaaaaaaaaacacaacaactatgtccacACGTAatct
catatgattcagattccaaggagaacaaaattaaaaacaaatctcgtaaacatacatat
acttcacataaaaacaaaagggtacagtataaccataaaatctccgagattcttttgatgt
atctgtccattttcattattacacaaactaggaaactgatatctctctattcacattcct
ctgattctattttctctttatatatattcaccatttaaccatctcaatcttataaccctc
aaaatcacaatcttctcttacaaaaaactttgaaagatg

14609 putative cytochrome P450

SEQ ID NO:

775

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taaaatataTgactagctaaaatgtgaggtatattgagaagtgagttcttaaaactact
tggaactgtctacttagaatttgagacattataagtacaattgatgttaatctaaaagt
gtagaacattgttaatttcttgaacagctgttagccaacaatgacggacgatcacgatca
ttgatcgaagaggcgattttgtttcacatcgatcagtggtatctcttggcgaagtacatg
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atactattaactttcaagtcgttatagtaattggacaatattattcgttaattatcaaaag
cgctttttcattttctatctgaacctaatgcctagcgagttgaaaacatagctacctaa
taggctactactacacaatcttgaagcacaaataatacaacgaaACGTcccttgggtat
gagattatttagaagtttcataagattctagtccttattcaattgtgcccacacagcac
aaagtacggaagcgataggaaggACGTCAcagtcctgttttgataatctaagatcgta
gaaagcGTTGGGtgcttttaagtttttctttcgctaaatattttaaggtcttttTgc
aggaatagaaatatgataaagtctattgagtttgtaagacctatgtatattgggtccgg
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acaaTGTCAAatataatttaacaaattatttaaaaccttttaaatatgtgcatagttttt
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gctttgtaataaattatatataattcaaaatcctcatcgtcgaaaacaattttaaaat
aaaacaaccaagatatatttccacaaattaaattaatttttagttttgaattcagatata
taacaaacaatgatataataagaatatttcattaaataaaaagatatcttaactgaat
ttatttattaatttggtatatacttattaccgaaataaaggattgtttatttcttacaac
tcgtcttattagtggtgcatagcataacaagggtgaaagagaaaacatg

16649 putative S-adenosyl-L-methionine:trans-caffeoyl-
Coenzyme A 3-O-methyltransferase (function:disease resistance) (promoter up to next ORF) SEQ ID NO: 776

catgtctcttgagtctcgtggttggtgcaaatgttcgttggtataaacgagagatgt
atgtcaatatatatattggcttctggtcaaactaattgagctactaataagacccaaat
taaggactaacacaccaattgatcttatccatgacttttcaaccatgggactagaaaat
caattatctagacagtacttgatgcgaatatattaacgtttatgtttcttaaggatttt

FIG. 2B

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ttttctctcttaagggttgcatatacaaatgttgaaatatgcaagcaggcgaacagtttgca
atgtagtttttattgactaatataaatttggtatgtgagatttaaaatgcaaaaaaagta
tatagtatagaattattttaagaatatatcaaattgaagggtactaaaaaacggatttg
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gtgttccagagatatgataagttgaccttttggattgtctaactctggaatcttttagtt
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attaaaaattgtaaaatatttttttattgtcgtaaaatgttttacttttctatttccat
taaagttgtaaatatgttttattaacgtcgtaaaatgttatttttttaataaaaaatat
ctgttgggccaaga

17653 (similarity to DNA damage inducible)
(promoter up to next ORF)

SEQ ID NO:
777

acaataatttccataattcaaagtctttcagaaaggatttctcaatacagggttaaaaat
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aaacaaatctcaaattttgtggctataaccaccattttcattgaaactaactactcaatt
aacggtctgaaagaggacaaaaagattttcacaaagtgtacaccaataaaagaaaatcgt
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cgaaatttacctgacgatttttttcttactgaaaattaccaagaaatcgcggtggaag
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gaatgagtacgttacttgcggttatggttgggttttctttttaatttttagaaactttc
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FIG. 2C

SEQ ID NO:
778

SUBSTITUTE SHEET (RULE 26)

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12778 Lipase/Acylhydrolase with GDSL-motif family SEQ ID NO:
(promoter up to next ORF) 780

catcatttagagagagggagaaacagaactgtgaaaagagaagaagattgcttttgtgc
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aataatagttcattttactatacaaaataataacgtgtagcgcgagggttcattttactat
acacctatttaacgcactagcaaacgattatcgatcaattatattatagttcgttta
atcacgtctgacgcattactggtttctcttctactttatttttaattctcaacaaaata
tctattgttactacgagtagcaagaagatcgtgcttttttttttttgggttcaacaaca
acttacaattacacaagagtctgaatacacataagctttaacccaatccggcaatatag
aatacaatttgggatcataattcagaaaagaaagagattccctagcaattctatctgcc
acacaattcccttctcatcgggtaaaagtcaactttaacctcttcgaagtgtgaaaaga
tcgtgcatttagaggcaagaagtagaattaaacatacaaatctcacggaaatatagggt
gtaaatggtaacactaaaccagattcagtaatttctgcagtaaccatttgcataaaact
aaattttgctgactagccaaattcaacaaaaaaatttcaacaccaacatatacgtagat
atgtttatttctgctaaaacttttggataatttacgagtacacaactcgaattaaaata
tttttaatatcaaaatacatatcaaatagatatttttaataagtcagattatactgat
acgatatatgaataatatagatacataaaatatcactaccagaatagacaagagacgaa
tatgttcggataaattatagataaatttggataaataattttaataacgtttagataactta
aatcaattattaaaattttgcaaaaaacaactcacacctatgctaagatatcttttaaaa
gataaattatagtaatttccctaatcatcctcatcatattattgattaaattacttgaa
aacaattaaaaaaaacaattaacaatctatattttatcatcatgttaatttttgaaatt
attttcttaatagtgttttgacaaagattttcggttaattatttacatatttttaatagt
tcaaatttaataaagaagaataaactcaattttgcgttgacacaatcttaatagtatatg

|| Subcluster B

20245 glutathione-conjugate transporter
AtMRP4

SEQ ID NO:
781

atttttctaataagacttttcttattctcatagactcttcttattcatctttcttaatc
aattcgaccaactcagtggaagacaaatctcacacgaccctttccactttttggtaact
ttattattaatttattagtagtggtgtagttcctttctttcttctgctgatctTGTCAC
aaaataactaaatttttccctaagcggctgtttatatattattaacaaagggttccgcgtg
tctcttggttaactagtagactaaaaacaaatcgtaaactcgattttctcaaccaaatt
tagaagatactacggcatgtaattagctaatagataaaaagattcgaattttcgttccaat
ggatttgccttttcttttgcacaaaaccaagaatttgccttctcttggcagtatttagc
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aaacttagtgtaaaagaaaataaaaatagcagacagtttacgggtaagactagatgacca
tatatgattgagtgcataaaacatcttttttcttcttttttgaaaaagcgaaactaa
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taaaatactgatttaataatcaattttctaattgggtTGACCCAACagacttttttttttt
ctatcctctaataatatataatcatatagtagtaattatttagtagataatatgattaa
cACGTgaatagcaaagtttctatcatttttattcaaaaaagattcataagtaataaaa
tgatAGTCAActtttctttttctttttgtgtttggccttttgtTGACGCGTCAAttgttg

FIG. 2E

SUBSTITUTE SHEET (RULE 26)

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tacaccaccaggtcacactattgtgggatgtgataatcggtaccttttaaatgtcaggagc
ttctttcttacattttccacttcaaacaaccgataattcagaggaattttctcttcct
ctctctctctcttttttatattttttcactgggaaaaatg

17051 CTF2B involved in hydroxylation
and oxidation of an aromatic ring

SEQ ID NO:
782

catagccgcgttccaagaggaGGTCAAgaggattcacttttctataatcaatattaaat
tgtagtcaaaaaattcaagaaacttatatagacctattttttttgaacatcaatag
ttgtcgttgaaaagtatcttggggatatttagatttagcatatgAGTCAATGTTGgggtc
cttaagagttgaggctacaaatttataactcagaaaaagtgtatatgccctttaatttt
tggcctattgggtcttttatggCGTCAactccaatttcagtttgaaaagaaaTGTCAAta
actaacaatgttgtcttTGACTttgaaatcttagaagtttcgacttaccattttctac
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tatgtgtatatgaagtcatttgaaatgaaatctcataaagtttcataagtaaattatta
gaataaaaacccaaggtaattgtatagattttgaaatccacacaataatatcgaattgt
aaaatctagagaattcaatttcaattcatgaaggagtggttaataatcatggatttttaa
agttagttgattgaatataaaagtaggaaagatgtgggattcatgtgggtgggttggccc
atctccatgatctctagtgaatttcagctTGACGcaactttcggttaagatcttacttca
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ttaagagtcctcgagtaagactctatcactatttaaataaattaatgtaattgagttatg
ataattcaaattggatctccttcattccatagttgcatTTGACAtttttatataaaactt
gctgattatctaagtcacaatttgagtccttggttaataattcagtttcaatcatcaggag
atgtctaataagattaaaaattaaagatagaaatgtctaattggattgaaatatataaag
gactcagccaaaaacatgttaactgaaaatcttgtataaaatggagattctctgataac

19640 putative glutathione S-transferase

SEQ ID NO:
783

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cttatgggtgttgatgggtcttgtgataaaacgacgacgaactttgccgttttatatgggc
ggcagtgatgtaaatgccaagagtcctagaaggaaacagatgTTGACTttacaacata
tttataACGTtccctttataattttttttttatctcttttttagtaagtggagatgtgtc
ctaattcctaaccttgcccttatccctggagcatgtgtaccTTGACTtgatccattcatt
ttctgaagacaaccccatgcttCGTCAagaatttcttctgcttccccaattatacccat
cactttatcgtgggttcttcataattgatccattttgtctgtgtatgaaacatcaacagc
tttaaaaccattttgtcattctcggttggttatattgacgcccaagaaaacaacaactct
atagtcctgagctataaaaaaagaattagtactaatctgttatttgatgttccttttggc
atatattaaaaatggttggtgttataataggcggtgggttttccgtttctccatctacga
acttggttgctgaattttccttccaacaatgtttataaagtatcggtgaattttctatgg
ttacaagactcaccacctcacgataactaaaaatataactaaagaaatttggttatattgtg
ccgcaacaaatagacccacatgtccgttgtaactttcctctgtttacacaacttcttACG
TgtcgaaatacatgttcacatttaatcatagttgtgggtttattaagaaggatgggtTTG

FIG. 2F

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ACTaaattatagcttttatctacttttctttcatatgaaaactccagggtttatgaacca
atttcttatgatttgaagaaattgaatactactacattttaaagtgtttataaatta
aTTGACAttagaatttagtaaaaacactaattgttcatacaaatgtttcatttattgtt
catacaaaactattataacaagattacacaaacatatagttaacatctactgatcgaaga
gtatcattggttgtctcttaggctgatttgattctttctacaactttcttcatatg

14248 PAD3_at member of the PF|00067
Cytochrome P450 family

SEQ ID NO:
784

gttctggtcgaaggatttgtcccgaatgccaatggcgattgctagtgtggaactagca
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tgctgttcaACGTtattgatgagcaataatataagctcgataacatggaaagtgtatg
aagcaaaaaacataagattcttttagattttgttgtgttatataagaaagaaatgttcca
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cacggattaagatctttttcattcaacaaaattctaaattttgttttttaagtaaaaa
atggttatagcataaatgttcagatttttatgtcgtattatattgaattaaatataggac
aaagaaaaataagatacagaacaaagagaaattttgatccaaaaaaaaaagaaagaga
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tttataattgaatttgatggaatttataatgtattttttgtcatggaaataataaagtt
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tggaagatgctggaatgatctctttttacaagaaagctcctctcattcttggtccggtt
aaacaccattaattgacatcggcacacaaaaattcaaacaccggtgaagattgtttgcta
tactttatttttatcaataataagttgcggtacttggttaactgtatACGTacttctat
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agagaaccattgggcccataaaacttattttattcccgcgaaagcctgagtggaatcgaac
cactaccacaaaaagtaagagtttgggttatttgatttttaattcattcactttgaattat
tatagacaccggacagtgacttatgataaagagatttttaacctttaaaactaaaacac
taaaatacataatccaaagaagacggaacaaaaaacaaaaacagagccaggaataatg

17500 athcallga_s_at calmodulin-like protein
(promoter up to next ORF)

SEQ ID NO:
785

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agcaccttcttcgaaattcccttgaggacaaaacatggacctctttttgttcacttg
gattttctcggaatatgacttgcatgtcttcttactatattttatgtatcccttcattc
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tttagacatgacaagtattttatcaaagtctccttcaattcaaactactgaatattgtt
tggaataagtactttttgggagacgtaagctatattttccaatccgaaatgaatgaacaa
atgtccatagttctgttttttttccctcctaaagtgaatatattaagagacactaaatt
ctagaaaatatgtttaaaataataatcagtaattgtccaaaaaatgtgaataactta

FIG. 2G

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aatcaaaatcaggatacgttgtcacaagaaacaaactttcctagataatgtatatttt
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gtttttcaaacaaaaaaaatattaatattatattataatttgattattttttattaaaaa
agtattttttgttaaaaaattaaaccaatagtaagatgagaatttgtcatgatgggttgta
caaagtatctcagagtatctcagagtttctcacttgagaaactttctacactctctctc
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tagagatgggtcttataaatttatcaacatgggtgaatctctcatgttatatatagagggtg
atttaaaggctaaatagaataacacactacagcatataaactcaatgatatg

18928 putative endochitinase (promoter up to SEQ ID NO:
next repeat region) 786

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aatgacacagttttttctcttgctgttatgagaaattccatgtcgggtcatagatcagat
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tcataaaaacttgattgagataatcaagtttagattagttcaaacggttgagatttttc
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cctgggtctagagactctagaaccatcggagctcaagtgaaaaacgacgcggttaagctg
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tcctccgttgtgtttcaggacgacgcaaaggggaaaaaaaattgaattctttctctcca
agcgaaactagggtttcgaaagtctctgtctcatcaaagcttcgaaaaggtagattttat
ggtttcttactctcctttctctatgatattccaatttcttgcgagcttgctcagtggtc
ttaccttatatttaccgaaccagtgcctttatattctatcacattcgaagttattgggtt
tctggttacttatattgcttattgttctatgactacgatataattatcccaaagatttg
ttcttttctccgaatttggattagaaatggatataactcaaattctgaacatgccagaa
gaatcct

14614 putative glucosyltransferase (promoter SEQ ID NO:
up to next repeat region) 787

ttaatttatccacacctcaacgaaaatttccggttgggtgcgctaacgaattcaggctgtg
aagttaaaagaaaaataaacaattatagcttcacataagcgatcgatcttcaaactct
acacatgacagaagcaataactaaattaaatagcgtaattttgttaataatactagaa
aacctaaaaaccaaattgtaaaaaaccttatgggaaaaaatgtgataaagcacctaaacc
atagaataacttaaaatttcaatttcccaatcaagggtatgatataaaaaccatggaaaa
caaattctcagccatattttctatctgaccgagtccttttcaaaaataatatatagacggt
agagtcttatatagtaaaaacatttttttaaaactaatttatcttctcatatgaaaatg
aatgcaataaaaaatgaccatatatgctgtaatgatattcaaggaagagatatcacac
aagggtcgaagaaatatacaatatctgaaagtcgactatatgggtccactttccaaattag

FIG. 2H

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agatggaaagaagaaacgattatgcagcaaaccattgatcggacgaagaagaataaa
tatggaggcccatctactatagtagtttggccttgaaatattttgggtccgagaaataataa
ataaacagttatggcttttcggatttggttgctttcaattttctcaaagtgttgacaa
gtgttattacactcacctaaaacaggatcattccaattttcttgggtcagagtcgtac
tttcttcttcttttaaaccaaggtcttataagtattctctaaaccaagtcactaaacaat
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caaaacaaaaattgtcttgcttttatatggaatgaagaaaaatcgaattttgtaacat
ttttgacttttaaagtcacactcgccgtatacggcacaccaaatagacaaaaacatttga
ccaccaactttgctttaatgttaaaactttttttttgcatcccactactctcttcttca
cctcctcaagtcacagtgaccaaatacacacacttcacaagaaacaacctatg

||| Additional genes showing early and transient RPP-triggered
expression

13176 Contains Myb DNA-binding domain
repeat signatures

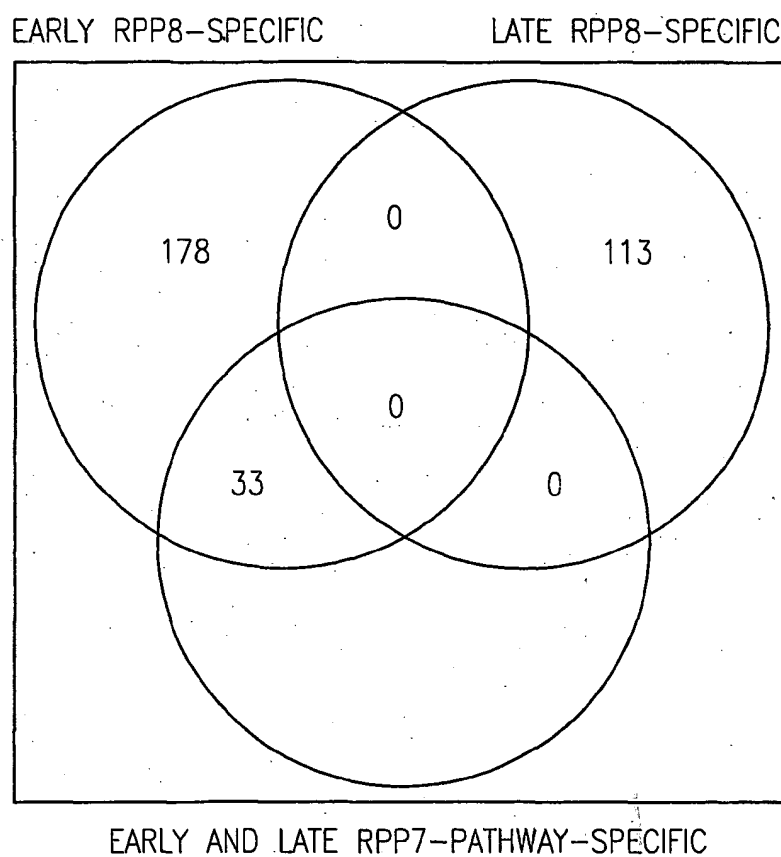
SEQ ID NO:
788

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cgttaattggagatcttctgaacatgacagtggaaggtatacaatgggctagttccaata
tcaccaataacaacccaagtgtctgcaaagcaagtatgagtttctttcctataaccagt
gtcctgaaaaaacacattaccaagttcaacaactcaatcagatcgaaaagtaaacaca
tgaagaagaagaagaacattcacacacaaatgtaacctcgatttcgtttttctgagtt
ccaggaatctcaagagcatctacatcgaaagAGTCAAcggcagggctagtgcaatcaa
acgctgctccacattgtcatcctcctcatcggaatccatttccgggtgattatgctcat
catatccatcatcgtcgtaatcttcattaacctcataatcatctttctcatcgaaacacc
catcgcgacaaTGACGTcggtgaatcgctccgccaactcctcatcaatctcagaccc
atcgctccactgctttcttcttcACGTgaaacatcaatcacggttggaacactga
agatctcgagattgtgattcagattcgtatctctgatccaaggaaacaggattggaatt
gggtgttttgagagattgagagatggaagagagagattgatctacatacactggagagg
acctggcacgaatgagaaagaagcttacACGTgtccaatcatgattggattcgagactc
acggtttaaggaaaaacaaaccagaccaaataggcttaaccgctaaaaaacgggttc
tcgttttgaaagattgagagagacgatctacaaaggaggacaggaccggcacgaatga
gaagaagcttacACGTgtccaatcaggattgaacgatttaatacaagcttaaccgtatgt
aaaccggatttttagctgggtccacaagtAGTCAAatataagattttttaatAGTCAAata
attttcataggggcgaagttcaagatgagttactacactcatcaaagctcacaaaaaga
gaagagaagagacgaggatcaatcaccattctcatg

FIG. 2I

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26 *Peronospora* (Hiks1 and Emco5) induced
RPP7, EDM1,2,3 and RPP8-Dependent genes

**FIG. 3**

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RPP4-pathway, RPP7-pathway and
RPP8-up-regulated transcription factor genes

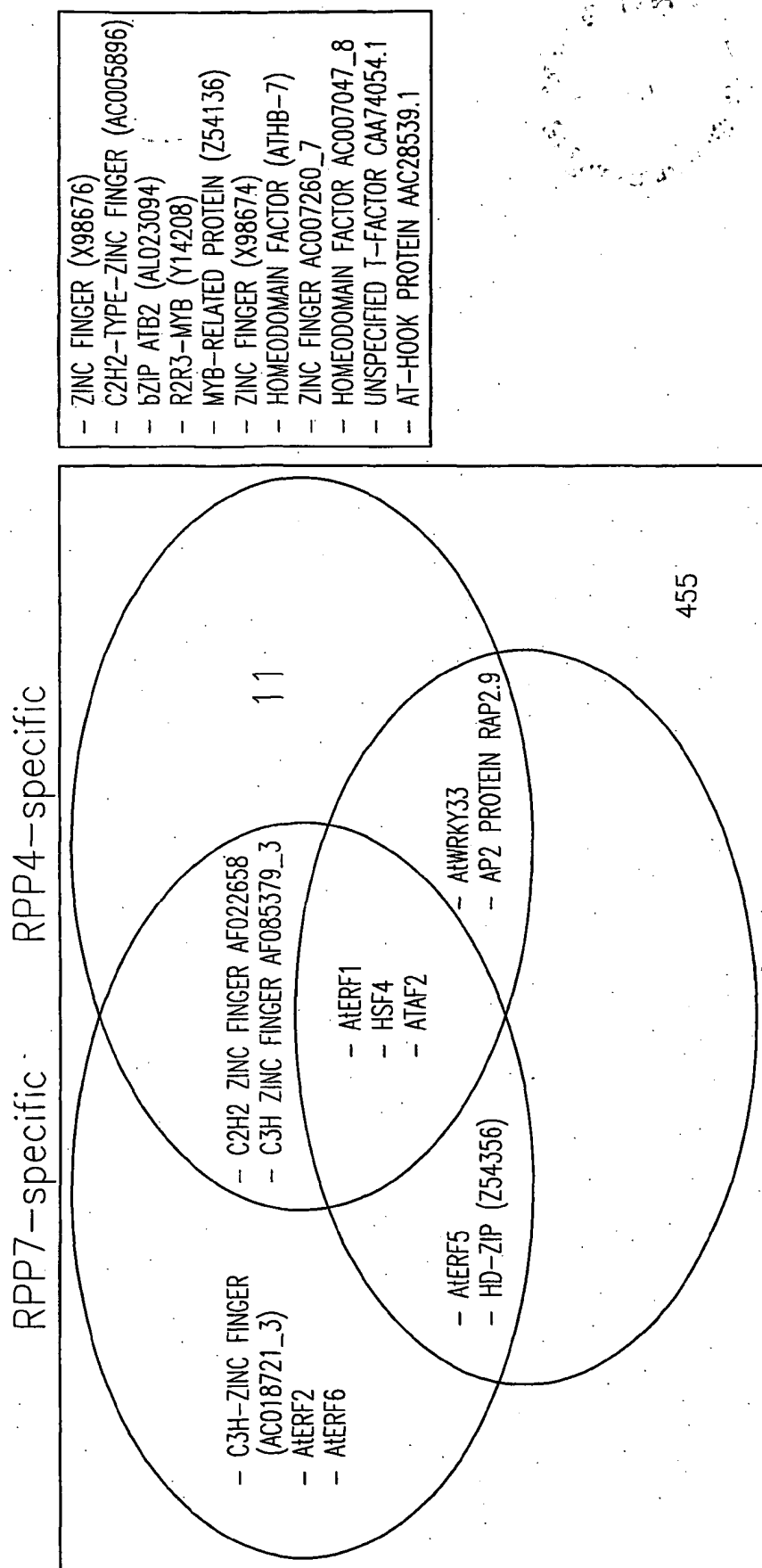


FIG. 4

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